

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 6.17442 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVPLFP 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4	44.4	11	2	I33098	173K exoantigen -
2	3	33.3	8	2	G33098	205K exoantigen -
3	3	33.3	9	2	PT0324	Ig heavy chain CRD
4	3	33.3	11	2	A57458	Gene Gax protein -
5	3	33.3	12	2	S21205	Ig heavy chain V r
6	3	33.3	12	2	S74196	3-hydroxy-3-methyl
7	3	33.3	13	2	S78766	ribosomal protein
8	3	33.3	13	2	PH0756	T-cell receptor be
9	3	33.3	13	2	I77387	AMP deaminase - ra
10	3	33.3	14	2	B36079	hypothetical prote
11	3	33.3	14	2	PL0152	metal-binding prot
12	3	33.3	14	2	A61308	hemocyanin chain 2
13	3	33.3	14	2	D61308	hemocyanin chain 5
14	3	33.3	14	2	PH1566	cerebrin 30 - huma
15	3	33.3	14	2	PH1614	Ig H chain V-D-J r
16	3	33.3	14	2	C59137	protein pf3 - gold
17	3	33.3	15	2	PA0059	protein QF200021 -
18	3	33.3	15	2	PA0080	translation elonga
19	3	33.3	15	2	S77988	cytochrome-c oxida
20	3	33.3	15	2	PH0772	T-cell receptor be
21	3	33.3	15	2	I67525	CD13 antigen homol
22	3	33.3	15	2	B59137	protein pf1 - gold
23	3	33.3	16	1	MTDFPS	melanotropin beta
24	3	33.3	16	2	T09741	photosystem I chai
25	3	33.3	16	2	PH0749	T-cell receptor be
26	3	33.3	16	2	B40291	cytochrome P450mtf
27	3	33.3	17	2	I55226	myosin heavy chain
28	3	33.3	17	2	S29165	quinaldine oxide
29	3	33.3	17	2	A61557	major merozoite su

30	33.3	17	2	S60171	sex-lethal protein
31	33.3	18	2	G02018	proteasome chain L
32	33.3	18	2	S09731	photosystem I prot
33	33.3	18	2	S36121	lectin - spurge (E
34	33.3	18	2	S40502	20-alpha-hydroxyst
35	33.3	18	2	B35910	neurofibromatosis-
36	33.3	18	2	S57518	T cell receptor be
37	33.3	19	2	PN0467	nitrogenase (EC 1.
38	33.3	19	2	B39845	pyrB leader peptid
39	33.3	19	2	S69153	Neb-collostatin -
40	33.3	19	2	A37968	neural surface pro
41	33.3	20	2	A39328	notechis II-5b non
42	33.3	20	2	C20554	hemocyanin subunit
43	33.3	4	2	A32039	tyrosine-melanocyt
44	33.3	4	2	A37832	phenol 2-monooxyge
45	33.3	4	2	S53508	starvation-induced
46	33.3	4	2	I54357	schwannomin - mous
47	33.3	5	2	A60521	glycogen phosphory
48	33.3	5	2	I40469	dnazx-like protein
49	33.3	5	2	B22565	R-phycocerythrin al
50	33.3	5	2	T14908	hypothetical prote
51	33.3	5	2	PT0308	Ig heavy chain CRD
52	33.3	5	2	JT0520	Ig kappa chain V-I
53	33.3	5	2	PT0610	T-cell receptor be
54	33.3	6	2	B34835	dnAA protein - Pse
55	33.3	6	2	A61049	halo-toxin - Pseud
56	33.3	6	2	A31263	dihydrofolate redu
57	33.3	6	2	B31263	dihydrofolate redu
58	33.3	6	2	I37263	Y protein - human
59	33.3	6	2	H48394	glycoprotein compo
60	33.3	6	2	I65546	MHC H2-L antigen -
61	33.3	7	1	XEYDGD	galactose oxidase
62	33.3	7	1	NYPG7	hypothalamic hepta
63	33.3	7	2	A60139	fatty-acid synthas
64	33.3	7	2	PH1408	Ig heavy chain V r
65	33.3	7	2	B34818	vicilin 57K chain
66	33.3	7	2	E61491	seed protein ws-5
67	33.3	7	2	I48105	dihydrofolate redu
68	33.3	7	2	I48086	DNA topoisomerase
69	33.3	7	2	A38081	amine oxidase (cop
70	33.3	7	4	I55382	hypothetical pepti
71	33.3	7	4	I56695	hypothetical L2 pr
72	33.3	8	2	PH1407	Ig heavy chain V r
73	33.3	8	2	B24749	neuropeptide B - b
74	33.3	8	2	PL0184	capsid protein VP-
75	33.3	8	2	PA0032	protein QA300040 -
76	33.3	8	2	S11078	glucose-6-phosphat
77	33.3	8	2	B33099	158K exoantigen -
78	33.3	8	2	A46306	spasmodic toxin
79	33.3	8	2	S66546	cardioacceleratory
80	33.3	8	2	B27867	homeotic protein U
81	33.3	8	2	A61328	trypsin (EC 3.4.21
82	33.3	8	2	S10783	enamelin f - bovin
83	33.3	8	2	A61597	cytochrome P450 AL
84	33.3	8	2	A42689	major postsynaptic
85	33.3	8	2	A35180	neutral proteinase
86	33.3	8	2	PC4373	telomeric and tetr
87	33.3	8	2	I57532	gene Tinslow prote
88	33.3	8	2	A25836	L-serine ammonia-1
89	33.3	8	4	I54017	granulocyte-colony
90	33.3	9	2	A91466	oxytocin - hippopo
91	33.3	9	2	A92774	oxytocin - spotted
92	33.3	9	2	A93147	oxytocin - finback
93	33.3	9	2	A93408	oxytocin - Austral
94	33.3	9	2	B90667	oxytocin - rabbit
95	33.3	9	2	A61230	calsequestrin, car
96	33.3	9	2	D28854	fibrinopeptide B -
97	33.3	9	2	E28854	fibrinopeptide B -
98	33.3	9	2	F28854	fibrinogen beta ch
99	33.3	9	2	C24180	fibrinogen beta ch
100	33.3	9	2	D24180	fibrinogen beta ch

## ALIGNMENTS

## RESULT 1

I33098  
 173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: I33098  
 R:Nichols, J.H.; Hager, L.P.  
 A:Title: Regulation of the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: I33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <NIC>

Query Match 44.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
 ||||  
 Db 7 PLFP 10

## RESULT 2

G33098  
 205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: G33098  
 R:Nichols, J.H.; Hager, L.P.  
 A:Title: Regulation of the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: G33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <NIC>

Query Match 33.3%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
 ||||  
 Db 2 VPL 4

## RESULT 3

PT0324  
 Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0324  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0324  
 A:Molecule type: DNA  
 A:Residues: 1-9 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
 ||||  
 Db 6 ESY 8

## RESULT 4

A57458  
 gene Gax protein - mouse (fragment)  
 C:Species: Mus sp. (mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999  
 C:Accession: A57458  
 R:Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.  
 Mol. Cell. Biol. 15, 4272-4281, 1995  
 A:Title: Regulation of Gax homeobox gene transcription by a combination of positive fact-  
 A:Reference number: A57458; MUID:95349593; PMID:7623821  
 A:Accession: A57458  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-11 <RES>  
 A:Cross-references: GB:S79168; NID:G1050991  
 C:Genetics:  
 A:Gene: Gax  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 33.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
 ||||  
 Db 4 PLF 6

## RESULT 5

S21205  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
 C:Accession: S21205  
 R:Makiya, R.; Stigbrand, T.  
 Eur. J. Biochem. 205, 341-345, 1992  
 A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-  
 A:Reference number: S21205; MUID:92209522; PMID:1555592  
 A:Accession: S21205  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <MAK>  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
 ||||  
 Db 5 VES 7

## RESULT 6

S74196  
 3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 01-May-1998  
 C:Accession: S74196  
 R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ino  
 Eur. J. Biochem. 230, 760-765, 1995  
 A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m  
 A:Reference number: S65629; MUID:95331315; PMID:7607249  
 A:Accession: S74196  
 A:Molecule type: protein  
 A:Residues: 1-12 <TAK>  
 A:Experimental source: liver

Query Match 33.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 5 VPL 7  
Db 6 VPL 8

RESULT 7  
S78766  
ribosomal protein MRP-S28, mitochondrial - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: S78766  
R:Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A:Reference number: S78760  
A:Accession: S78766  
A:Molecule type: protein  
A:Residues: 1-13 <GRA>  
C:Keywords: mitochondrion  
F,1-13/Product: ribosomal protein MRP-S28 (fragment) #status experimental <MAT>

Query Match 33.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
Db 6 VES 8

RESULT 8  
PH0756  
T-cell receptor beta chain (I7) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: PH0756  
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0756  
A:Molecule type: mRNA  
A:Residues: 1-13 <CAS>  
A:Cross-references: EMBL:X60850; NID:951482; PIDN:CAA43241.1; PID:951483  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
Db 10 PLF 12

RESULT 9  
I77387  
AMP deaminase - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I77387  
R:Mineo, I.; Clarke, P.R.H.; Sabina, R.L.; Holmes, E.W.  
Mol. Cell. Biol. 10, 5271-5278, 1990  
A:Title: A novel pathway for alternative splicing: Identification of an RNA intermediate  
A:Reference number: I57509; MUID:90377216; PMID:2398891  
A:Accession: I77387  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-13 <RES>  
A:Cross-references: GB:M58689; NID:9202877; PIDN:AAA40727.1; PID:9554414  
C:Genetics:

---

A:Gene: AMPD1  
A:Introns: 8/1

Query Match 33.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
Db 2 PLF 4

RESULT 10  
B36079  
hypothetical protein insulin-like growth factor I 5'-region - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 30-Nov-1990 #sequence\_revision 13-Sep-1991 #text\_change 18-Aug-2000  
C:Accession: B36079  
R:Kajimoto, Y.; Rotwein, P.  
Mol. Endocrinol. 4, 217-226, 1990  
A:Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of  
A:Reference number: A36079; MUID:90231335; PMID:2330002  
A:Accession: B36079  
A:Molecule type: mRNA  
A:Residues: 1-14 <KAJ>  
A:Cross-references: GB:M29857; NID:9214287; PIDN:AAA70329.1; PID:903887  
A:Note: the authors translated the codon CAG for residue 4 as Gly  
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9  
Db 5 LFP 7

RESULT 11  
PL0152  
metal-binding protein - reticulate nassa (fragment)  
C:Species: Nassarius reticulatus (reticulate nassa)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Jun-2000  
C:Accession: PL0152  
R:Andersen, R.A.; Eriksen, K.D.H.; Bakke, T.  
Comp. Biochem. Physiol. B 94, 285-291, 1989  
A:Title: Evidence of presence of a low molecular weight, non-metallothionein-like metal  
A:Reference number: PL0152  
A:Accession: PL0152  
A:Molecule type: protein  
A:Residues: 1-14 <AND>  
C:Comment: This protein is induced in environments contaminated with heavy metal.

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
Db 11 PLF 13

RESULT 12  
A61308  
hemocyanin chain 2 - Sahara scorpion (fragment)  
C:Species: Androctonus australis (Sahara scorpion)  
C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C:Accession: A61308  
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 289-291, 1979  
A:Title: Structural characterization of seven different subunits in Androctonus australis  
A:Reference number: A61308; MUID:80047238; PMID:499512  
A:Accession: A61308

A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <JOL>

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 11 PLF 13

## RESULT 13

D61308  
hemocyanin chain 5A - Sahara scorpion (fragment)  
C:Species: Androctonus australis (Sahara scorpion)  
C>Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C:Accession: D61308  
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 289-291, 1979  
A>Title: Structural characterization of seven different subunits in Androctonus australis  
A:Reference number: A61308; MUID:80047238; PMID:499512  
A:Accession: D61308  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <JOL>

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 11 PLF 13

## RESULT 14

PH1566  
cerebrin 30 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: PH1566  
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993  
A>Title: Micropurification of two human cerebrospinal fluid proteins by high performance  
A:Reference number: PH1566; MUID:93329419; PMID:8336140  
A:Accession: PH1566  
A:Molecule type: protein  
A:Residues: 1-14 <LEO>

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 10 PLF 12

## RESULT 15

PH1614  
Ig H chain V-D-J region (clone B-less 18) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1614  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1614  
A:Molecule type: DNA  
A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 5 PLF 7

## RESULT 16

C59137  
protein Pf3 - golden needle mushroom (fragment)  
C:Species: Flammulina velutipes (golden needle mushroom)  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: C59137  
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A>Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A:Reference number: A59137  
A:Accession: C59137  
A:Molecule type: protein  
A:Residues: 1-14 <SAK>

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|||  
Db 8 YVP 10

## RESULT 17

PA0059  
protein QF200021 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0059  
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A>Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0059  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>

Query Match 33.3%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
|||  
Db 11 VPL 13

## RESULT 18

PA0080  
translation elongation factor eEF-2 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0080  
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A>Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0080  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
C:Keywords: protein biosynthesis

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
 |||  
 Db 9 VPL 11

RESULT 19  
 S77988  
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIa - bigeye tuna (fragment)  
 C:Species: Thunnus obesus (bigeye tuna)  
 C:Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 04-Sep-1998  
 C:Accession: S77988  
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
 submitted to the Protein Sequence Database, June 1997  
 A:Reference number: S77980  
 A:Accession: S77988  
 A:Molecule type: protein  
 A:Residues: 1-15 <ARN>  
 A:Experimental source: heart; liver  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Pathway: oxidative phosphorylation; respiratory chain  
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6  
 |||  
 Db 3 YVP 5

RESULT 20  
 PH0772  
 T-cell receptor beta chain (J4) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C:Accession: PH0772  
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A:Reference number: PH0746; MUID:92078846; PMID:1836010  
 A:Accession: PH0772  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <CAS>  
 A:Cross-references: EMBL:X60866; NID:g52749; PIDN:CAA43256.1; PID:g52750  
 A:Experimental source: T lymphocyte  
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
 |||  
 Db 12 PLF 14

RESULT 21  
 I67525  
 CD33 antigen homolog - mouse (fragment)  
 C:Species: Mus sp. (mouse)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Jun-1998  
 C:Accession: I67525  
 R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.  
 Eur. J. Immunol. 24, 1657-1664, 1994  
 A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is n

A:Reference number: I53392; MUID:94298870; PMID:8026526  
 A:Accession: I67525  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <RES>  
 A:Cross-references: GB:S71349; NID:g550037  
 C:Genetics:  
 A:Gene: Ig VH7183

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5  
 |||  
 Db 11 SYV 13

RESULT 22  
 B59137  
 protein Pf1 - golden needle mushroom (fragment)  
 C:Species: Flamulina velutipes (golden needle mushroom)  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: B59137  
 R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
 submitted to the Protein Sequence Database, November 1999  
 A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
 A:Reference number: A59137  
 A:Accession: B59137  
 A:Molecule type: protein  
 A:Residues: 1-15 <SAK>  
 A:Experimental source: strain FV-4

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6  
 |||  
 Db 8 YVP 10

RESULT 23  
 MDPFBS  
 melanotropin beta - spiny dogfish  
 C:Species: Squalus acanthias (spiny dogfish)  
 C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 23-Aug-1996  
 C:Accession: A01471  
 R:Bennett, H.P.J.; Lowry, P.J.; McMartin, C.; Scott, A.P.  
 Biochem. J. 141, 439-444, 1974  
 A:Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel  
 A:Reference number: A90277; MUID:75127390; PMID:4375978  
 A:Accession: A01471  
 A:Molecule type: protein  
 A:Residues: 1-16 <BEN>  
 C:Superfamily: corticotropin-lipotropin  
 C:Keywords: hormone

Query Match 33.3%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
 |||  
 Db 14 VPL 16

RESULT 24  
 T09741  
 photosystem I chain psaI - upland cotton chloroplast (fragment)  
 C:Species: chloroplast Gossypium hirsutum (upland cotton)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T09741

R;Small, R.L.; Ryburn, J.A.; Cronn, R.C.; Seelanan, T.; Wendel, J.F.

Am. J. Bot. 85, 1301-1315, 1998

A;Title: The tortoise and the hare: choosing between noncoding plastome and nuclear Adh

A;Reference number: Z16323

A;Accession: T09741

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <SMA>

A;Cross-references: EMBL:AF031581; NID:g2623684; PID:g3723945

C;Genetics:

A;Gene: psal

A;Genome: chloroplast

C;Keywords: chloroplast; photosynthesis; photosystem I

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7

Db 12 VPL 14

#### RESULT 25

PH0749

T-cell receptor beta chain (B83) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0749

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I

allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0749

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60840; NID:g501116; PIDN:CAA43233.1; PID:g50117

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8

Db 13 PLF 15

#### RESULT 26

B40291

cytochrome P450mtf - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 30-Sep-1993

C;Accession: B40291

R;Addya, S.; Zheng, Y.M.; Shaviv, R.M.; Fan, J.; Avadhani, N.G.

Biochemistry 30, 8323-8330, 1991

A;Title: Characterization of a female-specific hepatic mitochondrial cytochrome P-450 wh

A;Reference number: A40291; MUID:91355184; PMID:1883820

A;Accession: B40291

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <ADD>

Query Match 33.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9

Db 14 LFP 16

#### RESULT 27

I55226

myosin heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999

C;Accession: I55226

R;Meydert, A.; Daubas, P.; Catavatti, M.; Minty, A.; Bugalsky, G.; Cohen, A.; Robert, B.

J. Biol. Chem. 258, 13867-13874, 1983

A;Title: Sequential accumulation of mRNAs encoding different myosin heavy chain isoforms

It fast myosin heavy chain from mouse skeletal muscle.

A;Reference number: I55226; MUID:84061805; PMID:6196357

A;Accession: I55226

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-17 <RES>

A;Cross-references: GB:K00986; NID:g199975; PIDN:AAA39792.1; PID:g199979

C;Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 33.3%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3

Db 7 VES 9

#### RESULT 28

S29165

quininaldine oxidoreductase (BC 1.5.99.-) alpha chain - Arthrobacter sp. (isolate Rue 61a)

C;Species: Arthrobacter sp.

A;Variety: isolate Rue 61a

C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

C;Accession: S29165

R;de Beyer, A.; Lingens, F.

Biol. Chem. Hoppe-Seyler 374, 101-110, 1993

A;Title: Microbial metabolism of quinoline and related compounds. XVI. Quinaldine oxidoreductase.

A;Reference number: S29165; MUID:93228843; PMID:8471177

A;Accession: S29165

A;Molecule type: protein

A;Residues: 1-17 <BEV>

A;Experimental source: isolate Rue 61a

C;Complex: heterohexamer; two alpha, two beta and two gamma chains

C;Function:

A;Description: catalyzes the oxidation of quinaldine to 1H-4-oxoquinaldine

A;Pathway: quinaldine degradation

C;Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3

Db 1 VES 3

#### RESULT 29

A61557

major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain FCB-1

C;Species: Plasmodium falciparum

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000

C;Accession: A61557

R;Heidrich, H.G.

Biol. Cell 64, 205-214, 1988

A;Title: Isolation and functional characterization of Plasmodium falciparum merozoite an

A;Reference number: A61557; MUID:89150734; PMID:3067799

A;Accession: A61557

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <HEI>

C;Keywords: surface antigen

Query Match 33.3%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
|||  
Db 4 ESY 6

RESULT 30  
S60171  
sex-lethal protein - fruit fly (Drosophila melanogaster) (fragment)  
C;Species: Drosophila melanogaster  
C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 17-Mar-1999  
C;Accession: S60171  
R;Hoshijima, K.; Kohyama, A.; Watakabe, I.; Inoue, K.; Sakamoto, H.; Shimura, Y.  
Nucleic Acids Res. 23, 3441-3448, 1995  
A;Title: Transcriptional regulation of the Sex-lethal gene by helix-loop-helix proteins.  
A;Reference number: S60171; MUID:96032836; PMID:7567454  
A;Accession: S60171  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-17 <HOS>  
A;Cross-references: EMBL:D50435  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995  
C;Genetics:  
A;Gene: FlyBase:Sxl  
A;Cross-references: FlyBase:FBgn0003659

Query Match 33.3%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
|||  
Db 5 VPL 7

RESULT 31  
G02018  
proteasome chain LMP7 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 22-Jun-1999  
C;Accession: G02018  
R;Kim, T.

submitted to the EMBL Data Library, July 1995  
A;Reference number: G09054  
A;Accession: G02018  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-18 <KIM>  
A;Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469  
C;Genetics:  
A;Gene: LMP7  
C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
|||  
Db 11 VES 13

RESULT 32  
S09731  
photosystem I protein psal - spinach chloroplast (fragment)  
C;Species: chloroplast Spinacia oleracea (spinach)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 19-Jan-1996  
C;Accession: S09731

R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.  
FEBS Lett. 263, 274-278, 1990

A;Title: Polypeptide composition of higher plant photosystem I complex. Identification c  
A;Reference number: S09730; MUID:90242987; PMID:2185953

A;Accession: S09731  
A;Molecule type: protein  
A;Residues: 1-18 <IKE>

C;Genetics:

A;Gene: psal

A;Genome: chloroplast

C;Superfamily: photosystem I protein psal

C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; thy

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
|||  
Db 8 VPL 10

RESULT 33  
S36121  
lectin - spurge (Euphorbia characias)  
C;Species: Euphorbia characias  
C;Date: 09-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
C;Accession: S36121  
R;Stirpe, F.; Licastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Boloc  
Biochim. Biophys. Acta 1158, 33-39, 1993  
A;Title: Purification and partial characterization of a mitogenic lectin from the latex  
A;Reference number: S36120; MUID:93357266; PMID:8353129  
A;Accession: S36121  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <SNI>

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
|||  
Db 2 ESY 4

RESULT 34  
S40502  
20-alpha-hydroxysteroid dehydrogenase - Tetrahymena pyriformis  
C;Species: Tetrahymena pyriformis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-Dec-1999  
C;Accession: S40502  
R;Inazu, A.; Sato, K.; Nakayama, T.; Deyashiki, Y.; Hara, A.; Nozawa, Y.  
Biochem. J. 297, 195-200, 1994  
A;Title: Purification and characterization of a novel dimeric 20-alpha-hydroxysteroid de  
A;Reference number: S40502; MUID:94107273; PMID:8280099  
A;Accession: S40502  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <INA>

C;Genetics:  
A;Genetic code: SGC5

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
|||  
Db 5 VPL 7

RESULT 35

B35910  
neurofibromatosis-related protein NF1, long splice form - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 23-Oct-1990 #sequence\_revision 23-Oct-1990 #text\_change 29-Aug-1997  
C:Accession: B35910  
R:Cawthon, R.M.; Weiss, R.; Xu, G.; Viskochil, D.; Culver, M.; Stevens, J.; Robertson, M.  
Cell 62, 608b, 1990  
A:Reference number: A35910  
A:Accession: B35910  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-18 <CAW>  
C:Genetics:  
A:Gene: GDB:NFI  
A:Cross-references: GDB:120231; OMIM:162200  
A:Map position: 17q11.2-17q11.2  
C:Keywords: alternative splicing; tumor suppressor

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
|||  
Db 14 LFP 16

RESULT 36  
S57518  
T cell receptor beta chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S57518  
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaeat, V.P.  
submitted to the EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b  
A:Reference number: S57494  
A:Accession: S57518  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-18 <BUR>  
A:Cross-references: EMBL:Z49920; NID:g887490; PIDN:CAA90166.1; PID:g887491  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
|||  
Db 5 LFP 7

RESULT 37  
PN0467  
nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Azotobacter chroococcum  
C:Species: Azotobacter chroococcum  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
C:Accession: PN0467  
R:Jones, R.; Woodley, P.; Birkmann-Zinoni, A.; Robson, R.L.  
Gene 123, 145-146, 1993  
A:Title: The nifH gene encoding the Fe protein Component of the molybdenum nitrogenase f  
A:Reference number: JN0516; MUID:93138425; PMID:8423000  
A:Accession: PN0467  
A:Molecule type: DNA  
A:Residues: 1-19 <JON>  
A:Cross-references: GB:M73020; NID:gl42326; PIDN:AAA22141.1; PID:g289238  
C:Genetics:  
A:Gene: nifD  
C:Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain  
C:Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3  
|||  
Db 9 VES 11

RESULT 38  
B39845  
pyrB leader peptide - Bacillus subtilis  
C:Species: Bacillus subtilis  
C>Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 12-Dec-1997  
C:Accession: B39845  
R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.  
J. Biol. Chem. 266, 9113-9127, 1991  
A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrimi  
A:Reference number: A39845; MUID:91225016; PMID:1709162  
A:Accession: B39845  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-19 <QUI>  
A:Cross-references: GB:M59757  
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 10 PLF 12

RESULT 39  
S69153  
Neb-colloostatin - flesh fly (Sarcophaga bullata)  
C:Species: Sarcophaga bullata  
C>Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 19-May-2000  
C:Accession: S69153  
R:Bylemans, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van  
Eur. J. Biochem. 228, 45-49, 1995  
A:Title: Neb-colloostatin, a second folliculastain of the grey fleshfly, Neobellieria bu  
A:Reference number: S69153; MUID:95188911; PMID:7883009  
A:Accession: S69153  
A:Molecule type: protein  
A:Residues: 1-19 <BYL>

Query Match 33.3%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
|||  
Db 3 VPL 5

RESULT 40  
A37968  
neural surface protein Bravo - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 15-Aug-1997  
C:Accession: A37968; A36345  
R:de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 112, 1049, 1991  
A:Reference number: A37968; MUID:91154309; PMID:1999455  
A:Contents: extratum  
A:Accession: A37968  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <DEL>  
R:de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 111, 3087-3096, 1990

A:Title: Topologically restricted appearance in the developing chick retinotectal system  
 A:Reference number: A36345; MUID:91100421; PMID:2269667  
 A:Accession: A36345  
 A:Molecule type: protein  
 A:Residues: 1-7,9-19 <DE2>

Query Match 33.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
 ||  
 Db 3 VPL 5

## RESULT 41

A39328

notechis II-5b nontoxic venom protein - common tiger snake (fragment)  
 C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 30-Sep-1993  
 C:Accession: A39328  
 R:fang, C.C.; Chang, L.S.; Wu, F.S.  
 Toxicon 29, 1337-1344, 1991

A:Title: Venom constituents of Notechis scutatus scutatus (Australian tiger snake) from  
 A:Reference number: A39328; MUID:92263371; PMID:1814009

A:Accession: A39328  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <YAN>  
 C:Superfamily: phospholipase A2

Query Match 33.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
 ||  
 Db 18 PLF 20

## RESULT 42

C20554

hemocyanin subunit IIa - Atlantic horseshoe crab (fragment)  
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-May-1997  
 C:Accession: C20554

R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiald, P.; Jolles, P.; Jolles, J.; Feldmann, R.J.  
 Biochemistry 22, 5573-5583, 1983  
 A:Title: Quaternary structure of Limulus polyphemus hemocyanin.  
 A:Reference number: A90478

A:Accession: C20554  
 A:Molecule type: protein  
 A:Residues: 1-20 <LAM>  
 C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunits  
 C:Superfamily: hemocyanin

Query Match 33.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
 ||  
 Db 11 PLF 13

## RESULT 43

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000

C:Accession: A32039  
 R:Horvath, A.; Kastin, A.J.  
 J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
 A:Reference number: A32039; MUID:89123285; PMID:2563371

A:Accession: A32039  
 A:Molecule type: protein  
 A:Residues: 1-4 <HOR>  
 A:Experimental source: brain  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end  
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 22.2%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7  
 ||  
 Db 2 PL 3

## RESULT 44

A37832

phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)  
 C:Species: Pseudomonas sp.

C:Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 23-Jun-1993  
 C:Accession: A37832

R:Powlowski, J.; Shingler, V.  
 J. Bacteriol. 172, 6834-6840, 1990

A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxyl  
 A:Reference number: A37832; MUID:91072231; PMID:2254259

A:Accession: A37832  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <POW>  
 C:Keywords: oxidoreductase

Query Match 22.2%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4  
 ||  
 Db 1 SY 2

## RESULT 45

S53508

starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)

C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C:Accession: S53508

R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
 Plant Mol. Biol. 27, 477-485, 1995

A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribo  
 A:Reference number: S53508; MUID:95201242; PMID:7894013

A:Accession: S53508  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <ROE>

Query Match 22.2%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FP 9  
 ||  
 Db 1 FP 2

## RESULT 46

I54357

schwannomin - mouse (fragment)  
 C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

```

C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2

Query Match      22.2%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      1 VP 2

RESULT 47
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A;Reference number: A60521; MUID:90227907; PMID:2103669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
A;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      4 VP 5

RESULT 48
I40469
dnaZ-like protein - Bacillus subtilis (fragment)
C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A;Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A;Reference number: I40469; MUID:89218958; PMID:2468993
A;Accession: I40469
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204
C;Genetics:
A;Start codon: GTG

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SY 4
      ||

C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2

Query Match      22.2%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      1 VP 2

RESULT 49
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)
C;Species: Gastrocionium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VP 6
      ||
Db      3 VP 4

RESULT 50
T14908
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weishaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14908
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VE 2
      ||
Db      4 VE 5

RESULT 51
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Sharn, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
A;Keywords: heterotetramer; immunoglobulin

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ES 3
      ||

```



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Db          3 ES 4
||
Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 52
JT0520
Ig kappa chain V-III region (SD1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C:Accession: JT0520
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A>Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157; PMID:2786547
A:Accession: JT0520
A:Molecule type: mRNA
A:Residues: 1-5 <ANK>
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
A:Keywords: heterotetramer; immunoglobulin
F:1-5/Domain: V kappa region <VRE>

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
||
Db          2 ES 3
||

RESULT 53
PT0610
T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0610
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0610
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <VEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      22.2%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
||
Db          4 ES 5
||

RESULT 54
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Fee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A>Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Escherichia coli
A:Reference number: A34835; MUID:90160310; PMID:2106132
A:Accession: B34835
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <VEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AA25916.1; PID:g151421
C:Keywords: DNA binding

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Query Match      22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 VE 2
||
Db          3 VE 4
||

RESULT 55
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A>Note: host mulberry tree
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A>Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A>Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match      22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 FP 9
||
Db          2 FP 3
||

RESULT 56
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A>Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match      22.2%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 ES 3
||
Db          4 ES 5
||

RESULT 57
B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C:Species: Plasmodium falciparum
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A>Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: B31263

```

A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-6 <PET>  
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 22.2%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ES 3  
 ||  
 Db 4 ES 5

## RESULT 58

I37263

Y protein - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
 C;Accession: I37263  
 R;Waerber, G.; Habener, J.F.  
 Endocrinology 131, 2010-2015, 1992  
 A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative exon  
 A;Reference number: I37263; MUID:93010691; PMID:1396344  
 C;Accession: I37263  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-6 <RES>  
 A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
 C;Genetics:  
 A;Gene: CREB

Query Match 22.2%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8  
 ||  
 Db 2 LF 3

## RESULT 59

H48394

glycoprotein component 16/major fat-globule membrane protein/WFG-E8 homolog - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
 C;Accession: H48394  
 R;Mather, I.H.; Banghart, L.R.; Lane, W.S.  
 Biochem. Mol. Biol. Int. 29, 545-554, 1993  
 A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig 11-like sequences.  
 A;Reference number: A48394; MUID:93250576; PMID:8485470  
 C;Accession: H48394  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-6 <MAT>  
 A;Experimental source: milk  
 A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
 C;Keywords: glycoprotein

Query Match 22.2%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VE 2  
 ||  
 Db 1 VE 2

## RESULT 60

I65546

MHC H2-L antigen - mouse (fragment)  
 C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C;Accession: I65546  
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.  
 Cell 44, 261-272, 1986  
 A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their function  
 A;Reference number: I52778; MUID:86106202; PMID:3510743  
 C;Accession: I65546  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-6 <RES>  
 A;Cross-references: GB:M12483; NID:gi199565; PIDN:AAA9663.1; PID:g554234

Query Match 22.2%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VP 6  
 ||  
 Db 2 VP 3

## RESULT 61

XEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)  
 C;Species: Cladobotryum dendroides  
 C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 31-Dec-1993  
 C;Accession: A01341  
 R;Avigad, G.; Markus, Z.  
 Fed. Proc. 31, 447, 1972  
 A;Reference number: A01341  
 C;Accession: A01341  
 A;Molecule type: protein  
 A;Residues: 1-7 <AVI>  
 C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase which, in the presence of copper, may inactivate the enzyme by binding to its prosthetic copper group.  
 C;Superfamily: galactose oxidase inhibitor  
 C;Keywords: copper

Query Match 22.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ES 3  
 ||  
 Db 6 ES 7

## RESULT 62

NYPG7

hypothalamic heptapeptide - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 23-Aug-1996  
 C;Accession: A01417  
 R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, I.  
 Horm. Metab. Res. 13, 228-232, 1981  
 A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity  
 A;Reference number: A01417; MUID:81213980; PMID:6263778  
 C;Accession: A01417  
 A;Molecule type: protein  
 A;Residues: 1-7 <CHA>  
 C;Superfamily: hypothalamic heptapeptide  
 C;Keywords: hypothalamus

Query Match 22.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SY 4  
 ||  
 Db 5 SY 6

## RESULT 63

```

A60139
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
C:Accession: A60139
R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain
A:Reference number: A60139; MUID:85175165; PMID:3921056
A:Accession: A60139
A:Molecule type: protein
A:Residues: 1-7 <HAR>
C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homodimerase
homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] synthetase
homology; acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzyme
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental
Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SY 4
DB 5 SY 6
RESULT 64
PH1408
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1408; PH1405
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Taniguchi, M.
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1408
A:Molecule type: DNA
A:Residues: 1-7 <SHI>
A:Experimental source: clone micro m+ 46-12-2
A:Accession: PH1405
A:Molecule type: DNA
A:Residues: 1-7 <SHI2>
A:Experimental source: clone micro m+ 46-6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 FP 9
DB 6 FP 7
RESULT 65
B34818
vicilin 57K chain - pigeon pea (fragment)
C:Species: Cajanus cajan (pigeon pea)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C:Accession: B34818
R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A:Reference number: A34818; MUID:90165956; PMID:2306256
A:Accession: B34818
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAW>
Query Match 22.2%; Score 2; DB 2; Length 7;
A60139
seed protein ws-5 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: E61491
R:Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional
A:Reference number: A61491; MUID:89351606; PMID:2765119
A:Accession: E61491
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <HIR>
C:Keywords: glycoprotein; seed
Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VP 6
DB 3 VP 4
RESULT 67
I48105
dihydrofolate reductase - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C:Accession: I48105
R:Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
Biochemistry 25, 6228-6236, 1986
A:Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydrofolate
reductase
A:Reference number: I48105; MUID:87076541; PMID:3024702
A:Accession: I48105
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056
Query Match 22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PL 7
DB 4 PL 5
RESULT 68
I48086
DNA topoisomerase II alpha - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48086
R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
J. Biol. Chem. 270, 25850-25858, 1995
A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster
DNA topoisomerase II alpha
A:Reference number: I48086; MUID:96029684; PMID:7592770
A:Accession: I48086
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

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Query Match      22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PL 7
      ||
Db      5 PL 6

RESULT 69
A38081
A:Title: amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)
C:Species: Pichia angusta
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C:Accession: A38081
R;Mu, D.; Jones, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A:Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine o
A:Reference number: A38081; MUID:92235001; PMID:1569055
A:Accession: A38081
A:Molecule type: Protein
A:Residues: 1-7 <DAW>
C:Keywords: copper; oxidoreductase; quinoprotein; topaquinone
F;4/Modified site: topaquinone (Tyr) #status experimental

Query Match      22.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YV 5
      ||
Db      6 YV 7

RESULT 70
I55382
hypothetical peptide PA11 promoter region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C:Accession: I55382
R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
A:Title: The two allele sequences of a common polymorphism in the promoter of the plasmi
A:Reference number: I55382; MUID:93226509; PMID:8398372
A:Accession: I55382
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <DAW>
A:Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
C:Comment: This is the hypothetical translation of a sequence from the PA11 gene promote
C:Genetics:
A:Gene: GDB:PA11
A:Cross-references: GDB:I20297; OMIM:173360
A:Map position: 7q21.3-7q22

Query Match      22.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ES 3
      ||
Db      5 ES 6

RESULT 71
I56695
hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)
C:Species: human papillomavirus type 16
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: I56695
R;Schneider-Maunoury, S.; Croissant, O.; Orth, G.
J. Virol. 61, 3295-3298, 1987

A:Title: Integration of human papillomavirus type 16 DNA sequences: a possible early ever
A:Reference number: I56695; MUID:87311896; PMID:3041049
A:Accession: I56695
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <SCH>
A:Cross-references: GB:M30709; NID:g190253; PIDN:AAA65995.1; PID:g553616
C:Comment: This is the hypothetical translation of a viral sequence integrated into the L
C:Comment: It is translated in an incorrect, -1, reading frame of the L2 protein.

Query Match      22.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SY 4
      ||
Db      2 SY 3

RESULT 72
PH1407
Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1407
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Tan
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in t
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1407
A:Molecule type: DNA
A:Residues: 1-8 <SHI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 FP 9
      ||
Db      7 FP 8

RESULT 73
B24749
neuropeptide B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C:Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b;
A:Reference number: A94074; MUID:86067985; PMID:3865193
A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <IAM>
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match      22.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LF 8
      ||
Db      2 LF 3

RESULT 74
PL0184
capsid protein VP-1 - murine poliovirus (fragment)

```

C;Species: murine poliovirus, Theiler's encephalomyelitis virus  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995  
C;Accession: PL0184  
R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.  
J. Exp. Med. 170, 2037-2049, 1989  
A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicity  
A;Reference number: PL0184; PMID:90063468; PMID:2479706  
A;Accession: PL0184  
A;Molecule type: genomic RNA  
A;Residues: 1-8 <ZUR>  
C;Keywords: capsid protein

Query Match 22.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9  
||  
Db 7 FP 8

RESULT 75  
PA0032  
protein QA300040 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0032  
R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JFID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A;Reference number: PA0001  
A;Accession: PA0032  
A;Molecule type: protein  
A;Residues: 1-8 <KAM>  
A;Experimental source: stem

Query Match 22.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LP 8  
||  
Db 2 LP 3

Search completed: November 25, 2003, 19:36:13  
Job time : 6.1742 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 3.19186 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVPLFP 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	44.4	9	UPA3_HUMAN	P30089 homo sapien
2	3	33.3	15	CHX2_THUOB	P80979 thunnus obe
3	3	33.3	15	PH2_PBRAM	P82695 periplaneta
4	3	33.3	16	MLB_SQUAC	P01207 squalus aca
5	3	33.3	17	PH3_PBRAM	P82896 periplaneta
6	3	33.3	18	AG1_EUPCH	P33888 euphorbia c
7	3	33.3	18	AND2_TETPY	P35430 tetrahymena
8	3	33.3	18	ALL2_CVDPO	P82153 cydia pomon
9	3	33.3	19	COOT_GARBU	Q09148 sarcophaga
10	3	33.3	19	LPGE_ECOLI	P33236 escherichia
11	2	22.2	5	PAR2_PARMA	P81864 pardachirus
12	2	22.2	6	EI01_LITRU	P82096 litoria rub
13	2	22.2	6	VP19_HSVIK	P01153 sus scrofa
14	2	22.2	7	HY7_PIG	P01153 sus scrofa
15	2	22.2	7	IGA0_DACDE	P06294 dactylium d
16	2	22.2	7	MNP1_LEPDE	P42984 leptinotars
17	2	22.2	7	PHR2_LYCES	P83379 lycopersico
18	2	22.2	7	TPFY_PACDA	P83455 pachymedusa
19	2	22.2	8	ALL6_CARMA	P81819 carcinus ma
20	2	22.2	8	ALL6_CVDPO	P82157 cydia pomon
21	2	22.2	8	CAD1_ENTPA	P13268 enterococcu
22	2	22.2	8	FUSS_FUSSO	P81010 fusarium so
23	2	22.2	8	NPB_BOVIN	P15507 bos taurus
24	2	22.2	8	PK3_PBRAM	P82618 periplaneta
25	2	22.2	8	UPA1_HUMAN	P30087 homo sapien
26	2	22.2	8	VGLG_HSV2B	P81780 herpes simp
27	2	22.2	9	COXE_THUOB	P80975 thunnus obe
28	2	22.2	9	FAR9_ASCSU	P43172 ascaris suu
29	2	22.2	9	FIBB_ERYPB	P19346 erythrocebu
30	2	22.2	9	FIBB_MACFU	P19345 macaca fusc
31	2	22.2	9	FIBB_PAPAN	P19344 papio anubi
32	2	22.2	9	FIBB_PAPHA	P19343 papio hamad
33	2	22.2	9	FIBB_THEGE	P19342 theropithec

34	2	22.2	9	1	FLA2_TREHY	P80159 treponema h
35	2	22.2	9	1	LMT3_LOCM1	P41489 locusta mig
36	2	22.2	9	1	NEUU_CAVPO	P34966 cavia porce
37	2	22.2	9	1	OXYA_SQUAC	P42999 squalus aca
38	2	22.2	9	1	OXYT_RABIT	P32878 oryctolagus
39	2	22.2	9	1	PGLR_DIAAB	P81179 diaprepes a
40	2	22.2	9	1	RT33_BOVIN	P82926 bos taurus
41	2	22.2	9	1	SAMP_MUSCA	P19095 mustelus ca
42	2	22.2	9	1	ULAE_HUMAN	P31931 homo sapien
43	2	22.2	9	1	UN19_CLOPA	P81355 clostridium
44	2	22.2	9	1	UPA7_HUMAN	P30093 homo sapien
45	2	22.2	10	1	ANG1_BOTJA	Q10581 bothrops ja
46	2	22.2	10	1	ANGT_BOVIN	P01017 bos taurus
47	2	22.2	10	1	ANGT_CHICK	P01018 gallus gall
48	2	22.2	10	1	APE_CAPGI	P80474 capnocytoph
49	2	22.2	10	1	BPP_VIPAS	P31351 vipera aspi
50	2	22.2	10	1	BRK_ONCMY	Q9P9Z1 oncorhynch
51	2	22.2	10	1	COXA_ONCMY	P80328 oncorhynch
52	2	22.2	10	1	COXH_ONCMY	P80331 oncorhynch
53	2	22.2	10	1	COXK_ONCMY	P80332 oncorhynch
54	2	22.2	10	1	GAJU_HUMAN	P80358 homo sapien
55	2	22.2	10	1	GON1_ALLMI	P37041 alligator m
56	2	22.2	10	1	GON3_ONCKE	P20367 oncorhynch
57	2	22.2	10	1	LPK2_LOCM1	P41488 locusta mig
58	2	22.2	10	1	NS1_MYCTU	P11135 mycobacteri
59	2	22.2	10	1	OPP2_BOVIN	P11180 bos taurus
60	2	22.2	10	1	PVK_LOCM1	P83382 locusta mig
61	2	22.2	10	1	QSOB_COMTE	P80465 comamonas t
62	2	22.2	10	1	SIAP_BACTG	P49325 bacillus th
63	2	22.2	10	1	TKL2_LOCM1	P16224 locusta mig
64	2	22.2	10	1	TRP7_LEUMA	P81739 leucophaea
65	2	22.2	10	1	UHA3_HUMAN	P40930 homo sapien
66	2	22.2	10	1	UPA4_HUMAN	P30090 homo sapien
67	2	22.2	10	1	UPA8_HUMAN	P30094 homo sapien
68	2	22.2	10	1	URE3_MORMO	P17339 morganella
69	2	22.2	11	1	ANGT_CRIGE	P09037 crinia geor
70	2	22.2	11	1	EPG_CLOPA	P81350 clostridium
71	2	22.2	11	1	HS70_PINPS	P81672 pinus pinas
72	2	22.2	11	1	MLG_THETS	P41989 theromyzon
73	2	22.2	11	1	MORN_HUMAN	P01163 homo sapien
74	2	22.2	11	1	NUHM_CANFA	P49820 canis fami
75	2	22.2	11	1	POQC_PSEFL	P55173 pseudomonas
76	2	22.2	11	1	TIN4_HOPTI	P82654 hoplobatr
77	2	22.2	12	1	LMT1_LOCM1	P22395 locusta mig
78	2	22.2	12	1	NUDM_CANFA	P54713 canis fami
79	2	22.2	12	1	PA21_MICFM	P25072 micrurus fu
80	2	22.2	12	1	PSF3_PHYPA	P80662 physcomitre
81	2	22.2	12	1	RF1_CONSP	P58805 conus spuri
82	2	22.2	12	1	TIN2_HOPTI	P82652 hoplobatr
83	2	22.2	12	1	TIN3_HOPTI	P82653 hoplobatr
84	2	22.2	12	1	TKN_KASSE	P08611 kassina sen
85	2	22.2	12	1	TM2A_METWA	P80652 methanosarc
86	2	22.2	12	1	YZPY_ECOLI	P17756 escherichia
87	2	22.2	13	1	ACT7_SOYEN	P15987 glycine max
88	2	22.2	13	1	ADFB_TENMO	P83109 tenebrio mo
89	2	22.2	13	1	AU11_LITRA	P82386 litoria ran
90	2	22.2	13	1	BU12_LITRA	P82387 litoria ran
91	2	22.2	13	1	BP37_LEUMA	P81754 leucophaea
92	2	22.2	13	1	CRBL_ICASP	P17237 icaria sp.
93	2	22.2	13	1	CRBL_VESCR	P01518 vespa crabr
94	2	22.2	13	1	CRTC_RANES	P31832 rana escul
95	2	22.2	13	1	EI21_LITRU	P82097 litoria rub
96	2	22.2	13	1	EI22_LITRU	P82098 litoria rub
97	2	22.2	13	1	FIBB_HYLLA	P14472 hylobates l
98	2	22.2	13	1	GER1_HORVU	P28525 hordium vul
99	2	22.2	13	1	GER2_HORVU	P28526 hordium vul
100	2	22.2	13	1	HPA1_RANES	P32415 rana escul

ALIGNMENTS

```

UPA3_HUMAN
ID   UPA3_HUMAN          STANDARD;          PRT;          9 AA.
AC   P30089;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=93092937; PubMed=1459097;
RA   Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA   Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA   Hochstrasser D.F.;
RT   "Plasma protein map: an update by microsequencing.";
RL   Electrophoresis 13:707-714 (1992).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC   PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR   SWISS-2DPAGE; P30089; HUMAN.
FT   NON TER          1
FT   NON TER          9
SQ   SEQUENCE          9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match          44.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches          4; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Qy          6 PLFP 9
Db          2 PLFP 5

RESULT 2
COXJ_THUOB
ID   COXJ_THUOB          STANDARD;          PRT;          15 AA.
AC   P80979;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIa (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart, and Liver;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103 (1997).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC   CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC   MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC   c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR   PIR; S77988; S77988.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   MOD RES          1
FT   MOD RES          15
FT   NON TER          15
SQ   SEQUENCE          15 AA; 1769 MW; C111B99419E69A1E CRC64;

Query Match          33.3%; Score 3; DB 1; Length 15;

UPA3_HUMAN
ID   UPA3_HUMAN          STANDARD;          PRT;          9 AA.
AC   P30089;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RX   MEDLINE=93092937; PubMed=1459097;
RA   Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA   Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA   Hochstrasser D.F.;
RT   "Plasma protein map: an update by microsequencing.";
RL   Electrophoresis 13:707-714 (1992).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC   PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR   SWISS-2DPAGE; P30089; HUMAN.
FT   NON TER          1
FT   NON TER          9
SQ   SEQUENCE          9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match          44.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches          4; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Qy          6 PLFP 9
Db          2 PLFP 5

RESULT 2
COXJ_THUOB
ID   COXJ_THUOB          STANDARD;          PRT;          15 AA.
AC   P80979;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIa (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart, and Liver;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103 (1997).
CC   -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC   CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC   MITOCHONDRIAL ELECTRON TRANSPORT.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC   c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR   PIR; S77988; S77988.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   MOD RES          1
FT   MOD RES          15
FT   NON TER          15
SQ   SEQUENCE          15 AA; 1769 MW; C111B99419E69A1E CRC64;

Query Match          33.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches          3; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Qy          4 YVP 6
Db          3 YVP 5

RESULT 3
PH2_PERAM
ID   PH2_PERAM          STANDARD;          PRT;          15 AA.
AC   P82695;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Peptide hormone 2 (Pea-VRAAcid 2).
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC   Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Abdominal perisymphathetic organs;
RA   Predel R.;
RL   Submitted (JUL-2000) to the SWISS-PROT data bank.
CC   -!- FUNCTION: UNKNOWN.
KW   Neuropeptide.
SQ   SEQUENCE          15 AA; 1603 MW; F353DC8B1F92B8BD CRC64;

Query Match          33.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches          3; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Qy          3 SYV 5
Db          11 SYV 13

RESULT 4
MLB_SQUAC
ID   MLB_SQUAC          STANDARD;          PRT;          16 AA.
AC   P01207;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Melanotropin beta.
OS   Squalus acanthias (Spiny dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75127390; PubMed=4375978;
RA   Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;
RT   "Structural studies of alpha-melanocyte-stimulating hormone and a
RT   novel beta-melanocyte-stimulating hormone from the neurointermediate
RT   lobe of the pituitary of the dogfish Squalus acanthias.";
RL   Biochem. J. 141:439-444 (1974).
CC   -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR   PIR; A01471; MTDIFS.
KW   Hormone.
SQ   SEQUENCE          16 AA; 1939 MW; 993AF43C8A640A0E CRC64;

Query Match          33.3%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches          3; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Qy          5 VPL 7
Db          14 VPL 16

```

## RESULT 5

PH3 PERAM  
ID PH3 PERAM STANDARD; PRT; 17 AA.  
AC P82696;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Peptide hormone 3 (Pea-VEAacid 1)  
OS Periplaneta americana (American cockroach)  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs;  
RX MEDLINE=20140865; PubMed=10676456;  
RA Predel R., Eckert M., Holman G.M.;  
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs  
of insects.";  
RL Ann. N.Y. Acad. Sci. 897:282-290 (1999).  
CC -!- FUNCTION: UNKNOWN.  
CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.  
KW Neuropeptide.  
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;

Query Match 33.3%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5  
|||  
DB 13 SYV 15

## RESULT 6

AGI EUPCH  
ID AGI EUPCH STANDARD; PRT; 18 AA.  
AC P3388;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Lectin (Fragment).  
OS Euphorbia characias (Spurge).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.  
OX NCBI\_TaxID=3991;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Latex;  
RX MEDLINE=93357266; PubMed=8353129;  
RA Stirpe F., Licastro F., Morini M.C., Parente A., Savino G.,  
RA Abondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;  
RT "Purification and partial characterization of a mitogenic lectin from  
the latex of Euphorbia marginata";  
RL Biochim. Biophys. Acta 1158:33-39 (1993).  
CC -!- FUNCTION: LECTIN THAT BINDS GALACTOSE, GALACTOSE-CONTAINING SUGARS  
AND GENTIOBIOSE. IT IS STRONGLY MITOGENIC FOR HUMAN T LYMPHOCYTES.  
CC -!- SUBUNIT: Homodimer.  
CC -!- PTM: N-GLYCOSYLATED.  
CC -!- SIMILARITY: TO E.MARGINATA LECTIN.  
DR PIR; S36121; S36121.  
KW Lectin.  
FT NON TER 18  
SQ SEQUENCE 18 AA; 1923 MW; C6F6A1A7B2AB124F CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
|||

Db 2 ESY 4

## RESULT 7

AHD2 TETPY  
ID AHD2 TETPY STANDARD; PRT; 18 AA.  
AC P35430;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD)  
(Fragment).  
OS Tetrahymena pyriformis.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
OC Tetrahymenina; Tetrahymena.  
OX NCBI\_TaxID=5908;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=W;  
RX MEDLINE=94107273; PubMed=8280099;  
RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;  
RT "Purification and characterization of a novel dimeric 20 alpha-  
hydroxysteroid dehydrogenase from Tetrahymena pyriformis.";  
RL Biochem. J. 297:195-200 (1994).  
CC -!- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA-HYDROXY  
GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-  
HYDROXYPROGESTENOLONE.  
CC -!- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxypregn-4-en-3-one +  
NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.  
CC -!- SUBUNIT: Homodimer.  
DR PIR; S40502; S40502.  
KW Oxidoreductase; NADP.  
FT NON TER 18  
SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
|||  
DB 5 VPL 7

## RESULT 8

ALL2 CYDPO  
ID ALL2 CYDPO STANDARD; PRT; 18 AA.  
AC P82153;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 2.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309 (1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 18  
SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 33.3%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY      3 SYV 5
Db      3 SYV 5

RESULT 9
COOT_SARBU STANDARD; PRT; 19 AA.
ID_COOT_SARBU
AC Q09148; 1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEB-colloostatin (Folliculostatin).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota, Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
NCBI_TaxID=7385;
[1]
SEQUENCE
RP MEDLINE=95188911; PubMed=7883009;
RX Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
RT "Neb-colloostatin, a second folliculostatin of the grey fleshfly,
RT Neobellieria bullata."
RL Eur. J. Biochem. 228:45-49 (1995).
CC -!- FUNCTION: HAS AN OSTIATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC -!- INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR: S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7
Db      7 VPL 9

RESULT 11
PAP2_PARMA STANDARD; PRT; 5 AA.
ID_PAP2_PARMA
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
NCBI_TaxID=31087;
[1]
SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarevici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER 5 AA; 614 MW; 7769C9C8100000 CRC64;
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FP 9
Db      4 FP 5

RESULT 12
E101_LITRU STANDARD; PRT; 6 AA.
ID_E101_LITRU
AC P82036;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 VP 6  
DB 2 VP 3  
  
RESULT 13  
VP19 HSV1K  
ID VP19 HSV1K STANDARD; PRT; 6 AA.  
AC P23210;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Capsid assembly and DNA maturation protein (Varion protein UL38)  
DE (Capsid protein VP19C) (Fragment).  
GN UL38.  
OS Herpes simplex virus (type 1 / strain KOS).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91101287; PubMed=1846198;  
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,  
RA Silverstein S., Wagner E.K.;  
RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
RT expression of UL38, a true late gene involved in capsid assembly.";  
RL J. Virol. 65:769-786(1991).  
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE  
CC EMBEDDED. BINDS DNA.  
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
CC  
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CC  
CC EMBL; M57646; AAA45830.1; .  
DR Capsid assembly; Coat protein; DNA-binding.  
KW NON TER 6  
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 VP 6  
DB 2 VP 3  
  
RESULT 13  
VP19 HSV1K  
ID VP19 HSV1K STANDARD; PRT; 6 AA.  
AC P23210;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Capsid assembly and DNA maturation protein (Varion protein UL38)  
DE (Capsid protein VP19C) (Fragment).  
GN UL38.  
OS Herpes simplex virus (type 1 / strain KOS).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91101287; PubMed=1846198;  
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,  
RA Silverstein S., Wagner E.K.;  
RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
RT expression of UL38, a true late gene involved in capsid assembly.";  
RL J. Virol. 65:769-786(1991).  
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE  
CC EMBEDDED. BINDS DNA.  
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
CC  
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CC  
CC EMBL; M57646; AAA45830.1; .  
DR Capsid assembly; Coat protein; DNA-binding.  
KW NON TER 6  
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PL 7  
DB 5 PL 6  
  
RESULT 14  
HY7\_PIG  
ID HY7\_PIG STANDARD; PRT; 7 AA.  
AC P01153;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE Hypothalamic heptapeptide.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS  
RX MEDLINE=81213980; PubMed=6263778;  
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,  
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;  
RT "Isolation, structure and synthesis of a heptapeptide with in vitro  
RT ACTH-releasing activity from porcine hypothalamus.";  
RL Horm. Metab. Res. 13:228-232(1981).  
DR PIR; A01417; NYPG7.  
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SY 4  
DB 5 SY 6  
  
RESULT 15  
IGAO\_DACDE  
ID IGAO\_DACDE STANDARD; PRT; 7 AA.  
AC P06294;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Galactose oxidase inhibitor.  
OS Dactylium dendroides (Cladobotryum dendroides).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
OX NCBI\_TaxID=5132;  
RN [1]  
RP SEQUENCE.  
RA Avigad G., Markus Z.;  
RT "Identification of a peptide inhibitor of galactose oxidase from  
RT Dactylium dendroides.";  
RL Fed. Proc. 31:447-447(1972).  
CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE  
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY  
CC BINDING TO ITS PROSTHETIC COPPER GROUP.  
DR PIR; A01341; KEYDGD.  
KW Copper; Metalloenzyme inhibitor.  
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 ES 3  
DB 6 ES 7  
  
RESULT 16  
MNP1\_LEPDE

ID MNFL\_LEPDE STANDARD; PRT; 7 AA.  
 AC P42984;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Myotropic neurotropic peptide 1 (Iued-MNP-I).  
 OS Leptinotarsa decemlineata (Colorado potato beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
 OC Chrysomelini; Leptinotarsa.  
 OK NCBI\_TaxID=7539;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=95380343; PubMed=7651886;  
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,  
 RA Grauwels L., van Leuven F., de Loof A.;  
 RT "Identification, characterization, and immunological localization of  
 RT a novel myotropic neurotropic peptide in the Colorado potato beetle,  
 RT Leptinotarsa decemlineata.";  
 RL Peptides 16:365-374 (1995).  
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
 CC OVIDUCT.  
 KW Neurotropic peptide; Amidation.  
 FT MOD RES 7 7  
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 PL 7  
 Db 5 PL 6  
 RESULT 17  
 ID \_LPCES STANDARD; PRT; 7 AA.  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OK NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures.";  
 RL Eur. J. Biochem. 269:6278-6286 (2002).  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Glycosylated.  
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of  
 CC purple acid phosphatase.  
 KW Hydrolase; Glycoprotein.  
 FT NON TER 1 1  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C79A0 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 LF 8  
 Db 2 LF 3  
 RESULT 18  
 ID TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-1 (PdT-1).  
 OS Pachymedusa dactylophora (Giant mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OK NCBI\_TaxID=75988;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactylophora tryptophyllin-1 (PdT-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD RES 3 3  
 FT MOD RES 7 7  
 SQ SEQUENCE 7 AA; 794 MW; 777D37DC7776350 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VP 6  
 Db 6 VP 7  
 RESULT 19  
 ID AL16\_CARMA STANDARD; PRT; 8 AA.  
 AC P81819;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 16.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OK NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Jommsen A.H., Maestri J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734 (1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4  
 DB 5 SY 6

RESULT 20  
 ALL6\_CVDPO STANDARD; PRT; 8 AA.

ID AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 6;  
 OS Cydia pomonella (Codling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7  
 DB 2 PL 3

RESULT 21  
 CAD1\_ENTFA STANDARD; PRT; 8 AA.

ID AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=13351;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 RT induces plasmid transfer in Streptococcus faecalis."  
 RL FEBS Lett. 178:97-100(1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC Pheromone.  
 KW HEMOLYSIN PLASMID PAD1.

SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8  
 DB 1 LF 2

RESULT 22  
 FUSF\_FUSSO STANDARD; PRT; 8 AA.

ID AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Allergen Fus s I3596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=IARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gangal S.V.;  
 RL Submitted (JUL-1997) to the SWISS-PROT data bank.  
 KW Allergen.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
 DB 7 VP 8

RESULT 23  
 NPB\_BOVIN STANDARD; PRT; 8 AA.

ID AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuroptide B.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;  
 RT "Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuroptides that modulate the action  
 RT of morphine."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
 DR PIR; B24749; B24749.  
 KW Neuroptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8

||  
2 LF 3

Db

## RESULT 24

ID PP3 PERAM STANDARD; PRT; 8 AA.  
AC P82618;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-3 (Pea-PR-3) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;  
OC Blattidae; Periplaneta.  
OC NCBI\_TaxID=6978;  
RN [1]  
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RP TISSUE=Retrocerebral complex;  
RC MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and  
RT abdominal neurohemal organs of the American cockroach.";  
RN Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
RN TISSUE SPECIFICITY.  
RP MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RN J. Comp. Neurol. 419:352-363(2000).  
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -I- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -I- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
CC -I- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 2 VP 3

## RESULT 25

ID UPAL HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Plasma;  
RC MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tisot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RN Electrophoresis 13:707-714(1992).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.

DR SWISS-2DPAGE; P30087; HUMAN.  
FT NON TER 1  
FT UNSURE 8  
FT NON TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3  
DB 3 ES 4

## RESULT 26

VGLG\_HSV2B  
ID VGLG\_HSV2B STANDARD; PRT; 8 AA.  
AC P81780;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Glycoprotein G (Fragment).  
OS Herpes simplex virus (type 2 / strain B4327UR).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OC NCBI\_TaxID=103921;  
RN [1]  
RN SEQUENCE.  
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;  
RL Submitted (APR-1999) to the SWISS-PROT data bank.  
CC -I- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND  
CC 2: GH, GB, GC, GG, GI, AND GE.  
CC -I- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN  
CC HSV-1.  
KW Glycoprotein.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 4 VP 5

## RESULT 27

ID COXE\_THUOB STANDARD; PRT; 9 AA.  
AC P80975;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).  
OS Thunus obesus (Bigeye tuna).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphia; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OC NCBI\_TaxID=8241;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Heart;  
RC MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottespeich F.,  
RA Kadenbach B.;  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
RT liver.";  
RN Eur. J. Biochem. 248:99-103(1997).  
CC -I- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN

```

CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1136 MW; 628072C9CB0776DB CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 7 VP 8

RESULT 28
FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AFG.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 6 PL 7

RESULT 29
FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 6 PL 7

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RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7979C732CB1B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
DB 5 LP 6

RESULT 30
FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 3 ES 4

RESULT 31
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RL evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE409C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
   ||
Db 5 LF 6

RESULT 32
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RL evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE409C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
   ||
Db 5 LF 6

RESULT 33
FIBB_THEGE
ID FIBB_THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RL evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; F28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 LF 8  
DB 5 LF 6

RESULT 34  
FLA2 TREHY STANDARD; PRT; 9 AA.  
AC P80159;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)  
DE (Fragment).  
GN FLA2.  
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).  
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.  
OX NCBI\_TaxID=159;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=C5;  
RX MEDLINE=93139764; PubMed=1487733;  
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,  
RA van der Zeijst B.A.M., Kusters J.G.;  
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are  
RT composed of two sheath proteins and three core proteins.";  
RL J. Gen. Microbiol. 138:2697-2706(1992).  
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.  
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO  
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE  
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND  
CC FLAB3 (32 kDa)  
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.  
KW Flagella; Periplasmic.  
FT UNSURE 2  
FT UNSURE 2  
FT NON TER 8 9  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 3 VP 4

RESULT 35  
LMT3 LOCM1 STANDARD; PRT; 9 AA.  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamyotropin 3 (LOM-MT-3).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
RA de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin III and  
RT IV, two additional neuropeptides of Locusta migratoria: members of the  
RT locustamyotropin peptide family.";  
RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A61620; A61620.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6  
DB 6 VP 7

RESULT 36  
NEUU CAVPO STANDARD; PRT; 9 AA.  
AC P34966;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuromedin U-9 (Nmu-9).  
GN NMU.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Small intestine;  
RX MEDLINE=90341105; PubMed=2381877;  
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;  
RT "Isolation and microsequence analysis of a novel form of neuromedin U  
RT from guinea pig small intestine.";  
RL Peptides 11:613-617(1990).  
CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.  
DR InterPro; IPR001942; NMU.  
DR Pfam; PF02070; NMU; 1.  
DR PROSITE; PS00967; NMU; 1.  
KW Amidation; Hormone.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8  
DB 4 LF 5

RESULT 37  
OXYA SQUAC STANDARD; PRT; 9 AA.  
AC P42999;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Aspartocin (Aspargtocin).  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squala; Squaloidei; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=73031727; PubMed=5083097;



RA Acher R., Chauvet J., Chauvet M.-T.;  
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides  
 RT isolated from a cartilaginous fish, *Squalus acanthias*.";  
 RN Eur. J. Biochem. 29:12-19(1972).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=72128038; PubMed=4622083;  
 RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;  
 RA "Identification of 2 new neurohypophysial hormones, valitocin (Val8-  
 RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the  
 RT spiny dog-fish (*Squalus acanthias*).";  
 RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).  
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro: IPR000981; Neurohyp\_horm.  
 DR PFam: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7  
 DB 7 PL 8

RESULT 38  
 ID OXYT\_RABIT STANDARD; PRT; 9 AA.  
 AC P32878; F01188;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Oxytocin (Oxytocin).  
 OS Oxyctolagus cuniculus (Rabbit).  
 OS Hippopotamus amphibius (Hippopotamus),  
 OS Balaenoptera physalus (Finback whale), (Common rorqual),  
 OS Tachyglousus aculeatus aculeatus (Australian echidna), and  
 OS Hydroglous colliiei (Spotted ratfish) (Pacific ratfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986, 9833, 9770, 49271, 7873;  
 [1]  
 RN SEQUENCE.  
 RC SPECIES=Rabbit;  
 RC MEDLINE=72215060; PubMed=5150741;  
 RA Chauvet J., Chauvet M.-T., Acher R.;  
 RA "Evolution of neurohypophysial hormones: isolation of active  
 RT principles from rabbits and rats.";  
 RL Biochimie 53:1099-1104(1971).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=H.amphibius;  
 RC MEDLINE=71232719; PubMed=5406007;  
 RX Ferguson D.R., Pickering B.T.;  
 RA Arginine and lysine vasopressins in the hippopotamus  
 RT neurohypophys. ";  
 RL Gen. Comp. Endocrinol. 13:425-429(1969).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=B.physalus;  
 RA Acher R., Chauvet J., Chauvet M.-T.;  
 RA "Isolation of finback whale oxytocin and vasopressin.";  
 RL Nature 201:191-192(1964).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=A.aculeatus;  
 RC MEDLINE=73223515; PubMed=4515919;  
 RX Acher R., Chauvet J., Chauvet M.-T.;

RT "Neurohypophysial hormones and evolution of tetrapods.";  
 RL Nature New Biol. 244:124-126(1973).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.colliiei;  
 RX MEDLINE=70088110; PubMed=5366118;  
 RA Pickering B.T., Heller H.;  
 RA "Oxytocin as a neurohypophysial hormone in the holocephalian  
 RT elasmobranch fish, *Hydrolagus colliiei*.";  
 RL J. Endocrinol. 45:597-606(1969).  
 CC -|- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE  
 CC UTERUS AND OF THE MAMMARY GLAND.  
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; A91466; A91466.  
 DR PIR; A92774; A92774.  
 DR PIR; A93147; A93147.  
 DR PIR; A93408; A93408.  
 DR PIR; B90667; B90667.  
 DR PDB; 1XV1; 15-OCT-90.  
 DR PDB; 1XV2; 15-OCT-90.  
 DR InterPro: IPR000981; Neurohyp\_horm.  
 DR PFam: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Hypothalamus; Amidation; 3D-structure.  
 FT DISULFID 1 6  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7  
 DB 7 PL 8

RESULT 39  
 ID PGLR\_DIAAB STANDARD; PRT; 9 AA.  
 AC P81179;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).  
 OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Phytophaga; Curculionidae; Entiminae; Entimini; Diaprepes.  
 OX NCBI\_TaxID=13040;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larval gut;  
 RA Doostdar H., McCollum T.G., Mayer R.T.;  
 RA "Purification and characterization of an endo-polygalacturonase from  
 RT the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes  
 RT abbreviatus L.) larvae.";  
 RL Comp. Biochem. Physiol. 118B:861-867(1997).  
 CC -|- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  
 CC galactosiduronic linkages in pectate and other galacturonans.  
 CC -|- INDUCTION: INHIBITED BY CITRUS PGIP.  
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 9.4, ITS MW IS: 44.5 kDa.  
 CC -|- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.  
 KW Hydrolase; Glycosidase; Cell wall.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5

KW	Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT	DOMAIN 1 >9 PENTAXIN.
FT	NON TER 9
SQ	SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;
Query Match 22.2%; Score 2; DB 1; Length 9;	
Best Local Similarity 100.0%; Pred. No. 1.3e+05;	
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	8 FP 9
Db	2 FP 3
RESULT 42	
ULAE_HUMAN	STANDARD; PRT; 9 AA.
ID	ULAE_HUMAN
AC	P31931;
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Liver;
RX	MEDLINE=94147969; PubMed=8313870;
RA	Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA	Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT	"Human liver protein map: update 1993.";
RL	Electrophoresis 14:1216-1222(1993).
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC	PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
DR	SWISS-2DPAGE; P31931; HUMAN.
FT	NON TER 9
SQ	SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;
Query Match 22.2%; Score 2; DB 1; Length 9;	
Best Local Similarity 100.0%; Pred. No. 1.3e+05;	
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	7 LF 8
Db	2 LF 3
RESULT 43	
UN19_CLOPA	STANDARD; PRT; 9 AA.
ID	UN19_CLOPA
AC	P81355;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DE	Unknown protein CP 19 from 2D-page (Fragment).
OS	Clostridium pasteurianum.
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC	Clostridium.
OX	NCBI_TaxID=1501;
RN	[1]
RP	SEQUENCE.
RC	STRAIN=W5;
RX	MEDLINE=98291870; PubMed=9629918;
RA	Flengsrud R., Skjeldal L.;
RT	"Two-dimensional gel electrophoresis separation and N-terminal
RT	sequence analysis of proteins from Clostridium pasteurianum W5.";
RL	Electrophoresis 19:802-806(1998).
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC	PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
FT	VARIANT 8 8 M -> D.
FT	NON TER 9

SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ES 3  
 ||  
 Db 4 ES 5

RESULT 44  
 UPA7 HUMAN  
 ID UPA7 HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Plasma;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RT Electrophoresis 13:707-714(1992).  
 RL -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 CC SWISS-2DPAGE; P30093; HUMAN.  
 DR NON\_TER 1 1  
 FT UNSURE 5 5  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VP 6  
 ||  
 Db 3 VP 4

RESULT 45  
 ANGI BOTJA  
 ID ANGI BOTJA STANDARD; PRT; 10 AA.  
 AC Q10581;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8724;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Plasma;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RA "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca".  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.

KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YV 5  
 ||  
 Db 4 YV 5

RESULT 46  
 ANGT BOVIN  
 ID ANGT BOVIN STANDARD; PRT; 10 AA.  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 DE (Fragment).  
 DE NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE.  
 RA Elliott D.F., Peart W.S.;  
 RA "The amino acid sequence in a hypertensin."  
 RL Biochem. J. 65:246-254(1957).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the  
 CC plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A90345; A90345.  
 DR PDB; 3ER5; 15-JUL-92.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEF5BDD761F2DB42 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YV 5  
 ||  
 Db 4 YV 5

RESULT 47  
 ANGT CHICK  
 ID ANGT CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]

(Fragment).  
 GN AGT OR SERPINA8.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OK NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RN SEQUENCE  
 RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RN SEQUENCE  
 RP SPECIES=C.C.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOGENIN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A60624; A60624.  
 DR PIR; A90917; A90917.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN, PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 2 8 ANGIOTENSIN II.  
 FT NON\_TER 10 10 ANGIOTENSIN III.  
 SQ SEQUENCE 10 AA; 1232 MW; CBFBD761F2DB42 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No.1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YV 5  
 DB ||  
 4 YV 5

RESULT 48  
 APE CAPGI  
 ID APE CAPGI STANDARD; PRT; 10 AA.  
 AC P80474;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Aminopeptidase (EC 3.4.11.-) (Fragment).  
 OS Capnocytophaga gingivalis.  
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
 OC Flavobacteriaceae; Capnocytophaga.  
 OK NCBI\_TaxID=1017;  
 RN [1]  
 RN SEQUENCE  
 RC STRAIN=ATCC 33624;  
 RX MEDLINE=96118234; PubMed=8574402;  
 RA Spratt D.A., Greenman J., Schaffer A.G.;  
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence  
 RT factor.";  
 RL Microbiology 141:3087-3093 (1995).

-!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-  
 CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.  
 CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5.. MAY BE IMPORTANT IN THE  
 CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL  
 CC CAVITY.  
 CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.  
 KW Hydrolase; Aminopeptidase; Magnesium; Calcium.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No.1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YV 5  
 DB ||  
 7 YV 8

RESULT 49  
 BPP VIPAS  
 ID BPP VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OK NCBI\_TaxID=8706;  
 RN [1]  
 RN SEQUENCE  
 RC TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RT enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No.1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 YP 6  
 DB ||  
 8 YP 9

RESULT 50  
 BRK ONCMY  
 ID BRK ONCMY STANDARD; PRT; 10 AA.  
 AC Q9PRZ1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OK NCBI\_TaxID=8022;

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RN [1]
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RL trout plasma.";
FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 8 PL 9

RESULT 51
COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C3D CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
DB 5 VE 6

RESULT 52
COXH_ONCMY
ID COXH_ONCMY STANDARD; PRT; 10 AA.
AC P80331;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

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DE Cytochrome c oxidase polypeptide VIc (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S43630; S43630.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 4 VP 5

RESULT 53
COXK_ONCMY
ID COXK_ONCMY STANDARD; PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIa-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
DB 4 VP 5

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Db          4 VP 5
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 54
GAJU HUMAN
ID_GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01356;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75150968; PubMed=5538385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXH1.
DR MTM; 137220;
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.
SQ SEQUENCE 10 AA; 1004 MW; CFEEC6AB02C3387D CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
DB 6 VE 7

RESULT 55
GONI ALLMI
ID_GONI_ALLMI STANDARD; PRT; 10 AA.
AC P370A1; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE
RX TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A60066; RHA01.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B3D7286B45A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 4 SY 5

RESULT 56
GON3 ONCKE
ID_GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-
DE RH III) (Luliberin III).
GN GNRH3.
OS Oncorhynchus keta (Chum salmon), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018; 30724;
RN [1]
RP SEQUENCE
RX MEDLINE=83195140; PubMed=6341999;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SEQUENCE AND FUNCTION
RX SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10850929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A21114; A21114.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 4 SY 5

RESULT 57
LPK2 LOCM1
ID_LPK2_LOCM1 STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

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OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
de Loof A.; identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPR-amide peptide
RT family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
CC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
KW Neuropeptide; Amidation; Pyrokinin; 1.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 3 VP 4

RESULT 58
NS1_MYCTU
ID NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
Db 4 PL 5

RESULT 59
ODP2_BOVIN
ID ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.

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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipote-attachment site on the E2
RT component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro; IPR003016; Lipoyl.
DR PROSITE; PS00189; LIPOYL; PARTIAL.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT NON_TER 1 1
FT BINDING 5 5 LIPOYL.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECDIADD33AB1 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
Db 1 VE 2

RESULT 60
PVK_LOCFI
ID PVK_LOCFI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; F:neuropeptide signaling pathway; IDA.

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KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LF 8
Db 4 LF 5

RESULT 61
Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni)
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995);
CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OKO-
CC 1,2-DIHYDROQUINOLINE.
CC -1- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -1- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
CC step.
CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
CC Oxidoreductase; Flavoprotein; FAD; Molybdenum.
KW NON TER 10
FT SEQUENCE 10 AA; 1241 MW; C2E2C25DD9DCD769 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9
Db 3 FP 4

RESULT 62
SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeivich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";

J. Bacteriol. 171:6656-6667(1989).
-1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH OBLIQUE (P2) SYMMETRY.
PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FP 9
Db 5 FP 6

RESULT 63
TKL2 LOCM STANDARD; PRT; 10 AA.
ID -TKL2 LOCM
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 2 PL 3

RESULT 64
TRP7 LEUMA STANDARD; PRT; 10 AA.
ID -TRP7 LEUMA
AC P81739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 7 (LemTRP 7).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE. AND MASS SPECTROMETRY.
RC TISSUE=Brain;

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RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1069.7; METHOD=MALDI.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 1 VP 2

RESULT 65
UPA3_HUMAN
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCD841A041B76B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2
Db 2 VE 3

RESULT 66
UPA4_HUMAN
ID UPA4_HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Fruiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 2 VP 3

RESULT 67
UPA8_HUMAN
ID UPA8_HUMAN STANDARD; PRT; 10 AA.
AC P30094;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Fruiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.2, ITS MW IS: 16 kDa.
DR SWISS-2DPAGE; P30094; HUMAN.
FT NON_TER 1 1
FT VARIANT 4 4
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VP 6
Db 9 VP 10

RESULT 68
URE3_MORMO
ID URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Urease gamma subunit (BC 3.5.1.5) (6 kDa subunit) (Urea  
DB amidohydrolase) (Fragment).  
GN UREA.  
OS Morganella morganii (Proteus morganii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OX Enterobacteriaceae; Morganella.  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=90264298; PubMed=2345135;  
RX Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
RT "Morganella morganii urease: purification, characterization, and  
RT isolation of gene sequences."  
RL J. Bacteriol. 172:3073-3080(1990).  
CC -|- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
CC -|- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.  
DR PIR; C35389; C35389.  
KW Hydrolase.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2  
DB 8 VE 9

RESULT 69  
ANGT CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Crinia.  
OX NCBI\_TaxID=8374;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=80024575; PubMed=488254;  
RA Espamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endecapeptide from the skin of the Australian  
RT frog Crinia georgiana." (1979).  
RL Experientia 35:1132-1133(1979).  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Skin.  
DR PIR; S07207; S07207.  
KW Vasoconstrictor.  
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5  
DB 7 YV 8

RESULT 70  
EFG\_CLOPA STANDARD; PRT; 11 AA.  
ID -EFG\_CLOPA  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
GN FUSA.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9623918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -|- FUNCTION: This protein promotes the GTP-dependent translocation of  
CC the nascent protein chain from the A-site to the P-site of the  
CC ribosome.  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -|- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-G/EF-2 SUBFAMILY.  
DR InterPro; IPR000795; EF\_GTPbind.  
DR PROSITE; PS00301; EFACTOR GTP; PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7  
DB 3 PL 4

RESULT 71  
HS70\_PINPS STANDARD; PRT; 11 AA.  
ID HS70\_PINPS  
AC P81672;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Heat shock 70 kDa protein (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN  
CC (SPOT N164) IS: 5.4, ITS MW IS: 73 kDa.  
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
KW ATP-binding; Heat shock; Multigene family.  
FT NON TER 1 1  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VE 2  
DB 1 VE 2

```

RESULT 72
MLG_THETS
ID_MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1] SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Watez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum."
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
KW Hormone; Amidation.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E9 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YV 5
DB 1 YV 2

RESULT 73
MORN_HUMAN
ID_MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1] SEQUENCE.
RP SPECIES=Human, Rat, and Bovine;
RC MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans."
RL Nature 293:579-580(1981).
RN [2] SEQUENCE.
RP SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3] SYNTHESIS.
RP MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;

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RT "Synthesis of a new neuropeptide, the head activator from hydra."
RL FEBS Lett. 131:317-321(1981).
RN [4] FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition."
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LF 8
DB 10 LF 11

RESULT 74
NUHM_CANEA
ID_NUHM_CANEA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1] SEQUENCE.
RP TISSUE=Heart;
RC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 24 kDa SUBUNIT FAMILY.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.

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FT NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LF 8
      ||
Db      6 LF 7

RESULT 75
PQQC_PSEFL
ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHAO;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "Tns-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)
CC -!- BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER BACTERIAL PQQC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
KW PQQ.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PL 7
      ||
Db      5 PL 6

Search completed: November 25, 2003, 19:28:26
Job time : 3.26329 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 16.9012 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVPLFP 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	44.4	16	10	O82407 fragaria vi
2	4	44.4	16	10	O82404 fragaria ni
3	4	44.4	16	10	O82406 fragaria mo
4	4	44.4	16	10	O82402 fragaria nu
5	4	44.4	16	10	O82403 fragaria ve
6	4	44.4	16	10	O82781 fragaria ve
7	4	44.4	16	10	O82405 fragaria il
8	3	33.3	7	13	O42564 fugu rubrip
9	3	33.3	8	4	Q15898 homo sapien
10	3	33.3	9	11	O35953 mus musculu
11	3	33.3	10	11	O8VHM9 mus musculu
12	3	33.3	10	12	O39957 hepatitis g
13	3	33.3	11	4	Q9NY38 homo sapien
14	3	33.3	11	7	O77876 oreochromis
15	3	33.3	12	6	Q9TRV4 sus sp. ins
16	3	33.3	13	8	Q9T2U1 bos taurus

17	3	33.3	13	11	O63047
18	3	33.3	13	13	P82881
19	3	33.3	13	15	O66746
20	3	33.3	14	4	P78359
21	3	33.3	14	4	Q9P2A2
22	3	33.3	14	5	P82219
23	3	33.3	14	10	Q9FYT0
24	3	33.3	14	13	Q91777
25	3	33.3	14	13	P82824
26	3	33.3	15	2	Q9R4U7
27	3	33.3	15	4	Q81ZQ0
28	3	33.3	15	8	Q35795
29	3	33.3	15	10	Q9S929
30	3	33.3	15	10	P82431
31	3	33.3	15	11	Q9QV16
32	3	33.3	15	11	O88175
33	3	33.3	15	12	Q86869
34	3	33.3	15	12	Q91PD8
35	3	33.3	15	12	Q91PE5
36	3	33.3	15	12	Q91PE4
37	3	33.3	16	2	Q9R566
38	3	33.3	16	2	Q53399
39	3	33.3	16	2	P83155
40	3	33.3	16	4	Q9UC53
41	3	33.3	16	6	Q9BGG8
42	3	33.3	16	8	O19977
43	3	33.3	16	8	O19975
44	3	33.3	16	8	O19973
45	3	33.3	16	8	O19971
46	3	33.3	16	8	Q9T2P6
47	3	33.3	16	11	Q9CW70
48	3	33.3	17	2	Q9R5B1
49	3	33.3	17	3	Q9URC6
50	3	33.3	17	4	Q9NY39
51	3	33.3	17	11	Q61932
52	3	33.3	17	15	Q78374
53	3	33.3	17	15	Q85463
54	3	33.3	18	2	Q9FAC6
55	3	33.3	18	5	Q9TWL5
56	3	33.3	18	8	Q9GB22
57	3	33.3	18	8	O19979
58	3	33.3	18	8	O19969
59	3	33.3	18	8	Q9ZV79
60	3	33.3	18	15	Q78376
61	3	33.3	18	17	Q825Z9
62	3	33.3	19	2	Q43964
63	3	33.3	19	4	Q9UCL1
64	3	33.3	19	4	Q9UCE4
65	3	33.3	19	10	Q947M7
66	3	33.3	19	10	Q41567
67	3	33.3	19	11	Q8K0N2
68	3	33.3	19	13	Q9PS17
69	3	33.3	19	13	Q9PS14
70	3	33.3	19	13	Q9PRT0
71	3	33.3	19	15	Q78351
72	3	33.3	20	2	Q9R4N0
73	3	33.3	20	4	Q96FU6
74	3	33.3	20	4	O8WX06
75	3	33.3	20	4	O8TR41
76	3	33.3	20	6	O62720
77	3	33.3	20	6	Q9TQX5
78	3	33.3	20	10	Q9S8J6
79	3	33.3	20	10	Q9S900
80	2	22.2	5	13	P83308
81	2	22.2	7	4	O8NH77
82	2	22.2	7	10	P93233
83	2	22.2	8	2	Q45615
84	2	22.2	8	2	Q8KEX4
85	2	22.2	8	2	Q9R3X0
86	2	22.2	8	2	Q49534
87	2	22.2	8	2	Q9X3K1
88	2	22.2	8	2	Q56140
89	2	22.2	8	2	Q938F2

O63047	tattus norv
P82881	rana clamit
O66746	equine infe
P78359	homo sapien
Q9P2A2	homo sapien
P82219	bombyx mori
Q9FYT0	allium cepa
Q91777	xenopus lae
P82824	rana catesb
Q9R4U7	acinetobact
Q81ZQ0	homo sapien
Q35795	saccharomyc
Q9S929	glycine max
P82431	nicotiana t
Q9QV16	tattus sp.
O88175	mus musculu
Q86869	lymphocytic
Q91PD8	rabies viru
Q91PE5	rabies viru
Q91PE4	rabies viru
Q9R566	micrococcu
Q53399	bacillus th
P83155	anabaena sp
Q9UC53	homo sapien
Q9BGG8	sorex arane
O19977	gossypium m
O19975	gossypium t
O19973	gossypium b
O19971	gossypium h
Q9T2P6	tattus sp.
Q9CW70	mus musculu
Q9R5B1	arthrobacte
Q9URC6	saccharomyc
Q9NY39	homo sapien
Q61932	mus musculu
Q78374	human immun
Q85463	avian sarco
Q9FAC6	streptomyce
Q9TWL5	lucilia cup
Q9GB22	calyptomena
O19979	gossypium d
O19969	gossypium a
Q9ZV79	idaris sp. c
Q78376	human immun
Q825Z9	pyrobaculum
Q43964	azotobacter
Q9UCL1	homo sapien
Q9UCE4	homo sapien
Q947M7	vitis vinif
Q41567	tritium ae
Q8K0N2	mus musculu
Q9PS17	gallus gall
Q9PS14	gallus gall
Q9PRT0	gallus gall
Q78351	human immun
Q9R4N0	rhodococcu
Q96FU6	homo sapien
O8WX06	homo sapien
O8TR41	homo sapien
O62720	oryctolagus
Q9TQX5	bos taurus
Q9S8J6	tritium ae
Q9S900	vigna sinen
P83308	gallus gall
Q8NH77	homo sapien
P93233	lycopersico
Q45615	bacillus su
Q8KEX4	microcystis
Q9R3X0	planktothri
Q49534	mycoplasma
Q9X3K1	prochloroco
Q56140	streptococc
Q938F2	pseudomonas

Q45899 clostridium  
Q96433 pseudomonas  
Q8gmms acinetobact  
O13591 saccharomyc  
Q9by75 homo sapien  
O15893 homo sapien  
O16468 homo sapien  
O60773 homo sapien  
Q9twh6 perinereis  
O15899 babesia ovi  
Q94623 manduca sex

## ALIGNMENTS

```

RESULT 1
O82407 PRELIMINARY; PRT; 16 AA.
AC O82407;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alcohohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria viridis (Wild strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64942;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 341;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000220; AAC36547.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db |||||
4 PLFP 7

RESULT 2
O82404 PRELIMINARY; PRT; 16 AA.
AC O82404;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria nilgerrensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berlin 1;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000217; AAC36544.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db |||||
4 PLFP 7

RESULT 3
O82406 PRELIMINARY; PRT; 16 AA.
AC O82406;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria moschata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 157;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000219; AAC36546.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db |||||
4 PLFP 7

RESULT 4
O82402 PRELIMINARY; PRT; 16 AA.
AC O82402;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria nubicola.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=60188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRAS20;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000213; AAC36540.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db |||||
4 PLFP 7

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QY      6 PLFP 9
Db      ||||
        4 PLFP 7

RESULT 5
ID O82403 PRELIMINARY; PRT; 16 AA.
AC O82403;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pawtuckaway;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000215; AAC36542.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1666 MW; CEF73B5B28A4CA87 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      ||||
        4 PLFP 7

RESULT 6
ID O82781 PRELIMINARY; PRT; 16 AA.
AC O82781;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Aldehyde reductase) (Fragment).
GN ADH.
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YELLOW WONDER, and BARON SOLEWACHER;
RA Yu H., Davis T.M.;
RL "Genetic relationships among Fragaria species based on RAPDs and an
RT alcohol dehydrogenase (ADH) gene.";
RL Genome 0:0-0(1997).
CC -|- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE +
CC NADH.
CC -|- COFACTOR: ZINC OR IRON.
DR EMBL; AF000216; AAC36543.1; -.
DR EMBL; AF000214; AAC36541.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      ||||
        4 PLFP 7

RESULT 7
ID O82405 PRELIMINARY; PRT; 16 AA.
AC O82405;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN ADH.
OS Fragaria inumae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64939;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 377;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000218; AAC36545.1; -.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
Db      ||||
        4 PLFP 7

RESULT 8
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RX Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7

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Db 1 VPL 3  
|||

## RESULT 9

Q15898 Q15898 PRELIMINARY; PRT; 8 AA.  
AC Q15898;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE (Clone XPeAllIB) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32078; AAA73888.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match 33.3%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4  
|||

Db 1 ESY 3

## RESULT 10

O35953 O35953 PRELIMINARY; PRT; 9 AA.  
AC O35953;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
GN SCN8A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJII;  
RA Plummer N.W., McBurney M.W., Meisler M.H.;  
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
RT two-domain protein in fetal brain and non-neuronal cells."  
RL J. Biol. Chem. 272:24008-24015(1997).  
DR EMBL; U97672; AAB80914.1; -.  
DR MGD; MGI:103169; Scn8a.  
KW Ionic channel.  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA; 898 MW; 2D92865B735B737 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
|||

Db 1 VPL 3

## RESULT 11

Q8VHM9 Q8VHM9 PRELIMINARY; PRT; 10 AA.  
AC Q8VHM9;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Interferon receptor 2a' (Fragment).  
GN IFNAR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;  
RT "The genomic structure and expression patterns of the gene encoding  
RT the second chain of the murine interleukin 10 receptor, IL-10R2."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;  
RT "The organization, transcriptional regulation and chromosomal  
RT localization of the locus encoding the gene for the murine type I  
RT interferon receptor, Ifnar2."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF440786; AAL40944.1; -.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||

Db 3 PLF 5

## RESULT 12

O39957 O39957 PRELIMINARY; PRT; 10 AA.  
AC O39957;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Hepatitis GB virus C.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC GBV-C/HGV group.  
OX NCBI\_TaxID=39839;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ed\_inburgh haemophilic;  
RX MEDLINE=97368412; PubMed=9225026;  
RA Smith D.B., Cuconu N., Davidson F., Jarvis L.M., Mokili J.L.,  
RA Hamid S., Ludlam C.A., Simmonds P.;  
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by  
RT analysis of the 5' non-coding region."  
RL J. Gen. Virol. 78:1533-1542(1997).  
DR EMBL; AF03175; AAC57986.1; -.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1067 MW; CC88FE27273772 CRC64;

Query Match 33.3%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 5 VPL 7  
|  
|  
|  
Db 3 VPL 5

## RESULT 13

Q9NY38 PRELIMINARY; PRT; 11 AA.  
AC Q9NY38; 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Heavy metal-responsive transcription factor (Fragment).  
GN MTF-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,  
RA Georgiev O., Schaffner W.;  
RT "Characterization of the mouse gene for the heavy metal-responsive  
RT transcription factor MTF-1."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ251891; CAB71327.1; -  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred.No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
|  
|  
|  
Db 5 VPL 7

## RESULT 14

O77876 PRELIMINARY; PRT; 11 AA.  
AC O77876; 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 1 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci."  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF049985; AAC41324.1; -  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;

Query Match 33.3%; Score 3; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred.No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5  
|  
|  
|  
Db 4 SYV 6

## RESULT 15

Q9TRY4 PRELIMINARY; PRT; 12 AA.  
AC Q9TRY4; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).  
OS Sus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9826;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92049376; PubMed=1719383;  
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;  
RT "Isolation and molecular cloning of insulin-like growth factor-binding  
RT protein-6."  
RL Mol. Endocrinol. 5:938-948(1991).  
FT NON\_TER 1 1  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1317 MW; 4DAAABE6CC72DB57 CRC64;

Query Match 33.3%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred.No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|  
|  
|  
Db 6 YVP 8

## RESULT 16

Q9T2U1 PRELIMINARY; PRT; 13 AA.  
AC Q9T2U1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE NADH:ubiquinone oxidoreductase (complex I) iron-sulfur protein  
DE fraction 20 kDa polypeptide peptide T-9 (Fragment).  
OS Bos taurus (Bovine).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92138662; PubMed=1778979;  
RA Masui R., Wakabayashi S., Matsubara H., Hatafi Y.;  
RT "The amino acid sequence of the 9 kDa polypeptide and partial amino  
RT acid sequence of the 20 kDa polypeptide of mitochondrial  
RT NADH:ubiquinone oxidoreductase."  
RL J. Biochem. 110:575-582(1991).  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1369 MW; 0E61A5EAB35FDB50 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred.No. 6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|  
|  
|  
Db 7 YVP 9

## RESULT 17

Q63047 PRELIMINARY; PRT; 13 AA.  
ID Q63047

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AC Q63047;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AMP deaminase (Fragment).
GN AMPD1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Soleus muscle;
RX MEDLINE=90377216; PubMed=2398891;
RA Mineo I., Clarke P.R.H., Sabina R.L., Holmes E.W.;
RT "A novel pathway for alternative splicing: Identification of an RNA
RT intermediate that generates an alternative 5' splice donor site not
RT present in the primary transcript of AMPD1."
RL Mol. Cell. Biol. 10:5271-5278(1990).
DR EMBL; MS8689; AAA40727.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1524 MW; 526CSA93EF6201A7 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db |||
2 PLF 4

RESULT 18
P82881
ID P82881 PRELIMINARY; PRT; 13 AA.
AC P82881;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Temporin-1CB.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RT skin of the North American green frog Rana clamitans."
RL Peptides 21:469-476(2000).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -|- SUBCELLULAR LOCATION: SECRETED.
CC -|- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1432 MW; C4A71A765A8935BD CRC64;

Query Match 33.3%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
Db |||
3 PLF 5

RESULT 19
Q66746

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ID Q66746 PRELIMINARY; PRT; 13 AA.
AC Q66746;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Polymerase (Fragment).
OS Equine infectious anemia virus.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90204701; PubMed=2157066;
RA Noiman S., Yaniv A., Sherman L., Tronick S.R., Gazit A.;
RT "Pattern of transcription of the genome of equine infectious anemia
RT virus."
RL J. Virol. 64:1839-1843(1990).
DR EMBL; M33845; AAA66411.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1493 MW; 978D390905A92321 CRC64;

Query Match 33.3%; Score 3; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db |||
1 VPL 3

RESULT 20
P78359
ID P78359 PRELIMINARY; PRT; 14 AA.
AC P78359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NF-kappa-B transcription factor p65 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pyde S., Nelles L., Huylebroeck D.;
RT "5' cDNA sequence Re1a isolated from Human umbilical vein endothelial
RT cells."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88316; AAB48487.1; -.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db |||
4 LFP 6

RESULT 21
Q9P2A2
ID Q9P2A2 PRELIMINARY; PRT; 14 AA.
AC Q9P2A2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated aldo-keto reductase (Fragment).
GN TRUNCATED AKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
RA Watanabe K., Ito S.;
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
RL three aldo-keto reductase genes.";
RL Genes Cells 5:111-125(2000).
DR EMBL; AB037903; BAA92888.1; --
FT NON_TER 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 5 VPL 7

RESULT 22
P82219 ID P82219 PRELIMINARY; PRT; 14 AA.
AC P82219;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCB1_TaxID=7091;
RN [1]
RP SEQUENCE.
RX STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 14
SQ SEQUENCE 14 AA; 1535 MW; 4E659A7257BAA3C7 CRC64;

Query Match 33.3%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
Db 6 PLF 8

RESULT 23
Q9FYTO ID Q9FYTO PRELIMINARY; PRT; 14 AA.
AC Q9FYTO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Alliinase (EC 4.4.1.4) (Fragment).
OS Allium cepa (Onion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCB1_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wase Showman Red;
RA Kaminishi A., Nomura K., Ohya T., Kita N.;

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RT "Cloning of Novel Promoter of Alliinase gene from Onion by Inverse
RT PCR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291183; AAG00599.1; --
FT NON_TER 14
SQ SEQUENCE 14 AA; 1573 MW; C3547CA8BE1B8162 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 2 ESY 4

RESULT 24
Q91777 ID Q91777 PRELIMINARY; PRT; 14 AA.
AC Q91777;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Hypothetical 1.6 kDa protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=90231335; PubMed=2330002;
RA Kajimoto Y., Kotwein P.;
RT "Evolution of insulin-like growth factor I (IGF-I): structure and
RL Mol. Endocrinol. 4:217-226(1990).
DR EMBL; M29857; AAA70329.1; --
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1627 MW; 3002F6B29B887BD7 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9
Db 5 LFP 7

RESULT 25
P82824 ID P82824 PRELIMINARY; PRT; 14 AA.
AC P82824;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RANATUERIN 9.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE.
RX TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RL American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.

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CC -!- SUBCELLULAR LOCATION: SECRETED.

KW Antibiotic. 14 AA; 1625 MW; 8941FA6337030BA1 CRC64;

SQ SEQUENCE 14 AA; 1625 MW; 8941FA6337030BA1 CRC64;  
Query Match 33.3%; Score 3; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
Db 2 LFP 4

RESULT 26

Q9R4U7 PRELIMINARY; PRT; 15 AA.  
AC Q9R4U7;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE Malonate decarboxylase gamma subunit (Fragment).  
OS Acinetobacter calcoaceticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=471;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95050812; PubMed=7961952;  
RA Kim Y.S., Byun H.S.;  
RT "Purification and Properties of a novel type of malonate decarboxylase  
from Acinetobacter calcoaceticus";  
RL J. Biol. Chem. 269:29636-29641(1994).  
SQ SEQUENCE 15 AA; 1816 MW; 4E14F10E389F9FEA CRC64;

Query Match 33.3%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
Db 10 LFP 12

RESULT 27

Q81ZQ0 PRELIMINARY; PRT; 15 AA.  
AC Q81ZQ0;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Protein kinase A catalytic subunit beta (Fragment).  
GN PKACB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wu K.-J., Mattioli M., Morse H.C., Dalla-Favera R.;  
RT "c-MYC activates protein kinase A (PKA) by direct transcriptional  
activation of the PKA catalytic subunit beta (PKA-CB) gene.";  
RL Oncogene 0:0-0(2002).  
DR ENBL; AF538872; AAN16454.1; -.  
KW Kinase.  
FT NON TER 15 15  
SQ SEQUENCE 15 AA; 1480 MW; 52FE569E5C19B70A CRC64;

Query Match 33.3%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3  
Db 1

Db 13 VES 15

RESULT 28

Q35795 PRELIMINARY; PRT; 15 AA.  
AC Q35795;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE OX13 locus in yeast MITOCHONDRION (Strain D273-10B) (CODES for  
cytochrome oxidase subunit 1).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system. Structure and  
nucleotide sequence of the gene coding for subunit 1 of yeast  
cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941(1980).  
DR ENBL; V00694; CAA24069.1; -.  
KW Mitochondrion.  
SQ SEQUENCE 15 AA; 1741 MW; 0E7A612E14FCC394 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3  
Db 3 VES 5

RESULT 29

Q9S929 PRELIMINARY; PRT; 15 AA.  
AC Q9S929;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Pyroline-5-carboxylate reductase, P5CR (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91378472; PubMed=1898034;  
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;  
RT "Pyroline-5-carboxylate reductase in soybean nodules:  
isolation/partial primary structure/evidence for isozymes.";  
RL Arch. Biochem. Biophys. 288:350-357(1991).  
FT NON TER 15 15  
SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4  
Db 9 ESY 11

RESULT 30

P82431 PRELIMINARY; PRT; 15 AA.  
ID P82431

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AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; famids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1694 MW; 5F3B8D2E48187626 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 13 VPL 15

RESULT 31
Q9QV16
ID O9QV16 PRELIMINARY; PRT; 15 AA.
AC O9QV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Prolactin-binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RA Cohen H., Cohen O., Gagnon J.;
RA "Serum prolactin-binding protein (PRL-BP) of human and rat are
RT identified as IgG.";
RL C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
SQ SEQUENCE 15 AA; 1469 MW; 35ED2512FF3FA369 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 5 VES 7

RESULT 32
O88175
ID O88175 PRELIMINARY; PRT; 15 AA.
AC O88175;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neutral cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RC MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RT of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31274.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1481 MW; 41868EF6117732C2 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 9 VPL 11

RESULT 33
O86869
ID O86869 PRELIMINARY; PRT; 15 AA.
AC O86869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN S-RNA PRODUCT.
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95190990; PubMed=7533851;
RA Moskophidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL; S75753; AAB33673.1; -.
DR InterPro; IPR001535; Arena_glycoprot.
DR Pfam; PF00798; Arena_glycoprot; 1.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1571 MW; 2D25ABF4F776C1A7 CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 4 VES 6

RESULT 34
O91PD8
ID O91PD8 PRELIMINARY; PRT; 15 AA.
AC O91PD8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=j598;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa."; EMBL/GenBank/DBJ databases.
DR EMBL; AF171117; AAK84649.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 35
Q91PE5
ID Q91PE5 PRELIMINARY; PRT; 15 AA.
AC Q91PE5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=j544;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF171109; AAK84642.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 36
Q91PF4
ID Q91PF4 PRELIMINARY; PRT; 15 AA.
AC Q91PF4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glycoprotein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=d352;
RA Sabeta C.T., Bingham J., Nel L.H.;
RT "Molecular epidemiology of rabies associated with canine species in
RL Zimbabwe and South Africa.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF171100; AAK84633.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1700 MW; 5E0F9BF995E1E09E CRC64;

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Query Match 33.3%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESY 4
Db 5 ESY 7

RESULT 37
Q9R596
ID Q9R596 PRELIMINARY; PRT; 16 AA.
AC Q9R596;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA topoisomerase I (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Micrococcaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE.
RX MEDLINE=93249439; PubMed=8387285;
RA Anderluzzi D., Pedrini A.M.;
RT "Structural similarities between M. luteus and E. coli DNA
RT topoisomerase I.";
RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
SQ SEQUENCE 16 AA; 1672 MW; 0B5A23304332200F CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 10 VPL 12

RESULT 38
Q53399
ID Q53399 PRELIMINARY; PRT; 16 AA.
AC Q53399;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CryII protein (Fragment).
GN CRYIIB.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94123945; PubMed=8293956;
RA Hodgman T.C., Ziniu Y., Shen J., Ellar D.J.;
RT "Identification of a cryptic gene associated with an insertion
RT sequence not previously identified in Bacillus thuringiensis.";
RL FEMS Microbiol. Lett. 114:23-29(1993).
DR EMBL; S68408; AAC60457.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1944 MW; 132368F185FD4F90 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVV 5
Db 14 SVV 16

RESULT 39

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P83155  
ID P83155 PRELIMINARY; PRT; 16 AA.  
AC P83155;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Fructose-bisphosphate aldolase (EC 4.1.2.13) (Fragment).  
OS Anabaena sp. (strain L31).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
OX NCBI\_TaxID=29412;  
RN [1]  
RP SEQUENCE.  
RA Apce S.K., Uhlemann E., Schmid R., Altendorf K.;  
RL Submitted (OCT-2001) to the SWISS-PROT data bank.  
CC -|- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE  
CC PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE.  
CC -|- COFACTOR: ZINC (BY SIMILARITY).  
CC -|- PATHWAY: SIXTH STEP IN GLYCOLYSIS.  
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -|- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE  
CC FAMILY.  
DR InterPro; IPR000771; K\_bp aldolase.  
DR PROSITE; PS00602; ALDOLASE CLASS II\_1; PARTIAL.  
DR PROSITE; PS00806; ALDOLASE CLASS II\_2; PARTIAL.  
KW Lyase; Glycolysis; Zinc; Metal-binding.  
FT NON TER 16  
SQ SEQUENCE 16 AA; 1702 MW; 5D2670D9E4833A8B CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
Db 3 VPL 5

## RESULT 40

Q9UC53  
ID Q9UC53 PRELIMINARY; PRT; 16 AA.  
AC Q9UC53;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 77 kDa SPONTANEOUS RECURRENT ABORTION-associated human embryonic  
DE antigen/IGVHII homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=96033130; PubMed=8582963;  
RA Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W.,  
RA Miki S., Tanaka T., Suzuki T., Soma H.;  
RT "diagnostic relevance of abortion-associated human embryonic antigen  
RT expressed on the cell surface of tumour promoter-treated Bloom syndrome  
RT cells."  
RL Hum. Reprod. 10:1694-1701(1995).  
SQ SEQUENCE 16 AA; 1626 MW; C9C5ED2512FF3FB9 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3  
Db 5 VES 7

## RESULT 41

Q9BGG8  
ID Q9BGG8 PRELIMINARY; PRT; 16 AA.

Q9BGG8;  
AC 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Thyroid hormone receptor alpha (Fragment).  
GN THRA1.  
OS Sorex araneus (Eurasian common shrew) (European shrew).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.  
OX NCBI\_TaxID=42254;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Latkin D., Serov O., Zhdanova N.;  
RT "Mapping of five genes from human chromosome 17 to chromosome 17 of  
RT the common shrew (Sorex araneus).";  
RL Acta Theriol. (Warsz) 45:143-146(2000).  
DR EMBL; AF314827; AAK13419.1; -.  
KW Receptor.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 33.3%; Score 3; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
Db 2 LFP 4

## RESULT 42

O19977  
ID O19977 PRELIMINARY; PRT; 16 AA.  
AC O19977;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Photosystem I subunit (Fragment).  
GN PSI.  
OS Gossypium mustelinum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
OX NCBI\_TaxID=34275;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Small R.L., Ryburn J.A., Cronm R.C., Seelanan T., Wendel J.F.;  
RT "The tortoise and the hare: choosing between noncoding plastome and  
RT nuclear Adh sequences for phylogeny reconstruction in a recently  
RT diverged plant group.";  
RL Am. J. Bot. 85:1301-1315(1998).  
DR EMBL; AF031584; AAC63566.2; -.  
KW Chloroplast.  
FT NON TER 16  
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7  
Db 12 VPL 14

## RESULT 43

O19975  
ID O19975 PRELIMINARY; PRT; 16 AA.

AC O19975;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

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DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium tomentosum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34277;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031583; AAC63564.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
DB 12 VPL 14

RESULT 44
O19973 PRELIMINARY; PRT; 16 AA.
AC O19973;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3634;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031582; AAC63562.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
DB 12 VPL 14

RESULT 45
O19971 PRELIMINARY; PRT; 16 AA.
AC O19971;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium hirsutum (Upland cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031581; AAC63560.2; -.
KW Chloroplast.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
DB 12 VPL 14

RESULT 46
O9T2P6 PRELIMINARY; PRT; 16 AA.
AC O9T2P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome P-450-FEMALE-specific isoform (Fragment).
OS Rattus sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9135184; PubMed=1883820;
RA Addya S., Zheng Y.M., Shayiq R.M., Fan J.Y., Avadhani N.G.;
RT "Characterization of a female-specific hepatic mitochondrial
RT cytochrome P-450 whose steady-state level is modulated by
RT testosterone.";
RL Biochemistry 30:8323-8330(1991).
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1837 MW; 7889F9F622765DAC CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
DB 14 LFP 16

RESULT 47
O9CW70 PRELIMINARY; PRT; 16 AA.
AC O9CW70;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adult male brain cDNA, RIKEN full-length enriched library,
DE clone:0710008B15, full insert sequence (fragment).
GN MAG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003029; BAB22519.1; -.
DR MGD; MGI:96912; Mag.
FT NON_TER 16
FT SEQUENCE 16 AA; 1867 MW; 65BB8C02CB69FDB5 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
DB 8 PLF 10

RESULT 48
Q9R5B1 PRELIMINARY; PRT; 17 AA.
AC Q9R5B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DE QUINALDINE oxidoreductase alpha-subunit (Fragment).
OS Arthrobacter.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Micrococcaceae.
OX NCBI_TaxID=1663;
RN [1]
RP SEQUENCE
RX MEDLINE=93228843; PubMed=8471177;
RA de Beyer A., Litgens F.;
RT "Microbial metabolism of quinaldine and related compounds. XVI.
RT Quinaldine oxidoreductase from Arthrobacter spec. Ru 61a: a molybdenum-
RT containing enzyme catalysing the hydroxylation at C-4 of the
RT heterocycle.";
RL Biol. Chem. Hoppe-Seyler 374:101-109(1993).
SQ SEQUENCE 17 AA; 1768 MW; A2EB35201E43B3E8 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
DB 1 VES 3

RESULT 49

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Q9URC6 PRELIMINARY; PRT; 17 AA.
AC Q9URC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipid-binding protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE
RX MEDLINE=91353077; PubMed=18825448;
RA Creutz C.E., Snyder S.L., Kambouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding
RT proteins of Saccharomyces cerevisiae.";
RL Yeast 7:229-244(1991).
FT NON_TER 1
FT NON_TER 17
FT SEQUENCE 17 AA; 1959 MW; C2EB6543287744D2 CRC64;

Query Match 33.3%; Score 3; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
DB 15 ESY 17

RESULT 50
Q9NY39 PRELIMINARY; PRT; 17 AA.
AC Q9NY39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHI3L1 protein (Fragment).
GN CHI3L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ammon C., Rehli M., Andreassen R., Krause S.W.;
RT "Alternative splicing of the human cartilage gp-39 gene generates
RT multiple mRNA transcripts encoding for at least four putative protein
RT isoforms with distinct carboxyl termini.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251847; CAB76474.1; -.
FT NON_TER 1
FT SEQUENCE 17 AA; 2099 MW; 086B9AA863393785 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8
DB 15 PLF 17

RESULT 51
Q61932 PRELIMINARY; PRT; 17 AA.
AC Q61932;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adult skeletal muscle myosin heavy chain mRNA carboxyl-end, segment 1
DE (Fragment).

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GN MVH4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=84061805; PubMed=6196357;  
 RA Weydert A., Daubas P., Caravatti M., Minty A., Bugaisky G., Cohen A.,  
 RA Robert B., Buckingham M.B.;  
 RT "Sequential accumulation of mRNAs encoding different myosin heavy  
 RT chain isoforms during skeletal muscle development in vivo detected  
 RT with a recombinant plasmid identified as coding for an adult fast  
 RT myosin heavy chain from mouse skeletal muscle.";  
 RL J. Biol. Chem. 258:13867-13874(1983).  
 DR EMBL: K00986; AAA39792.1; --  
 DR MGD; MGI:1339713; Wnt4.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1985 MW; 40EA696BP87181E2 CRC64;  
 Query Match 33.3%; Score 3; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VES 3  
 Db 7 VES 9  
 RESULT 52  
 ID Q78374 PRELIMINARY; PRT; 17 AA.  
 AC Q78374;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Viral sample FLPBR4E (Florida patient B), partial env cds, V4 region  
 DE (Fragment).  
 DE Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11676;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=92271245; PubMed=1589796;  
 RA Ou C.-Y., Ciesielski C.A., Myers G., Bandea C.I., Luo C.C.,  
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,  
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,  
 RA Jaffe H.W.;  
 RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";  
 RL Science 256:1165-1171(1992).  
 DR EMBL: M92121; AAA44491.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1877 MW; 9925A5E497E51505 CRC64;  
 Query Match 33.3%; Score 3; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 LFP 9  
 Db 1 LFP 3  
 RESULT 53  
 Q85463  
 ID Q85463 PRELIMINARY; PRT; 17 AA.  
 AC Q85463;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Pol gene (Fragment).  
 OS Avian sarcoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_TaxID=11876;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=88275035; PubMed=2839694;  
 RA Katz R.A., Kotler M., Skalka A.M.;  
 RT "cis-acting intron mutations that affect the efficiency of avian  
 RT retroviral RNA splicing: Implication for mechanisms of control.";  
 RL J. Virol. 62:2686-2695(1988).  
 DR EMBL: M21395; AAA42414.1; --  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1835 MW; F43A1834E07A2C3A CRC64;  
 Query Match 33.3%; Score 3; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 PLF 8  
 Db 4 PLF 6  
 RESULT 54  
 ID Q9FAC6 PRELIMINARY; PRT; 18 AA.  
 AC Q9FAC6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Transposase (Fragment).  
 OS Streptomyces coelicolor A3(2).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=100226;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21080545; PubMed=11212918;  
 RA Yamasaki M., Redenbach M., Kinashi H.;  
 RT "Integrated structures of the linear plasmid SCP1 in two bidirectional  
 RT donor strains of Streptomyces coelicolor A3(2).";  
 RL Mol. Gen. Genet. 264:634-642(2001).  
 DR EMBL: AB042600; BAB17790.1; --  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1855 MW; 7B38501811F74BFE CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VES 3  
 Db 3 VES 5  
 RESULT 55  
 ID Q9TWL5 PRELIMINARY; PRT; 18 AA.  
 AC Q9TWL5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 24 kDa chymotrypsin-like enzyme (Fragment).  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Lucilia.  
 OX NCBI\_TaxID=7375;

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RN SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA.";
RL Insect Mol. Biol. 3:201-211(1994).
SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 33.3%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 11 LFP 13

RESULT 56
Q9GB22 PRELIMINARY; PRT; 18 AA.
AC Q9GB22;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Cytochrome c oxidase subunit II (Fragment).
GN CoII.
OS Calyptomena viridis (Lesser green broadbill).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoseauria; Aves; Neognathae; Passeriformes; Eurylaimidae;
OC Calyptomena.
OC NCBI_TaxID=135972;
RN [1]
RP SEQUENCE FROM N.A.
RA Slikas B., Jones I.B., Derrickson S.R., Fleischer R.C.;
RT "Phylogenetic relationships of Micronesian white-eyes (Zosteropidae)
RT based on mitochondrial sequence data.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF168455; AAG12310.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 18 AA; 1993 MW; 59773229B49CF327 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 1 VES 3

RESULT 57
O19979 PRELIMINARY; PRT; 18 AA.
AC O19979;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium darwinii (Darwin's cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OC NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and

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RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031585; AAC63568.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEPB57 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 12 VPL 14

RESULT 58
O19969 PRELIMINARY; PRT; 18 AA.
AC O19969;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAL.
OS Gossypium arboreum (Tree cotton).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OC NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031580; AAC63558.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEPB57 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 12 VPL 14

RESULT 59
Q9ZY79 PRELIMINARY; PRT; 18 AA.
AC Q9ZY79;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Idris sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastroidae;
OC Scellionidae; Idris.
OC NCBI_TaxID=81086;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";

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RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF082922; AAD1782.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 18 AA; 2131 MW; BBB4F268AEA31D08 CRC64;
Query Match 33.3%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PLF 8
DB 9 PLF 11

RESULT 60
Q78376 PRELIMINARY; PRT; 18 AA.
AC Q78376;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Viral sample FLPR4I (Florida patient B), partial env cds, V4 region
DE (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Gieselski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
RL Science 256:1165-1171(1992).
DR EMBL; M92122; AAA44492.1; -.
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2000 MW; OB1E4794679R050A CRC64;
Query Match 33.3%; Score 3; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LFP 9
DB 1 LFP 3

RESULT 61
Q82S29 PRELIMINARY; PRT; 18 AA.
AC Q82S29;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE3501a.
GN PAE3501a.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;

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RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AR00934; AAL64964.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 18 AA; 2362 MW; BCF4D6923A98943 CRC64;
Query Match 33.3%; Score 3; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ESY 4
DB 3 ESY 5

RESULT 62
Q43964 PRELIMINARY; PRT; 19 AA.
ID Q43964;
AC Q43964;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nitrogenase molybdenum-iron protein (Fragment).
GN NIFD.
OS Azotobacter chroococcum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93138425; PubMed=8423000;
RA Jones R.L., Woodley P., Zinoni A.B., Robson R.L.;
RT "The nifH gene encoding the Fe protein of the molybdenum nitrogenase
RT from Azotobacter chroococcum.";
RL Gene 123:145-146(1993).
DR EMBL; M73020; AAA22141.1; -.
FT NON TER 19
FT NON TER 19
SQ SEQUENCE 19 AA; 2165 MW; OAC46CC8BF500CD7 CRC64;
Query Match 33.3%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VES 3
DB 9 VES 11

RESULT 63
Q9UC11 PRELIMINARY; PRT; 19 AA.
ID Q9UC11;
AC Q9UC11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Gelatinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099930; PubMed=1464361;
RA Kjeldsen L., Bjerrum O.W., Hovgaard D., Johnsen A.H., Sehested M.,
RA Borregaard N.;
RT "Human neutrophil gelatinase: a marker for circulating blood
RT neutrophils. Purification and quantitation by enzyme linked
RT immunosorbent assay.";
RL Eur. J. Haematol. 49:180-191(1992).
SQ SEQUENCE 19 AA; 2200 MW; 968209EF26B87375 CRC64;
Query Match 33.3%; Score 3; DB 4; Length 19;

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Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 10 LFP 12

RESULT 64
Q9UCB4 PRELIMINARY; PRT; 19 AA.
ID AC Q9UCB4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE PROCATHEPSIN E (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93349047; PubMed=8346912;
RA Takeda-Ezaki M., Yamamoto K.;
RT "Isolation and biochemical characterization of procathepsin E from
RT human erythrocyte membranes."
RL Arch. Biochem. Biophys. 304:352-358(1993)
SQ SEQUENCE 19 AA; 2293 MW; 3217ABB8670A65FC CRC64;

Query Match 33.3%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 5 VPL 7

RESULT 65
Q947M7 PRELIMINARY; PRT; 19 AA.
ID AC Q947M7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Leucoanthocyanidin dioxygenase (Fragment).
GN LDOX.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RA Gollop R., Farhi S., Perl A.;
RT "Regulation of the leucoanthocyanidin dioxygenase gene expression in
RT Vitis vinifera."
RL Plant Sci. 161:579-588(2001).
DR EMBL; AF290432; AAK96258.1; -.
KW Dioxygenase.
FT NON_TER
SQ SEQUENCE 19 AA; 1935 MW; 95D58D008AE5E27F CRC64;

Query Match 33.3%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 9 VES 11

RESULT 66
Q9PS17 PRELIMINARY; PRT; 19 AA.
ID AC Q9PS17;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Puromycin-sensitive aminopeptidase isozyme II (Fragment).

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Q41567 PRELIMINARY; PRT; 19 AA.
ID AC Q41567;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Heat shock protein 16.9 (Fragment).
GN HSP16.9-3LC2.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Mustang;
RX MEDLINE=96382426; PubMed=8790290;
RA Joshi C.P., Nguyen H.T.;
RT "Differential display-mediated rapid identification of different
RT members of a multigene family, HSP 16.9 in wheat."
RL Plant Mol. Biol. 31:575-584(1996).
DR EMBL; L37074; AAA51394.1; -.
FT NON_TER
SQ SEQUENCE 19 AA; 1769 MW; 7A77E05EFD609CEF CRC64;

Query Match 33.3%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7
Db 4 VPL 6

RESULT 67
Q8KON2 PRELIMINARY; PRT; 19 AA.
ID AC Q8KON2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030921; AAH30921.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 19 AA; 2255 MW; 66C5F38861B749AE CRC64;

Query Match 33.3%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9
Db 6 LFP 8

RESULT 68
Q9PS17 PRELIMINARY; PRT; 19 AA.
ID AC Q9PS17;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Puromycin-sensitive aminopeptidase isozyme II (Fragment).

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OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93250542; PubMed=8485450;  
 RA Hui K.S., Saito M., Hui M., Saito M., Lajtha A., Yamamoto K.,  
 RA Osawa T.;  
 RL Neurochem. Int. 22:445-453 (1993).  
 DR HSP; P29312; 1QJA.  
 SQ SEQUENCE 19 AA; 2159 MW; 8091278C84691774 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
 Db 16 ESY 18

RESULT 69  
 Q9PS14  
 ID Q9PS14 PRELIMINARY; PRT; 19 AA.  
 AC Q9PS14;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Puromycin-sensitive aminopeptidase isozyme I (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93250542; PubMed=8485450;  
 RA Hui K.S., Saito M., Hui M., Saito M., Lajtha A., Yamamoto K.,  
 RA Osawa T.;  
 RL Neurochem. Int. 22:445-453 (1993).  
 DR HSP; P29312; 1QJA.  
 SQ SEQUENCE 19 AA; 2132 MW; 8091278C8478E774 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4  
 Db 16 ESY 18

RESULT 70  
 Q9PRT0  
 ID Q9PRT0 PRELIMINARY; PRT; 19 AA.  
 AC Q9PRT0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE 23A7 antigen (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95332492; PubMed=7608337;  
 RA Denburg J.L., Caldwell R.T., Marner J.M.;  
 RT "Developmental changes in epitope accessibility as an indicator of  
 multiple states of an immunoglobulin-like neural cell adhesion

RT molecule."  
 RL J. Comp. Neurol. 354:533-550 (1995).  
 SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EED03 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
 Db 3 VPL 5

RESULT 71  
 Q78351  
 ID Q78351 PRELIMINARY; PRT; 19 AA.  
 AC Q78351;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Viral sample FLPBR4A (Florida patient B), partial env cds, V4 region (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L.Q., Leigh-Brown A.J.;  
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92271245; PubMed=1589796;  
 RA Ou C.-Y., Ciesielecki C.A., Myers G., Bandea C.I., Luo C.C.,  
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,  
 RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,  
 RA Jaffe H.W.;  
 RT "Molecular Epidemiology of HIV Transmission in a Dental Practice."  
 RL Science 256:1165-1171 (1992).  
 DR EMBL; M92118; AAA44488.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 1985 MW; 5FFC8787D98CEA1C CRC64;

Query Match 33.3%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9  
 Db 1 LFP 3

RESULT 72  
 Q9R4N0  
 ID Q9R4N0 PRELIMINARY; PRT; 20 AA.  
 AC Q9R4N0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Muconate cycloisomerase (EC 5.5.1.1) (Fragment).  
 OS Rhodococcus erythropolis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=1833;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95270600; PubMed=7751292;  
 RA Solyanikova I.P., Maltseva O.V., Vollmer M.D., Golovleva L.A.,  
 RA Schliemann M.;  
 RT "Characterization of muconate and chloromuconate cycloisomerase from  
 Rhodococcus erythropolis 1CP: indications for functionally convergent  
 evolution among bacterial cycloisomerases."  
 RL J. Bacteriol. 177:2821-2826 (1995).

SQ SEQUENCE 20 AA; 2167 MW; 1490DD0BA27A5773 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
DB 15 VPL 17

## RESULT 73

Q96FJ6 PRELIMINARY; PRT; 20 AA.  
AC Q96FJ6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010734; AAH10734.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 20 AA; 2406 MW; CC51FC8C824E6D52 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
DB 18 PLF 20

## RESULT 74

Q8WX06 PRELIMINARY; PRT; 20 AA.  
AC Q8WX06;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE B212B22.1 (Diaphanous (Drosophila, homolog 2) (Fragment).  
GN DIAPH2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Heath P.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL391821; CAD13462.1; -.  
FT NON\_TER  
SQ SEQUENCE 20 AA; 2321 MW; 8821A82DF9B73B78 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
DB 4 VPL 6

## RESULT 75

Q8TE41

ID Q8TE41 PRELIMINARY; PRT; 20 AA.  
AC Q8TE41;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Truncated steroid 11beta-hydroxylase (Fragment).  
GN CYP11B1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Penachioni J.Y.; de Castro M., Bachega T.A., Mendonca B.B.,  
RA de Mello M.P.;  
RT "CYP11B1 new mutations R404+C and G267S leading to 11beta-hydroxylase  
RT deficiency in Brazilian patients."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Penachioni J.Y.;  
RT "Mutations and polymorphisms in CYP11B1 human gene in individuals with  
RT 11-beta-Hydroxylase deficiency."  
RL Thesis (2001), Department of College of Medical Sciences,  
RL Campinas State University, Campinas, SP, Brazil.  
DR EMBL; AJ431375; CAD24087.1; -.  
FT NON\_TER  
SQ SEQUENCE 20 AA; 2130 MW; 78B715D5A3CD45BF CRC64;

Query Match 33.3%; Score 3; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPL 7  
DB 6 VPL 8

Search completed: November 25, 2003, 19:34:13  
Job time : 17.9012 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 22.9709 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLPFP 9

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
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23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	AAW42101	Colostrinin derive
2	9	100.0	9	AAW72276	Colostrinin derive
3	9	100.0	9	AAW72529	Colostrinin peptid
4	9	100.0	9	AAW72561	Colostrinin peptid
5	9	100.0	9	AAW20258	Colostrinin consti
6	9	100.0	9	AAW51067	Colostrinin consti
7	9	100.0	9	AAW14607	Neural cell regula
8	88.9	8	22	AAW07189	Colostrinin peptid
9	8	88.9	9	AAW07199	Modified colostrin

10	5	55.6	15	22	AAW98131	Interferon-gamma s
11	5	55.6	15	22	AAW98132	Interferon-gamma s
12	5	55.6	15	22	AAW98133	Interferon-gamma s
13	5	55.6	15	22	AAW97741	gp100 derived IFN-
14	5	55.6	15	22	AAW97742	gp100 derived IFN-
15	5	55.6	15	22	AAW97743	gp100 derived IFN-
16	5	55.6	15	23	ABP46299	Human Blys binding
17	5	55.6	16	23	ABP46252	Human Blys binding
18	4	44.4	7	12	AAW12158	Cyclo-octa peptide
19	4	44.4	7	19	AAW46013	Peptide #45 based
20	4	44.4	7	20	AAW17016	Heat shock protein
21	4	44.4	7	22	AAW72158	Melanoma antigen,
22	4	44.4	7	23	AAW80708	Javelin peptide #1
23	4	44.4	8	15	AAW58322	Hypotensive polype
24	4	44.4	8	20	AAW16845	Heat shock protein
25	4	44.4	8	22	ABW04380	Carrot partial ant
26	4	44.4	8	22	ABW20475	Mouse contactin pr
27	4	44.4	8	23	ABW78590	Multiple sclerosis
28	4	44.4	8	24	ABW20030	MHC binding peptid
29	4	44.4	9	14	AAW46514	Plasmodium yoelii
30	4	44.4	9	19	AAW68359	MHC binding peptid
31	4	44.4	9	21	AAW23654	Cytotoxic T lympho
32	4	44.4	9	21	AAW96361	HLA-A24 binding pe
33	4	44.4	9	21	AAW86776	Telomerase peptide
34	4	44.4	9	21	AAW68305	Altered MHC determ
35	4	44.4	9	21	AAW52959	Altered MHC determ
36	4	44.4	9	22	AAW98253	Human peptide #152
37	4	44.4	9	22	AAW63512	Amino acid sequenc
38	4	44.4	9	22	AAW63517	Amino acid sequenc
39	4	44.4	9	22	AAW66424	Circumsporozoite p
40	4	44.4	9	23	AAW79591	Malarial epitope #
41	4	44.4	9	24	ABW06327	Human cancer-relat
42	4	44.4	9	24	ABW07074	Human cancer-relat
43	4	44.4	9	24	ABW07293	Human cancer-relat
44	4	44.4	9	24	ABP72311	Plasmodium yoelii
45	4	44.4	9	24	ABP58362	CSP peptide. Mus
46	4	44.4	10	16	AAW79143	Fructosyltransfera
47	4	44.4	10	22	AAW85227	Saccharomyces cere
48	4	44.4	10	23	ABW83032	Transferrin recept
49	4	44.4	10	24	ABW06228	Human cancer-relat
50	4	44.4	10	24	ABW06458	Human cancer-relat
51	4	44.4	10	24	ABW06590	Human cancer-relat
52	4	44.4	10	24	ABW07254	Human cancer-relat
53	4	44.4	10	24	ABW07442	Human cancer-relat
54	4	44.4	11	16	AAW72659	Cladosporium herba
55	4	44.4	11	22	AAW11116	Tryptic peptide #1
56	4	44.4	11	22	AAW99185	Vaccine related MH
57	4	44.4	11	22	AAW63527	An epitope which m
58	4	44.4	11	24	ABP99426	Beta-amyloid bindi
59	4	44.4	12	21	AAW67307	Malarial epitope o
60	4	44.4	12	22	AAW99153	Vaccine related MH
61	4	44.4	12	22	AAW63518	Amino acid sequenc
62	4	44.4	13	13	AAW21802	Epitope, from alle
63	4	44.4	13	22	AAW17675	Novel signal trans
64	4	44.4	13	22	AAW68132	Peptide derived fr
65	4	44.4	13	24	ABP53814	Human CNTF potenti
66	4	44.4	13	24	ABP53834	Human CNTF potenti
67	4	44.4	13	24	ABP53835	Human CNTF potenti
68	4	44.4	13	24	ABP53854	Human CNTF potenti
69	4	44.4	13	24	ABP53874	Human CNTF potenti
70	4	44.4	14	16	AAW83142	Human CNTF potenti
71	4	44.4	14	22	ABW56665	[4-Leu, 12-D-Arg,
72	4	44.4	14	22	AAW97755	Human peptide #103
73	4	44.4	14	22	AAW99155	Vaccine related MH
74	4	44.4	14	22	ABW70401	Rabies matrix prot
75	4	44.4	14	23	ABP46338	Human Blys binding
76	4	44.4	14	23	ABP46377	Human Blys binding
77	4	44.4	14	23	ABP46412	Human Blys binding
78	4	44.4	14	23	ABP46436	Human Blys binding
79	4	44.4	14	23	ABP46456	Human Blys binding
80	4	44.4	14	23	ABP46522	Human Blys binding
81	4	44.4	14	23	ABP46629	Human Blys binding
82	4	44.4	14	23	ABP46646	Human Blys binding



83 Human BlyS binding  
 84 Purified cis-9,10-  
 85 Purified cis-9,10-  
 86 Beta (1 -> 4)-N-ac  
 87 Patten acid amide h  
 88 Patten acid amide h  
 89 Transforming growth  
 90 Transforming growth  
 91 Human cytomagalovi  
 92 Human cytomagalovi  
 93 Human cytomagalovi  
 94 Human cytomagalovi  
 95 Human myosin heavy  
 96 Human BlyS binding  
 97 Human BlyS binding  
 98 Human BlyS binding  
 99 Human BlyS binding  
 100 Human BlyS binding

## ALIGNMENTS

RESULT 1  
 AAW42101  
 ID AAW42101 standard; peptide; 9 AA.  
 XX AAW42101;  
 XX  
 DT 09-SEP-1998 (first entry)  
 XX  
 DE Colostrinin derived nanopptide.  
 XX  
 KW Colostrinin; nanopptide; NP; central nervous system; CNS;  
 KW neurological disorder; mental disorder; dementia; Alzheimer's disease;  
 KW motor neurone disease; Parkinson's disease; psychosis; neurosis;  
 KW immunological deficiency; cancer therapy; stimulant; modulator;  
 KW dietary supplement; cachexia; inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9814473-A1.  
 XX  
 XX 09-APR-1998.  
 XX  
 XX 03-OCT-1997; 97WO-GB02721.  
 XX  
 XX 03-OCT-1996; 96PL-0316416.  
 XX  
 XX (GEOR-) GEORGIADIS BIOTECH LTD.  
 XX (HRS-) HIRSZPFLD INST IMMUNOLOGY & EXPERIMENTAL.  
 XX  
 XX Dubowska-Inglot A, Janusz M, Lisowski J;  
 XX WPI; 1998-250967/22.  
 XX  
 XX Use of colostrinin, or derived nanopptide for treating chronic  
 XX diseases of the central nervous system - and immune system, also as  
 XX dietary supplement and for inhibiting development of Alzheimer's  
 XX disease  
 XX  
 XX Claim 51; Page 27; 34pp; English.  
 XX  
 XX This is the amino acid sequence of the colostrinin derived nanopptide  
 XX (NP). In the method of the invention colostrinin, and its NP are used  
 XX to treat chronic disorders of the central nervous system (CNS),  
 XX particularly neurological and mental disorders such as dementia  
 XX (Alzheimer's disease); motor neurone disease (e.g. Parkinson's disease);  
 XX psychosis and neurosis (including assisting withdrawal from addictive  
 XX drugs) and the immune system, particularly bacterial or viral infections  
 XX or acquired immunological deficiency (e.g. where caused by cancer  
 XX therapy). Colostrinin is a stimulant/modulator of the immune system and  
 XX may also be used as a dietary supplement, e.g. in babies who have not

CC received colostrinum, young children or adults being given chemotherapy or  
 CC suffering from cachexia due to chronic disease, and to inhibit  
 CC development of Alzheimer's disease.  
 XX  
 XX Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 9; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VESYVPLFP 9  
 Db 1 VESYVPLFP 9  
 RESULT 2  
 AAB72276  
 ID AAB72276 standard; peptide; 9 AA.  
 XX AAB72276;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 31.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 17-AUG-2000; 2000WO-US22818.  
 XX  
 XX 17-AUG-1999; 99US-0149311.  
 XX  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 XX  
 XX Inducing a cytokine and modulating an immune response, useful for  
 XX treating central nervous system diseases and bacterial and viral  
 XX infections, comprises administering colostrinin as an immunological  
 XX regulator -  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 XX  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 XX a proline rich polypeptide aggregate contained in colostrinum. The  
 XX peptides have immune response modulatory activity, and are capable of  
 XX inducing cytokines. Colostrinin and its derived peptides are useful for  
 XX inducing cytokine production, for modulating an immunological response  
 XX and for inducing blood cell proliferation. The peptides are useful in the  
 XX treatment of disorders of the central nervous system, neurological  
 XX disorders, mental disorders, dementia, neurodegenerative diseases,  
 XX Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 XX disorders of the immune system, bacterial and viral infections and  
 XX acquired immunological deficiencies.  
 XX  
 XX Sequence 9 AA;  
 XX  
 Query Match 100.0%; Score 9; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VESYVPLFP 9

Db 1 VESYVPLFP 9  
|||||

RESULT 3  
AAB72529  
ID AAB72529 standard; Peptide; 9 AA.

XX AC AAB72529;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #30.  
XX NW Dermatological; oxidative stress regulator; colostrinin.  
XX OS Unidentified.  
XX PN WO200112650-A2.

XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22665.  
XX PR 17-AUG-1999; 99US-0149310.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX DR WPI; 2001-218342/22.  
XX PT Modulating oxidative stress level in a cell, involves contacting the  
XX cell with an oxidative stress regulator selected from colostrinin, its  
XX constituent peptide, analog or their combinations -  
XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
XX stress level in a cell or a patient, comprising contacting the cell with,  
XX or administering to the patient, an oxidative stress regulator selected  
XX from colostrinin, or its constituent peptide (e.g. the present peptide),  
XX to change the level of an oxidizing species in the cell. The method can  
XX be used to treat oxidative damage to skin, by decreasing or preventing an  
XX increase in the level of damage to a biomolecule of the patient.  
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
|||||

Db 1 VESYVPLFP 9  
|||||

RESULT 4  
AAB72561  
ID AAB72561 standard; Peptide; 9 AA.

XX AC AAB72561;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #30.  
XX NW Neuroprotective; neural cell differentiation regulator; colostrinin;  
XX colostrinin.  
XX OS Unidentified.  
XX PN WO200112651-A2.

XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22774.  
XX PR 17-AUG-1999; 99US-0149633.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I;  
XX DR WPI; 2001-226545/23.  
XX DE Use of colostrinin, its constituent peptide or analog as a neural cell  
XX regulator, for promoting neural cell differentiation and treating  
XX damaged neural cells in a patient -  
XX PS Claim 6; Page 22; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell  
XX differentiation and treating damaged neural cells, using colostrinin and  
XX colostrinin constituent peptides (e.g. the present peptide) as a neural  
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
|||||

Db 1 VESYVPLFP 9  
|||||

RESULT 5  
AAE20258  
ID AAE20258 standard; peptide; 9 AA.

XX AC AAE20258;  
XX DT 18-JUN-2002 (first entry)  
XX DE Colostrinin constituent peptide #30.  
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX transplantation; implantation; dermatological; vulnery.

XX OS Unidentified.

XX PH Key Location/Qualifiers  
XX FT Modified-site 9  
XX FT /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.  
XX PF 17-AUG-2000; 2000WO-US22776.  
XX PR 17-AUG-2000; 2000WO-US22776.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX DR WPI; 2002-269151/31.

XX PT Composition useful for the modulation of blood cell proliferation in a  
XX patient comprises a blood cell regulator selected from colostrinin, its  
XX constituent peptide and/or analog -

XX Claim 6; Page 26; Sipp; English.

XX The invention relates to a composition which comprises a blood cell

CC regulator selected from colostrin, its constituent peptide and/or

CC analogue. The invention is used for modulating the oxidative stress

CC level in a cell e.g. mammalian or human cell present in a cell culture,

CC tissue, organ, or organism; or for treating oxidative damage to the skin

CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a

CC patient, enhancing wound healing, and the reduction of side effects of

CC cosmetic procedures. The method changes the level of an oxidising species

CC in the cell, such as decreases or prevents increase in the level of

CC damage to a biomolecule of the patient selected from DNA, protein and/or

CC lipid, compared to the same conditions when the oxidative stress

CC regulator is not present. The modulation of oxidative stress results in

CC enhanced repair, regeneration, and replacement of cells, tissues and

CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and

CC external organs), as well as enhanced preservation of such organs for

CC transplantation, implantation, or scientific research. The present

CC sequence is a colostrin constituent peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VESYVPLFP 9

Db 1 VESYVPLFP 9

|||||

RESULT 6

AA051067

ID AA051067 standard; Peptide; 9 AA.

XX AA051067;

XX 30-MAY-2002 (first entry)

XX Colostrin constituent peptide.

XX Colostrin; colostrum; beta-casein; human.

XX Homo sapiens.

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of

PT blood cell regulator selected from colostrin, its constituent peptide

PT and/or analogue -

XX Example 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrin constituent peptide

CC that has been classified as having a beta-casein homologue precursor.

CC The peptide has previously been identified as being useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis,

CC chronic disorders of the immune system, diseases with a bacterial

CC or viral aetiology, and acquired immunological deficiencies. The

CC present invention provides claimed colostrin constituted peptides

CC (see AM51036-66) that are useful as immunological regulators and

CC as blood cell regulators. These are used in claimed methods of the

CC invention to modulate specific or nonspecific immune responses in

CC patients, and to modulate cellular proliferation or differentiation

CC of blood cells, such as leucocytes. These methods specifically do

CC not use the present colostrin peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VESYVPLFP 9

Db 1 VESYVPLFP 9

|||||

RESULT 7

AA014607

ID AAO14607 standard; peptide; 9 AA.

XX AAO14607;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrin peptide 30.

XX Neural cell differentiation; neural cell regulator; colostrin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 9 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell

PT regulator selected from colostrin, its constituent peptide and/or

PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a

CC neural cell regulator (i.e. a colostrin peptide) in order to change the

CC cells in morphology to form neural cells. Colostrin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrin peptide used in

CC the method of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESYVPLFP 9  
 |||||  
 Db 1 VESYVPLFP 9

## RESULT 8

AAE07189  
 ID AAE07189 standard; peptide; 8 AA.

AC AAE07189;

DT 06-NOV-2001 (first entry)

DE Colostrinin peptide 5.

KW Colostrinin; neurotropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.

OS Unidentified.

FN WO200155199-A1.

PD 02-AUG-2001.

PF 26-JAN-2001; 2001WO-GB00329.

PR 26-JAN-2000; 2000GB-0001825.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

PS Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 5 related to the invention.

XX Sequence 8 AA;

XX Query Match 88.9%; Score 8; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYVPLFP 9  
 |||||  
 Db 1 ESYVPLFP 8

## RESULT 9

AAE07199  
 ID AAE07199 standard; peptide; 9 AA.

XX AAE07199;

DT 06-NOV-2001 (first entry)

DE Modified colostrinin cyclic peptide #5.

KW Colostrinin; neurotropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.

OS Synthetic.

FN Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic

FT linkage with Pro found at the C-terminal end"

XX WO200155199-A1.

PD 02-AUG-2001.

PF 26-JAN-2001; 2001WO-GB00329.

PR 26-JAN-2000; 2000GB-0001825.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

PS Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is modified colostrinin cyclic peptide #5 related to  
 CC the invention.

```

XX SQ Sequence 9 AA;
Query Match      88.9%; Score 8; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYVPLFP 9
Db 2 ESYVPLFP 9
|||||

RESULT 10
AAB98131
ID AAB98131 standard; Peptide; 15 AA.
XX AC AAB98131;
XX DT 17-AUG-2001 (first entry)
XX DE Interferon-gamma stimulation gp100 derived peptide 1366.
XX DX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
XX KW modified gp100; vaccine; gene therapy; cancer.
XX OS Homo sapiens.
XX PN WO200130847-A1.
XX PD 03-MAY-2001.
XX PF 20-OCT-2000; 2000WO-CA01254.
XX PR 22-OCT-1999; 99US-0160879.
XX PR 07-AUG-2000; 2000US-0223325.
XX PA (AVET ) AVENTIS PASTEUR LTD.
XX PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
XX DR WPI; 2001-316326/33.
XX PT New isolated and purified gp100 useful for the prophylactic treatment
XX PS of cancer -
XX PS Example 4; Page 61; 89pp; English.
XX CC The present invention describes an isolated and purified modified gp100
XX CC molecule (gp100M) capable of modulating an immune response in an animal.
XX CC gp100M has cytostatic activity and can be used in vaccine production and
XX CC gene therapy. Nucleic acids and proteins of the invention are useful as
XX CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
XX CC AAH98098 to AAB98206 represent sequence used in the exemplification of
XX CC the present invention. More specifically AAB98098 to AAB98205 represent
XX CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
XX CC AAH22106 represent primers used in the present invention; AAH22099
XX CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
XX CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
XX CC gp100M protein given in AAB22106.
XX SQ Sequence 15 AA;
Query Match      55.6%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7
Db 6 SYVPL 10
|||||

RESULT 12
AAB98133
ID AAB98133 standard; Peptide; 15 AA.
XX AC AAB98133;
XX DX 17-AUG-2001 (first entry)
XX DE Interferon-gamma stimulation gp100 derived peptide 1366.
XX DX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
XX KW modified gp100; vaccine; gene therapy; cancer.
XX OS Homo sapiens.
XX PN WO200130847-A1.

```

XX PD 03-MAY-2001.  
 XX PF 20-OCT-2000; 2000WO-CA01254.  
 XX PR 22-OCT-1999; 99US-0160879.  
 XX PR 07-AUG-2000; 2000US-0223325.  
 XX PA (AVET ) AVENTIS PASTEUR LTD.  
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B, Tine JA;  
 XX PI WPI; 2001-316326/33.  
 XX DR New isolated and purified gp100 useful for the prophylactic treatment  
 XX PT of cancer -  
 XX PS Example 4; Page 61; 89pp; English.  
 XX CC The present invention describes an isolated and purified modified gp100  
 XX CC molecule (gp100M) capable of modulating an immune response in an animal.  
 XX CC gp100M has cytostatic activity and can be used in vaccine production and  
 XX CC gene therapy. Nucleic acids and proteins of the invention are useful as  
 XX CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and  
 XX CC AAB98098 to AAB98206 represent sequence used in the exemplification of  
 XX CC the present invention. More specifically AAB98098 to AAB98205 represent  
 XX CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to  
 XX CC AAH22106 represent primers used in the present invention; AAH22099  
 XX CC represents the plasmid nucleotide sequence comprising the Vaccinia virus  
 XX CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human  
 XX CC gp100M protein given in AAB22106.  
 XX SQ Sequence 15 AA;  
 Query Match 55.6%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SYVPL 7  
 DB 1 SYVPL 5  
 RESULT 13  
 AAB97741  
 ID AAB97741 standard; Peptide; 15 AA.  
 XX AC AAB97741;  
 XX DT 08-AUG-2001 (first entry)  
 XX DE gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:34.  
 XX KW Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;  
 XX KW tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;  
 XX KW cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.  
 XX OS Virus.  
 XX OS Synthetic.  
 XX PN WO200130382-A1.  
 XX PD 03-MAY-2001.  
 XX PF 20-OCT-2000; 2000WO-CA01253.  
 XX PR 22-OCT-1999; 99US-0160879.  
 XX PR 07-AUG-2000; 2000US-0223325.  
 XX PA (AVET ) AVENTIS PASTEUR LTD.  
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B;  
 XX PI WPI; 2001-308587/32.  
 XX DR Inducing immune response to tumor antigen, useful in immunotherapy of  
 XX PT cancer, by administering the antigen to a lymphatic site -

DR WPI; 2001-308587/32.  
 XX Inducing immune response to tumor antigen, useful in immunotherapy of  
 XX PT cancer, by administering the antigen to a lymphatic site -  
 XX PS Example 1; Page 39; 60pp; English.  
 XX CC The present invention describes a method for inducing an immune response,  
 XX CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or  
 XX CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys  
 XX CC (Macaca fascicularis) were injected with a modified form of gp100 antigen  
 XX CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals  
 XX CC of (a) developed a cell-mediated response (indicated by production of  
 XX CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but  
 XX CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far  
 XX CC greater antibody response to gp100. The method is used in immunotherapy  
 XX CC of a wide range of cancers through induction of a specific immune  
 XX CC response (humoral and cellular) against the tumour antigens. When  
 XX CC administered to a lymphatic site, Ag (or (I)) induces a stronger immune  
 XX CC response than administration by other routes and may also break tolerance  
 XX CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to  
 XX CC AAB97815 represent peptides derived from gp100 which stimulate interferon  
 XX CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given  
 XX CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)  
 XX CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen  
 XX CC peptide, all of which are used in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 15 AA;  
 Query Match 55.6%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SYVPL 7  
 DB 11 SYVPL 15  
 RESULT 14  
 AAB97742  
 ID AAB97742 standard; Peptide; 15 AA.  
 XX AC AAB97742;  
 XX DT 08-AUG-2001 (first entry)  
 XX DE gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:35.  
 XX KW Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;  
 XX KW tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;  
 XX KW cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.  
 XX OS Virus.  
 XX OS Synthetic.  
 XX PN WO200130382-A1.  
 XX PD 03-MAY-2001.  
 XX PF 20-OCT-2000; 2000WO-CA01253.  
 XX PR 22-OCT-1999; 99US-0160879.  
 XX PR 07-AUG-2000; 2000US-0223325.  
 XX PA (AVET ) AVENTIS PASTEUR LTD.  
 XX PI BerinSTEIN N, Tartaglia J, Moingeon P, Barber B;  
 XX PI WPI; 2001-308587/32.  
 XX DR Inducing immune response to tumor antigen, useful in immunotherapy of  
 XX PT cancer, by administering the antigen to a lymphatic site -

XX Example 1; Page 39; 60pp; English.

XX The present invention describes a method for inducing an immune response,

XX in an animal, to a tumour antigen (Ag) comprising administering Ag, or

XX nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys

XX (Macaca fascicularis) were injected with a modified form of gp100 antigen

XX (a) into the left inguinal lymph node or (b) subcutaneously. Both animals

XX of (a) developed a cell-mediated response (indicated by production of

XX interferon-gamma from T lymphocytes when exposed to gp100 peptides), but

XX only 2 of 4 animals of (b) did so. Also animals in (a) produced a far

XX greater antibody response to gp100. The method is used in immunotherapy

XX of a wide range of cancers through induction of a specific immune

XX response (humoral and cellular) against the tumour antigens. When

XX administered to a lymphatic site, Ag (or I) induces a stronger immune

XX response than administration by other routes and may also break tolerance

XX to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to

XX to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to

XX AAB97815 represent peptides derived from gp100 which stimulate interferon

XX (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given

XX in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)

XX protein given in AAB97817; and AAB97818 represents a CEA modified antigen

XX peptide, all of which are used in the exemplification of the present

XX invention.

XX Sequence 15 AA;

SQ Query Match 55.6%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVPL 7

Db |||||

6 SYVPL 10

RESULT 15

AAB97743

ID AAB97743 standard; Peptide; 15 AA.

XX AC AAB97743;

XX 08-AUG-2001 (first entry)

XX gp100 derived IFN-gamma production stimulation peptide SEQ ID NO:36.

XX Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;

XX tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;

XX cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.

XX Virus.

XX Synthetic.

XX WO200130382-A1.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-CA01253.

XX 22-OCT-1999; 99US-0160879.

XX 07-AUG-2000; 2000US-0223325.

XX (AVET ) AVENTIS PASTEUR LTD.

XX Berinstein N, Tartaglia J, Moingeon P, Barber B;

XX WPI; 2001-308587/32.

XX Inducing immune response to tumor antigen, useful in immunotherapy of

XX cancer, by administering the antigen to a lymphatic site -

XX Example 1; Page 39; 60pp; English.

XX The present invention describes a method for inducing an immune response,

CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or

CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys

CC (Macaca fascicularis) were injected with a modified form of gp100 antigen

CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals

CC of (a) developed a cell-mediated response (indicated by production of

CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but

CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far

CC greater antibody response to gp100. The method is used in immunotherapy

CC of a wide range of cancers through induction of a specific immune

CC response (humoral and cellular) against the tumour antigens. When

CC administered to a lymphatic site, Ag (or I) induces a stronger immune

CC response than administration by other routes and may also break tolerance

CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to

CC AAB97815 represent peptides derived from gp100 which stimulate interferon

CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given

CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)

CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen

CC peptide, all of which are used in the exemplification of the present

CC invention.

XX Sequence 15 AA;

SQ Query Match 55.6%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVPL 7

Db |||||

1 SYVPL 5

RESULT 16

ABP46299

ID ABP46299 standard; peptide; 15 AA.

XX AC ABP46299;

XX 19-AUG-2002 (first entry)

XX Human BlyS binding scFv VH CDR3 SEQ ID 2310.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

XX the diagnosis and treatment of cancers and immune disorders -

XX Claim 2; Page 2968; 3149pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS  
 CC and so may be used to detect and quantitate the presence of BLYS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLYS. They may also be  
 CC administered to treat diseases associated with aberrant BLYS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 15 AA;

Query Match 55.6%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7  
 Db 8 SYVPL 12

RESULT 17  
 ABP46252  
 ID ABP46252 standard; peptide; 16 AA.  
 XX  
 AC ABP46252;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human BLYS binding scFv VH CDR3 SEQ ID 2263.

BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX

(HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR

Antibodies against B lymphocyte stimulating polypeptides, useful for  
 the diagnosis and treatment of cancers and immune disorders -  
 Claim 2; Page 2960; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS  
 CC and so may be used to detect and quantitate the presence of BLYS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLYS. They may also be  
 CC administered to treat diseases associated with aberrant BLYS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 16 AA;

Query Match 55.6%; Score 5; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVPL 7  
 Db 8 SYVPL 12

RESULT 18  
 AAR12158  
 ID AAR12158 standard; peptide; 7 AA.  
 XX  
 AC AAR12158;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 05-AUG-1991 (first entry)  
 XX  
 DE Cyclo-octa peptide, hymenistatin.

KW Tumour growth inhibitor; cyclic.  
 XX  
 OS Hymeniadon sp.

PN EP430538-A.  
 XX  
 PD 05-JUN-1991.  
 XX  
 PF 20-NOV-1990; 90EP-0312606.  
 XX  
 PR 30-NOV-1989; 89US-0443882.  
 XX  
 PA (UYAR-) UNIV ARIZONA STATE.  
 PA (YUAR-) ARIZONA BOARD REGEN.

PI Pettitt GR;  
 XX  
 XX WPI; 1991-166026/23.

New cyclo-octa peptide, hymenistatin - having inhibiting tumour  
 growth activity e.g. against national cancer institute P-388  
 leukaemia cell line.

PS Claim 1; Page 8; 10pp; English.

XX The cpd., isolated from South Pacific sponge, is active as a  
 CC tumour growth inhibitor against P388 murine leukaemia cell line  
 CC (ED50 = 3.5ug/ml). The peptide sequence was determined by -NOE  
 CC expts. and FAB ms/ms.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;



```

Query Match          44.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
Db 2 YVPL 5

RESULT 19
AAW46013
ID AAW46013 standard; peptide; 7 AA.
XX
AC AAW46013;
XX
DT 03-JUL-1998 (first entry)
XX
DE Peptide #45 based on human SSTR 5 (residues 1-7).
XX
KW Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
KW insulin-like growth factor binding protein; ILGFBP; SSTR; diabetes;
KW somatostatin receptor; insulin-like growth factor.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9744352-A1.
XX
PD 27-NOV-1997.
XX
PF 22-MAY-1997; 97WO-AU00312.
XX
PR 22-MAY-1996; 96AU-0009990.
XX
PA (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
XX
PI Gerraty NL, Kingston DU, Westbrook SL;
XX
DR WPI; 1998-018427/02.
XX
PT New non-naturally occurring peptide(s) - which are based on portions
PT of somatostatin, somatostatin receptors and insulin-like growth
PT factor binding protein
XX
PS Disclosure; Page 9; 136pp; English.
XX
CC Peptides AAW45983-W456025 are based on portions of somatostatin,
CC somatostatin receptors (SSTR) and insulin-like growth factor binding
CC proteins (IGFBP). They are capable of increasing weight gain, birth
CC weight, growth rates, milk production, levels of circulating insulin,
CC IGF-I and IGF-III, fibre production and muscle weight. They may be used
CC to modulate carbohydrate metabolism and in treatment of diabetes. The
CC oil carrier may be used for delivery of the peptides.
XX
SQ Sequence 7 AA;

Query Match          44.4%; Score 4; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
    ||||
Db 3 PLFP 6

RESULT 20
AAV17016
ID AAV17016 standard; peptide; 7 AA.
XX
AC AAV17016;
XX
DT 20-JUL-1999 (first entry)
XX

```

```

DE Heat shock protein (hsp) binding peptide.
XX
KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
KW acquired immune deficiency; autoimmune disease.
XX
OS Synthetic.
XX
PN WO922761-A1.
XX
PD 14-MAY-1999.
XX
PF 22-OCT-1998; 98WO-US22335.
XX
PR 31-OCT-1997; 97US-0961707.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
PI Querfelli O, Rothman JE;
XX
DR WPI; 1999-313177/26.
XX
PT Identifying peptides which bind heat shock proteins
XX
PS Examples; Page 24; 155pp; English.
XX
CC The invention relates to conjugate peptides engineered to noncovalently
CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
CC peptide comprises (a) contacting a phage display library having
CC bacteriophage expressing, in a surface protein, inserted peptides with a
CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
CC physiologic binding buffer; (b) isolating a phage binding to the hsp
CC target; and (c) identifying the inserted peptide expressed. The peptides
CC which bind to a hsp can be used as tethering peptides for a hsp which may
CC serve as an accessory in a chaperone process and/or may comprise a
CC cytokine. They can also be coupled to antigens to induce an immune
CC response. Such compositions can be used for treating neoplastic disease,
CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
CC disease of the immune system, e.g. acquired immune deficiencies or
CC autoimmune diseases.
XX
SQ Sequence 7 AA;

Query Match          44.4%; Score 4; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
Db 2 YVPL 5

RESULT 21
AAU72158
ID AAU72158 standard; Peptide; 7 AA.
XX
AC AAU72158;
XX
DT 26-FEB-2002 (first entry)
XX
DE Melanoma antigen, javelin peptide #144.
XX
KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;
KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
KW javelin molecule; melanoma antigen recognised by T cells-1; human.
XX
OS Bacteriophage M13.
XX
PN WO200178655-A2.

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XX PD 25-OCT-2001.  
 XX PF 17-APR-2001; 2001WO-US12449.  
 XX PR 17-APR-2000; 2000US-197462P.  
 XX PA (HOUG//) HOUGHTON A.  
 XX PA (LIVI//) LIVINGSTON P.  
 XX PA (ALAW//) AL-AWOATI Q.  
 XX PA (MAYH//) MAYHEW M.  
 XX PA (HOEM//) HOE M.  
 XX PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;  
 XX DR WPI; 2001-663092/76.  
 XX PT Anti cancer vaccine for the treatment of melanoma comprises a heat  
 XX PT shock protein and a melanoma antigen i.e. tyrosinase -  
 XX PS Disclosure; Page 19; 150pp; English.  
 XX CC The invention relates to a method of induction of an immune response,  
 XX CC comprising administration of an immunotherapeutic composition, comprising  
 XX CC a heat shock protein, and a melanoma antigen, where the melanoma  
 XX CC antigen is selected from tyrosinase, tyrosinase related protein 1,  
 XX CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,  
 XX CC NYEs01, MART antigens, GM2, antigenic portions and combinations of these.  
 XX CC The melanoma antigen is covalently bound to a javelin molecule, where the  
 XX CC melanoma antigen bound to the javelin molecule is non-covalently bound to  
 XX CC the heat shock protein. The composition is useful for inducing an immune  
 XX CC response for the treatment of melanoma. AAU71980-AAU72481 represent  
 XX CC melanoma antigen peptides of the invention.  
 XX SQ Sequence 7 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YVPL 7  
 DB 2 YVPL 5  
 RESULT 22  
 AAU80708  
 ID AAU80708 standard; peptide; 7 AA.  
 AC AAU80708;  
 DT 26-MAR-2002 (first entry)  
 DE Javelin peptide #138 for conjugation to multi-component viral particles.  
 XX Immunogenic complex; non-pathogenic multi-component viral particles;  
 KW javelin; heat shock protein; humoral immunity; cellular immunity;  
 KW anti-viral immune response; viral infection; hepatitis; influenza;  
 KW mumps; HIV infection; human immunodeficiency virus; polio;  
 KW tick-borne encephalitis; ebola virus infection.  
 XX Synthetic.  
 OS  
 PN WO200178772-A1.  
 XX  
 XX PD 25-OCT-2001.  
 XX PF 17-APR-2001; 2001WO-US12568.  
 XX PR 17-APR-2000; 2000US-197462P.  
 XX PA (MOJA-) MOJAVE THERAPEUTICS INC.

PI Hoe M, Landsberger F;  
 XX WPI; 2002-049177/06.  
 XX PT New heat shock protein-based viral vaccines, useful for enhancing  
 XX PT anti-viral immune response in an organism, particularly as a vaccine  
 XX PT for preventing or ameliorating viral infections, e.g. hepatitis,  
 XX PT influenza or HIV infection -  
 XX PS Disclosure; Page 13; 75pp; English.  
 XX CC The present invention relates to the use of an immunogenic complex,  
 XX CC comprising a non-pathogenic multi-component viral particle covalently  
 XX CC linked to a javelin molecule (preferably a peptide) that selectively  
 XX CC binds to a heat shock protein. The immunogenic complex is useful for  
 XX CC inducing both humoral and cellular immunity, especially for enhancing  
 XX CC the anti-viral immune response, in a human or non-human subject. The  
 XX CC immunogenic complex is particularly useful as a vaccine for preventing  
 XX CC or ameliorating viral infections, e.g. hepatitis, influenza, mumps,  
 XX CC HIV (human immunodeficiency virus) infection, polio, tick-borne  
 XX CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent  
 XX CC javelin peptides which may be covalently conjugated to multi-component  
 XX CC viral particles.  
 XX SQ Sequence 7 AA;  
 Query Match 44.4%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YVPL 7  
 DB 2 YVPL 5  
 RESULT 23  
 AAR58322  
 ID AAR58322 standard; peptide; 8 AA.  
 XX AAR58322;  
 AC AAR58322;  
 DT 22-SEP-1994 (first entry)  
 DE Hypotensive polypeptide.  
 XX Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 KW Lactobacillus helveticus.  
 OS  
 PN JP06041191-A.  
 XX  
 XX PD 15-FEB-1994.  
 XX PF 03-MAR-1993; 93JP-0043047.  
 XX PR 04-MAR-1992; 92JP-0047340.  
 XX (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 PA  
 XX WPI; 1994-089332/11.  
 XX New polypeptide - used in physiologically active agents having  
 XX e.g. hypotensive antioxidative and calcium absorption promoting  
 XX activity  
 XX Claim 1-2; Page 7; 10pp; Japanese.  
 XX Sequences (AAR58319-341) are used in conjunction with  
 XX physiologically active agents showing a property such as  
 XX hypotensive activity, calcium absorption promoting activity and  
 XX antioxidative activity. The peptides are non-toxic and can be  
 XX used in physiologically active agents.

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XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
DB 5 YVPL 8

RESULT 24
AA116845
ID AAY16845 standard; peptide; 8 AA.
AC AAY16845;
XX
XX DT 20-JUL-1999 (first entry)
XX DE
XX DE Heat shock protein (hsp) binding peptide.
XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
XX KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
XX KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
XX KW acquired immune deficiency; autoimmune disease.
XX OS Synthetic.
XX PN WO9922761-AL.
XX PD 14-MAY-1999.
XX PF 22-OCT-1998; 98WO-US22335.
XX PR 31-OCT-1997; 97US-0961707.
XX PS (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;
XX PI Querfelli O, Rothman JE;
XX DR WPI; 1999-313177/26.
XX DR N-PSDB; AAXG0745.
XX PT Identifying peptides which bind heat shock proteins
XX PS Disclosure; Fig 2H; 155pp; English.
XX CC The invention relates to conjugate peptides engineered to noncovalently
XX CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
XX CC peptide comprises (a) contacting a phage display library having
XX CC bacteriophage expressing, in a surface protein, inserted peptides with a
XX CC hsp target, and bound to a benzquinone ansamycin antibiotic (BAA), in a
XX CC physiologic binding buffer; (b) isolating a phage binding to the hsp
XX CC target; and (c) identifying the inserted peptide expressed. The peptides
XX CC which bind to a hsp can be used as tethering peptides for a hsp which may
XX CC serve as an accessory in a chaperone process and/or may comprise a
XX CC cytokine. They can also be coupled to antigens to induce an immune
XX CC response. Such compositions can be used for treating neoplastic disease,
XX CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
XX CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
XX CC disease of the immune system, e.g. acquired immune deficiencies or
XX CC autoimmune diseases.
XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
    ||||
DB 5 YVPL 8

RESULT 25
ABB04380
ID ABB04380 standard; peptide; 8 AA.
XX
XX AC ABB04380;
XX DT 02-MAY-2002 (first entry)
XX DE
XX DE Carrot partial antifreeze peptide D.
XX KW Carrot; frozen food; anti-freeze peptide; AFP; confectionery; ice-cream;
XX KW Daucus carota; Autumn King.
XX OS Daucus carota.
XX PN WO9822591-A2.
XX PD 28-MAY-1998.
XX PF 06-NOV-1997; 97WO-EP06181.
XX PR 19-NOV-1996; 96EP-0308362.
XX PS (UNIL ) UNILEVER NV.
XX PS (UNIL ) UNILEVER PLC.
XX PI Byass LJ, Doucet CJ, Fenn RA, McArthur AJ, Sidebottom CM;
XX PI Smallwood WF, Warrell D;
XX DR WPI; 2001-227110/08.
XX PT Frozen food product mfg. process - using anti-freeze peptides to
XX PT produce specific elongated ice crystals with desirable ice
XX PT recrystallisation properties and relatively hard and brittle texture
XX PS Example 6; Page 25; 37pp; English.
XX CC The invention relates to a process for the production of a frozen food
XX CC product comprising anti-freeze peptides (AFP), where the conditions are
XX CC chosen so that the ice crystals in the product have an aspect ratio of
XX CC 1.9 or greater. The process is used for preparing frozen confectionery
XX CC products and ice-cream mixes. The present sequence is part of a peptide
XX CC with antifreeze properties isolated from carrot (Daucus carota, cultivar
XX CC Autumn King).
XX SQ Sequence 8 AA;
Query Match 44.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YVPL 8
    ||||
DB 3 YVPL 6

RESULT 26
AAB20475
ID AAB20475 standard; Peptide; 8 AA.
XX
XX AC AAB20475;
XX DT 21-JUN-2001 (first entry)
XX DE
XX DE Mouse contactin precursor peptide isolated in database screening.
XX KW Contactin; mouse; PSK; seizure related protein; epilepsy;
XX KW neurological disorder; diagnosis; therapy.
XX OS Mus sp.

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XX PN WO200125268-A1.  
 XX PD 12-APR-2001.  
 XX PF 04-OCT-2000; 2000WO-DK00556.  
 XX PR 04-OCT-1999; 99DK-0001420.  
 XX PA (SCHR/) SCHROTZ-KING P.  
 XX PA (KING/) KING A.  
 XX PA (MANN/) MANN M.  
 XX PA (ANDE/) ANDERSEN J.  
 XX PA (KUES/) KUESTER B.  
 XX PI Schrotz-King P, King A, Mann M, Andersen J, Kuester B;  
 XX DR WPI; 2001-290605/30.  
 XX PT Novel human seizure related proteins useful for controlling epileptic  
 PT seizures and neurological disorders, and for identifying potential drug  
 PT targets for use in diagnosis and/or prognosis of neurological disorders  
 PT  
 XX PS Disclosure; Page 59; 150pp; English.  
 XX CC The present sequence is that of a mouse contactin precursor peptide  
 CC identified during a proteomics screening approach for membrane  
 CC receptors in the brain. 9 proteins from an RP-HPLC preparation  
 CC from the mouse E16 brain plasma membrane were analyzed by  
 CC nanoelectrospray tandem mass spectrometry. Peptide sequences were  
 CC found by searching NRDB or EST databases with peptide sequence tags.  
 CC Sample 9 was identified as contactin. Sample 7 was novel, and named  
 CC PSK-1. Human PSKs (see AAB20446-48) were subsequently identified.  
 CC These are novel transmembrane receptor or secreted proteins that  
 CC are potentially involved in the control or generation of seizures  
 CC such as epileptic seizures or other neurological disorders.  
 CC PSK-1, -2 and -3 polynucleotides and polypeptides can be used to  
 CC identify potential drug targets. They can also be used in the  
 CC diagnosis of seizure related conditions or other neurodegeneration  
 CC such as Alzheimer, Rasmussen's Encephalitis, Parkinson's disease,  
 CC multiple sclerosis, cerebrovascular disorders (stroke syndromes),  
 CC like ischaemia, Huntington's disease or schizophrenia (claimed),  
 CC and in the treatment of conditions caused by PSK upregulation,  
 CC deficiency or impaired function.  
 XX SQ Sequence 8 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VESY 4  
 ||||  
 Db 2 VESY 5  
 RESULT 27  
 ABG78590  
 ID ABG78590 standard; Peptide; 8 AA.  
 XX AC ABG78590;  
 XX DT 29-NOV-2002 (first entry)  
 XX DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #78.  
 XX KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;  
 KW human; multiple sclerosis-associated protein isoform; MSPI;  
 KW antiinflammatory; neuroprotective.  
 XX OS Homo sapiens.  
 XX

PN WO200259604-A2.  
 XX PD 01-AUG-2002.  
 XX PF 25-JAN-2002; 2002WO-GB00330.  
 XX PR 26-JAN-2001; 2001US-264404P.  
 XX PR 20-NOV-2001; 2001US-331647P.  
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX PI Herath HMAc, Perekh RB, Rohlf C;  
 XX DR WPI; 2002-599812/64.  
 XX PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.  
 PT determining the stage or severity of MS, comprises detecting the  
 PT presence of MS-associated features or protein isoforms by 2-dimensional  
 PT electrophoresis -  
 XX PS Disclosure; Page 22; 128pp; English.  
 XX CC This invention relates to a novel method for screening or diagnosing  
 CC multiple sclerosis (MS) in a subject to determine the stage or severity  
 CC of MS, to identify a subject at risk of developing MS or to monitor the  
 CC effect of a therapy administered. The method comprises analysing a  
 CC sample body fluid from the subject by two-dimensional electrophoresis  
 CC and detecting the presence of multiple sclerosis-associated features  
 CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).  
 CC The MSF's of the invention correspond to spots identified on a 2D gel  
 CC these proteins may have antiinflammatory or neuroprotective activity.  
 CC The methods of the invention and the compositions are useful for  
 CC clinical screening, diagnosis and treatment of MS, for monitoring the  
 CC effectiveness of MS treatment, for selecting participants in clinical  
 CC trials, for identifying patients most likely to respond to a particular  
 CC therapeutic treatment and for screening and developing drugs for  
 CC treatment of MS. Agents that modulate the expression or activity of an  
 CC MSPI are useful for treating MS, for preventing or delaying the onset or  
 CC development of MS, to prevent or delay the progression of MS, or to  
 CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding  
 CC an MSPI, MSPI-related polypeptide, or their fragments are useful for  
 CC promoting MSPI function by gene therapy. The present sequence represents  
 CC a human multiple sclerosis associated feature tryptic digest  
 CC peptide of the invention.  
 XX SQ Sequence 8 AA;  
 Query Match 44.4%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VESY 4  
 ||||  
 Db 2 VESY 5  
 RESULT 28  
 ABJ20030  
 ID ABJ20030 standard; Peptide; 8 AA.  
 XX AC ABJ20030;  
 XX DT 10-APR-2003 (first entry)  
 XX DE MHC binding peptide SEQ ID No 195.  
 XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.  
 XX OS Synthetic.

XX PN WO200294981-A2.  
 XX PD 28-NOV-2002.  
 XX PF 16-MAY-2002; 2002WO-IL00383.  
 XX PR 16-MAY-2001; 2001US-230959P.  
 XX PR 29-MAY-2001; 2001US-0865548.  
 XX PA (TECR ) TECHNION RES & DEV FOUND LTD.  
 XX PI Barnea E, Beer I, Ziv T, Admon A, Daseau L, Buchsbaum S;  
 XX WPI; 2003-210043/20.  
 XX PT Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -  
 XX Claim 37; Page 194; 238pp; English.  
 XX CC The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
 CC sequences of the invention may be used in a gene therapy application.  
 CC This sequence represents a peptide relating to the method for identifying  
 CC MHC binding peptides of the invention.  
 XX SQ Sequence 8 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 YVPL 7  
 Db ||||  
 4 YVPL 7  
 RESULT 29  
 AAR46514  
 ID AAR46514 standard; peptide; 9 AA.  
 XX AC AAR46514;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 30-MAR-1994 (first entry)  
 XX DE Plasmodium yoelii CSP residues 276-288.  
 XX KW Vaccine; polar lipid; targeting; immune response; antigenic  
 KW peptide; antigen; circumsporozoite protein.  
 XX OS Synthetic.  
 XX PN US5256641-A.  
 XX PD 26-OCT-1993.  
 XX PF 09-JUL-1992; 92US-0911209.  
 XX PR 01-NOV-1990; 90US-0607982.  
 XX PA (OREG-) STATE OF OREGON.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.

XX PI Malkovsky M, Stowell MHB, Yatvin MB, Mcclard RW;  
 XX PI Parks DW, Wittejf;  
 XX WPI; 1993-350862/44.  
 XX PT New covalent conjugate of antigenic peptide and polar lipid e.g.  
 PT sphingosine - useful in protective vaccines, treatment of  
 PT auto-immune disease and preventing of transplant rejection  
 XX PS Disclosure; Page 13; 15pp; English.  
 XX CC The peptide is an example of an antigenic peptide which may be  
 CC joined via a functional linker group, opt. at the two ends of a  
 CC spacer group, to a polar lipid carrier, e.g. sphingosine, ceramide,  
 CC phosphatidyl choline, ethanolamine, inositol or serine, cardiolipin  
 CC or phosphatidic acid. The compsn. may be used as a vaccine against  
 CC Plasmodium (malaria) infection. An advantage of the system is that  
 CC when incorporated into the compsn. entry of the antigenic peptide into  
 CC the cells of the immune system is facilitated (no need for endocytosis)  
 CC and targeting to specific organelles becomes possible. Unlike known  
 CC vaccines, intracellular synthesis of viral antigens is not necessary  
 CC for presentation via the MHC class I antigen pathway, nor intracellular  
 CC proteolysis for presentation via the MHC class II antigen pathway, so  
 CC both humoral and cellular immunity is achieved. Also, when a spacer is  
 CC present, the antigen release rate may be controlled.  
 CC See also AAR46507-47  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 SYVP 6  
 Db ||||  
 1 SYVP 4  
 RESULT 30  
 AAW68359  
 ID AAW68359 standard; peptide; 9 AA.  
 XX AC AAW68359;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 14-OCT-1998 (first entry)  
 XX DE MHC binding peptide CSP 276-288.  
 XX KW Antigen; major histocompatibility complex; MHC; lymphocyte; detection;  
 KW immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma;  
 XX KW viral infection.  
 XX OS Synthetic.  
 OS Plasmodium yoelii.  
 XX PN WO9744667-A2.  
 XX PD 27-NOV-1997.  
 XX PF 21-MAY-1997; 97WO-FR00892.  
 XX PR 21-MAY-1996; 96US-0651925.  
 XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR.  
 XX PI Langladedemoyen P, Lone Y, Kourilsky P, Abastado J;  
 XX WPI; 1998-018653/02.  
 DR

CC	as active ingredient; (2) a DNA encoding (1); (3) an expression vector
CC	containing the DNA of (2); and (4) a transformant which can retain the
CC	expression vector of (3). (1) has cytostatic, immunostimulant and
CC	protooncogene activities, and can be used as a cellular immune response
CC	inducer. The protein is useful as an active ingredient for drug
CC	compositions in preventing and/or treating infectious diseases such as
CC	malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC	The present sequence represents a specifically claimed CTL epitope
CC	for use in a fused protein of the present invention.
XX	
SQ	Sequence 9 AA;
	Query Match 44.4%; Score 4; DB 21; Length 9;
	Best Local Similarity 100.0%; Pred.No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	3 SVYP 6
DB	1 SVYP 4
RESULT 32	
AAAY96361	
ID	AAAY96361 standard; peptide; 9 AA.
XX	AAAY96361;
AC	
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	HLA-A24 binding peptide hTERT T1088.
XX	
XX	hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer
XX	human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine
KW	major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy
XX	
XX	Homo sapiens.
OS	
XX	WO200025813-A1.
PN	
XX	
PD	11-MAY-2000.
XX	
PF	29-OCT-1999; 99WO-US25438.
XX	
PR	29-OCT-1998; 98US-0106106.
XX	
XX	(DAND ) DANA FARBER CANCER INST INC.
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX	
PI	Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
XX	
DR	WPI; 2000-365402/31.
XX	
PT	Universal tumor-associated antigens such as telomerase catalytic
PT	subunit capable of binding major histocompatibility complex molecule
PT	useful for diagnosis, prevention and treatment of cancer
XX	
PS	Disclosure; Page 74; 136pp; English.
XX	
CC	Human telomerase complex reverse transcriptase (hTERT) is expressed in
CC	more than 85 percent of human cancers. hTERT is useful as a universal
CC	tumour-associated antigen (TAA) that binds to a major histocompatibility
CC	complex molecule (MHC). hTERT peptides were analyzed for the ability to
CC	bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
CC	lymphocytes (CTL) were then generated that kill a cell expressing hTERT
CC	or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
CC	Antigen-presenting cells (APC) were also generated ex vivo for
CC	presentation of a TAA peptide or hTERT. The APC can be used to activate
CC	CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
CC	CTL are useful for cancer immunotherapy. Measuring the level of CTL in
CC	sample is useful for assessing the level of immunity of a patient to a
CC	TAA or a peptide, where the sample is obtained before or after a cancer
CC	treatment is given to the patient. TAA peptides (e.g. hTERT) are also
CC	useful for diagnosis and prophylactic treatment of cancer.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
|  
|  
|  
Db 2 YVPL 5

## RESULT 33

AA96776  
ID AAY86776 standard; Peptide; 9 AA.

AC AAY86776;  
XX 05-MAY-2000 (first entry)  
DT Telomerase peptide #191.  
DE  
XX Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;  
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;  
KW telomerase T lymphocyte.  
XX Homo sapiens.

OS WO200002581-A1.  
PN 20-JAN-2000.  
XX 30-JUN-1999; 99WO-NO00220.  
XX 08-JUL-1998; 98NO-0003141.  
XX (NH9D ) NORSK HYDRO AS.

PA Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;  
PI Saeboe-Larsen S;  
XX WPI: 2000-145727/13.  
XX Protein or peptide fragments useful in the treatment and prophylaxis of  
PT cancer in mammals -  
PS Claim 12; Page 35; 53pp; English.

CC This sequence represents a telomerase peptide of the invention, and can  
CC be used in a method for the treatment or prophylaxis of cancer. The  
CC sequences are useful in the treatment or prophylaxis of cancer  
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or  
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary  
CC tract carcinomas. They are useful for generating telomerase T lymphocytes  
CC capable of recognising and destroying tumour cells in a mammal,  
CC comprising culturing T lymphocytes obtained from the mammal with the  
CC peptides. Telomerase protein is expressed only by tumour cells, hence,  
CC other body cells are not targeted or destroyed by telomerase specific T  
CC cells.  
CC Note: This sequence was indexed from WO200002581, which is the first  
CC major country equivalent to NO9803141.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
|  
|  
|  
Db 5 YVPL 8

## RESULT 34

AA968305  
ID AAY68305 standard; Peptide; 9 AA.

XX AAY68305;  
DT 13-APR-2000 (first entry)  
XX  
XX Altered MHC determinant binding peptide SEQ ID NO:137.

DE MHC class I; major histocompatibility complex; microglobulin; antigen;  
KW immune response; immunisation; AIDS; multiple sclerosis; toxic shock;  
KW cancer; lupus erythematosus; snake bite; cytostatic; antiviral;  
KW immunomodulatory; dermatological; immunosuppressive; antiinflammatory;  
KW neuroprotective.

XX Plasmodium yoelii.

OS US6011146-A.

PN 04-JAN-2000.

XX 07-JUN-1995; 95US-0481985.

XX 15-NOV-1991; 91US-0792473.

PR 05-DEC-1991; 91US-0801818.

XX (INSP ) INST PASTEUR.

PA (INRM ) INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Mottez E, Abastado J;

XX WPI: 2000-125951/11.

XX New recombinant DNA encoding covalently linked form of major  
PT histocompatibility complex Class I determinant, used for immune system  
PT stimulation, e.g. for treating cancer -

PS Disclosure; Column 11; 88pp; English.

XX The present invention describes a recombinant DNA molecule (I)  
CC containing a sequence (Ia) that encodes an altered MHC (major  
CC histocompatibility complex ) Class I determinant (II) comprises a  
CC polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin  
CC domains, in which alpha3 and beta2 are covalently linked, thorough C-  
CC polypeptide. (III) includes an antigen-binding site and when (II) and  
CC the antigen are associated they are recognized by a mammalian T cell  
CC receptor (TCR). (I) are used to produce (II) which are used to study  
CC functional interactions between the various MHC domains. They can also  
CC be used to modulate (in vivo or in vitro) the immune system by inducing  
CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)  
CC of immune system cells, typically for treating, or immunising against;  
CC cancer, acquired immune deficiency syndrome, lupus erythematosus,  
CC multiple sclerosis, toxic shock and snake bite, but also for selective  
CC destruction of autoreactive cells, diagnostically to assay T cell  
CC receptors and to raise specific antibodies (useful for diagnosis,  
CC therapy, studying MHC-associated cellular processes and for affinity  
CC purification). AA257558 and AAY68186 to AAY68316 are sequences used in  
CC the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
|  
|  
|  
Db 1 SYVP 4

## RESULT 35

AA52959  
ID AA52959 standard; Peptide; 9 AA.  
XX AC  
XX AA52959;  
XX DT  
XX 14-FEB-2000 (first entry)  
XX DE  
XX Altered MHC determinant binding peptide SEQ ID NO:137.  
XX KW Major histocompatibility complex; MHC class I; MHC class II; antigen;  
KW immune response; diagnosis; antibody; immunisation; autoimmune disease;  
KW acquired immune deficiency syndrome; AIDS; cytostatic; dermatological;  
KW anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;  
KW vaccine; lupus erythematosus; multiple sclerosis; thyroiditis;  
KW toxic shock; tumour; snakebite.  
XX OS  
XX Synthetic.  
XX Plasmodium yoelii.  
XX PN  
XX US5976551-A.  
XX PD  
XX 02-NOV-1999.  
XX PF  
XX 07-JUN-1995; 95US-0484905.  
XX PR  
XX 05-DEC-1991; 91US-0801818.  
XX PR  
XX 15-NOV-1991; 91US-0792473.  
XX XX  
XX (INSP ) INST PASTEUR.  
XX PA  
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX PI  
XX Kourilsky P, Mottez E, Abastado J;  
XX WPI; 2000-037081/03.  
XX DR  
XX Composition containing an antigen and altered major histocompatibility  
PT Class II determinant, used to immunize against autoimmune diseases,  
PT e.g. acquired immune deficiency syndrome -  
XX  
XX Claim 8; Column 11; 96pp; English.  
XX  
XX The present invention describes a composition capable of eliciting  
CC anti-major histocompatibility (MHC) antibodies. The composition  
CC comprises an antigen associated with an altered MHC Class II determinant  
CC (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains  
CC encoded by a mammalian MHC Class II locus covalently linked to form a  
CC polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in  
CC sequence. The resulting Antigen-MHC complex is recognizable by the T cell  
CC receptor. The compositions are used for immunisation against, or  
CC treatment of, a wide range of autoimmune diseases, e.g. acquired immune  
CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,  
CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature  
CC of antigen. (I) is also used to analyse functional interactions between  
CC the various domains and for targeting lymphocyte receptors. Antibodies  
CC against (I) are produced by usual methods of immunisation or cell fusion,  
CC and may be humanised by standard methods. These antibodies are useful for  
CC diagnosis (detection or purification of MHC gene products), therapy  
CC (neutralising MHC on cell surfaces) and in the study of MHC and cellular  
CC processes. AA523240 to AA533242 and AA52840 to AA52970 represent  
XX sequences used in the exemplification of the present invention.  
XX SQ  
XX Sequence 9 AA;  
XX  
XX Query Match 44.4%; Score 4; DB 21; Length 9;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 3 SYVP 6  
XX Db 1 SYVP 4  
XX  
XX RESULT 36  
XX AAG63512  
XX ID AAG63512 standard; peptide; 9 AA.  
XX

AA98253  
ID AA98253 standard; Peptide; 9 AA.  
XX AC  
XX AA98253;  
XX DT  
XX 24-JAN-2002 (first entry)  
XX DE  
XX Human peptide #1528 encoded by a SNP oligonucleotide.  
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX OS  
XX Homo sapiens.  
XX PN  
XX WO200147944-A2.  
XX PD  
XX 05-JUL-2001.  
XX PF  
XX 28-DEC-2000; 2000WO-US35498.  
XX PR  
XX 28-DEC-1999; 99US-0173419.  
XX PR  
XX 27-DEC-2000; 2000US-0173419.  
XX XX  
XX (CURA-) CURAGEN CORP.  
XX PI  
XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX DR  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
XX Disclosure; Page 4003; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The oligonucleotides and the peptides encoded by one such oligonucleotide.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms.  
XX SQ  
XX Sequence 9 AA;  
XX  
XX Query Match 44.4%; Score 4; DB 22; Length 9;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 2 ESYV 5  
XX Db 3 ESYV 6  
XX  
XX RESULT 37  
XX AAG63512  
XX ID AAG63512 standard; peptide; 9 AA.  
XX



AC AAG63512;  
 XX 15-OCT-2001 (first entry)  
 DT Amino acid sequence of an antigen derived from Plasmodium.  
 DE  
 XX Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;  
 KW macrophage; dendritic cell; cytokine production; immunocompetent cell;  
 KW autoimmune disease.  
 XX Plasmodium sp.  
 OS WO200146126-A1.  
 XX 28-JUN-2001.  
 PD  
 XX 21-DEC-2000; 2000WO-FR03650.  
 PF  
 XX 22-DEC-1999; 99WO-IB02038.  
 PR  
 XX (OMPH-) OM-PHARMA.  
 PA Bauer J, Martin OR, Rodriguez S;  
 XX WPI; 2001-496651/54.  
 DR  
 XX New amphiphilic acylated pseudopeptides having a functionalized  
 PT auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in  
 PT vaccines -  
 XX Disclosure; Page 34; 267pp; French.  
 PS  
 XX The specification describes N-Acylated pseudopeptides, which have  
 CC a neutral or charged acidic group at one terminal and a functionalized  
 CC auxiliary spacer at the other. The pseudopeptides show immunomodulatory  
 CC and adjuvant action, based on activation of antigen presenting cells  
 CC (e.g. macrophages or dendritic cells), induction of differentiation of  
 CC dendritic cells, induction of cytokine production and induction of  
 CC maturation of immunocompetent cell strains originating from hematopoietic  
 CC and lymphoid organs. They reinforce humoral and cellular immunity. They  
 CC can be grafted onto antigens (to modulate immune response) or onto  
 CC drugs (to improve the therapeutic activity or targeting). The  
 CC pseudopeptides are thus useful in human or veterinary medicine as  
 CC immunizing or diagnostic agents. Typically, the pseudopeptides are used  
 CC as adjuvants together with (or covalently bonded to) antigens for  
 CC vaccination against viral, parasitic/protozoal, microbial or fungal  
 CC infections; incubated with blood cells ex vivo, to render the cells  
 CC immunocompetent before reintroduction in vivo; or used in therapy of  
 CC certain autoimmune diseases. The present sequence represents a  
 CC Plasmodium antigen, which may be used with the pseudopeptides of the  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SYVP 6  
 Db |||||  
 1 SYVP 4  
 RESULT 38  
 AAG63517  
 ID AAG63517 standard; peptide; 9 AA.  
 XX  
 AC AAG63517;  
 XX 15-OCT-2001 (first entry)  
 DT Amino acid sequence of an antigen derived from Plasmodium.  
 DE

KW Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;  
 KW macrophage; dendritic cell; cytokine production; immunocompetent cell;  
 KW autoimmune disease.  
 XX Plasmodium sp.  
 OS WO200146126-A1.  
 XX 28-JUN-2001.  
 PD  
 XX 21-DEC-2000; 2000WO-FR03650.  
 PF  
 XX 22-DEC-1999; 99WO-IB02038.  
 PR  
 XX (OMPH-) OM-PHARMA.  
 PA Bauer J, Martin OR, Rodriguez S;  
 XX WPI; 2001-496651/54.  
 DR  
 XX New amphiphilic acylated pseudopeptides having a functionalized  
 PT auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in  
 PT vaccines -  
 XX Example 3.5; Page 90; 267pp; French.  
 PS  
 XX The specification describes N-Acylated pseudopeptides, which have  
 CC a neutral or charged acidic group at one terminal and a functionalized  
 CC auxiliary spacer at the other. The pseudopeptides show immunomodulatory  
 CC and adjuvant action, based on activation of antigen presenting cells  
 CC (e.g. macrophages or dendritic cells), induction of differentiation of  
 CC dendritic cells, induction of cytokine production and induction of  
 CC maturation of immunocompetent cell strains originating from hematopoietic  
 CC and lymphoid organs. They reinforce humoral and cellular immunity. They  
 CC can be grafted onto antigens (to modulate immune response) or onto  
 CC drugs (to improve the therapeutic activity or targeting). The  
 CC pseudopeptides are thus useful in human or veterinary medicine as  
 CC immunizing or diagnostic agents. Typically, the pseudopeptides are used  
 CC as adjuvants together with (or covalently bonded to) antigens for  
 CC vaccination against viral, parasitic/protozoal, microbial or fungal  
 CC infections; incubated with blood cells ex vivo, to render the cells  
 CC immunocompetent before reintroduction in vivo; or used in therapy of  
 CC certain autoimmune diseases. The present sequence represents a  
 CC Plasmodium antigen, which may be used with the pseudopeptides of the  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SYVP 6  
 Db |||||  
 1 SYVP 4  
 RESULT 39  
 AAG66424  
 ID AAG66424 standard; Peptide; 9 AA.  
 XX  
 AC AAG66424;  
 XX 23-OCT-2001 (first entry)  
 DT Circumsporozoite protein, CSP, used as a peptide antigen.  
 DE  
 XX Immunomodulator; vaccine; immune response; immunogenic; CSP;  
 KW Circumsporozoite protein.  
 XX Plasmodium yoelii.  
 OS WO200154720-A1.  
 PN

XX PD 02-AUG-2001.  
 XX PF 05-JAN-2001; 2001WO-EP00087.  
 XX PR 28-JAN-2000; 2000AT-0000129.  
 XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
 XX PI Lingnau K, Mattner F, Schmidt W, Birnstiel M, Buschle M;  
 XX DR WPI; 2001-536419/59.  
 XX PT Pharmaceutical composition useful for inducing immune response  
 XX PT comprises antigen, immunogenic oligodeoxynucleotide containing  
 XX PT cytosine-guanine dinucleotide motifs and polycationic polymer -  
 XX PS Example 2; Page 22; 39pp; English.  
 XX CC The present invention relates to a pharmaceutical composition which  
 XX CC comprises an antigen, an immunogenic oligodeoxynucleotide containing  
 XX CC cytosine-guanine dinucleotide (CpG) motifs (CpG-ODN) and a polycationic  
 XX CC polymer. The composition is useful for making a vaccine to induce potent  
 XX CC immune responses, or to decrease or ablate undesired immune responses.  
 XX CC The present sequence, CSP, is a peptide from the circumsporozoite protein  
 XX CC of Plasmodium yoelii. This sequence was used as a peptide antigen in the  
 XX CC method of the present invention.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SYVP 6  
 Db 1 SYVP 4  
 RESULT 40  
 AAG79591  
 ID AAG79591 standard; Peptide; 9 AA.  
 AC AAG79591;  
 DT 09-JAN-2003 (first entry)  
 DE Malarial epitope #3.  
 XX KW Yellow fever; YF; virus; flavivirus; vector; antigen; envelope protein;  
 XX KW E protein; immunization; immune response; parasite; vaccine; malaria;  
 XX KW dengue; Japanese encephalitis; tick-borne encephalitis; fungi;  
 XX KW monkey neurovirulence testing.  
 XX OS Plasmodium malariae.  
 XX PN GB2372991-A.  
 XX PD 11-SEP-2002.  
 XX PF 09-MAR-2001; 2001GB-0005877.  
 XX PR 09-MAR-2001; 2001GB-0005877.  
 XX PA (FIOC-) FIOCRUZ FUNDACAO CRUZ OSWALDO.  
 XX PI Bonaldo MC, Galler R, Da Silva Freire M, Garrat RC;  
 XX DR WPI; 2002-735136/80.  
 XX PT Novel Flavivirus vector useful for expressing heterologous antigens,  
 XX PT comprises foreign gene sequences inserted at sites in the level of its  
 XX PT envelope protein -

XX PS Claim 18; Page 94; 96pp; English.  
 XX CC The sequences given in AAG79586-91 are insertion sequences which  
 XX CC may be inserted into the envelope protein derived from yellow  
 XX CC fever virus (yF) in the vector of the invention. The vector  
 XX CC has foreign gene sequences inserted at sites in the level of its  
 XX CC envelope protein, where the sites are structurally apart from areas  
 XX CC known to interfere with the overall Flavivirus E protein structure.  
 XX CC Vectors such as these may be useful for immunization against Flavivirus  
 XX CC and other infectious agents. It is useful for expressing heterologous  
 XX CC antigens and for eliciting an immune response to foreign antigens.  
 XX CC The vector of the invention is useful for eliciting an adequate immune  
 XX CC response to cope with different parasite stages. Vaccines containing  
 XX CC the vectors of the invention are useful for treating yellow fever  
 XX CC and other diseases such as malaria, dengue, Japanese encephalitis,  
 XX CC tick-borne encephalitis, and fungi infections. The vector of the  
 XX CC invention is a safe and effective virus. It has several advantages  
 XX CC such as well-defined and efficient production methodology,  
 XX CC strict quality control including monkey neurovirulence testing, long  
 XX CC lasting immunity, cheapness, single doses, and estimated use is over  
 XX CC 200 million doses with excellent records of safety.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SYVP 6  
 Db 1 SYVP 4  
 RESULT 41  
 ABR06327  
 ID ABR06327 standard; Peptide; 9 AA.  
 AC ABR06327;  
 DT 19-MAY-2003 (first entry)  
 DE Human cancer-related protein 109P1D4 HLA peptide #262.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 XX PI Morrison K, Morrison RK, Raitano AB;  
 XX DR WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 XX PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX PT diagnostic reagents for eliciting cellular or humoral immune response  
 XX PT in cancer patients -  
 XX PS Claim 13; Page 175; 1021pp; English.  
 XX

CC	therapeutic, prognostic and diagnostic reagents for cancer
CC	sequence is a human leukocyte antigen (HLA) peptide, use
CC	from the invention.
XX	
SQ	Sequence 9 AA;
	Query Match 44.4%; Score 4; DB 24; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 4; Conservative 0; Mismatches 0; Indels
QV	6 PLFP 9

```

Db      2 PLFP 5
|||||
RESULT 44
ABP72311
ID   ABP72311 standard; Peptide; 9 AA.
AC
AC
XX
XX
DT   08-MAY-2003 (first entry)
XX
XX
DE   Plasmodium yoelii circumsporozoite protein T cell epitope.
XX
XX
DE   Malaria; antigen; epitope; circumsporozoite; infection; vaccine;
KW   glycosylceramide; adjuvant; antiparasitic; protozoacide;
KW   animalarial.
XX
XX
OS   Plasmodium yoelii.
XX
XX
PN   WO2003009812-A2.
XX
XX
PD   06-FEB-2003.
XX
XX
PF   24-JUL-2002; 2002WO-US23673.
XX
XX
PR   25-JUL-2001; 2001US-308056P.
XX
XX
PA   (UJNY ) UNIV NEW YORK STATE.
XX
XX
PI   Tsuji M, Gonzalez-Aseguinolaza G, Nussenzweig RS, Koezuka Y;
XX
XX
WPI; 2003-268011/26.
XX
XX
PT   Augmenting the immunogenicity of an antigen in a mammal, useful for
PT   treating cancer, viral infection and malaria, comprises immunizing the
PT   mammal with the antigen conjointly with adjuvant comprising a
PT   glycosylceramide -
XX
XX
PS   Claim 41; Page 73; 97pp; English.
XX
XX
CC   The present sequence is that of a malaria-specific antigen
CC   comprising a CD8+ T cell epitope of the Plasmodium yoelii
CC   circumsporozoite protein. The malaria-specific antigen is used in
CC   a claimed method for conferring immunity against the sporozoite
CC   stage of malaria in a mammalian (human) host. This method
CC   comprises the co-administration of the antigen and the natural
CC   killer T cell ligand alpha-galactosylceramide as adjuvant. The
CC   malaria-specific antigen may be presented by a recombinant virus
CC   such as a recombinant adenovirus, pox virus or Sindbis virus.
CC   Co-administration of the antigen with alpha-galactosylceramide
CC   enhances malaria-specific T cell responses, particularly those of
CC   CD8+ T cells and prolongs the duration of protective immunity
CC   induced by the malaria vaccine. This is an example of the method
CC   of the invention for augmenting the immunogenicity of an antigen in
CC   a mammal by immunising the mammal with the antigen and with a
CC   glycosylceramide adjuvant. Glycosylceramides can be used as
CC   adjuvants for vaccines against infections and cancer.
XX
XX
SQ   Sequence 9 AA;

Query Match      44.4%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      1 SYVP 4
|||||

RESULT 45
ABP58362
ID   ABP58362 standard; Peptide; 9 AA.

```

```

XX
AC
AC
DT   07-APR-2003 (first entry)
XX
XX
DE   CSP peptide.
XX
XX
KW   Mouse; mastocytoma; immunostimulant; oligodeoxynucleic acid; ODN;
KW   vaccine.
XX
XX
OS   Mus sp.
XX
XX
PN   WO200295027-A2.
XX
XX
PD   28-NOV-2002.
XX
XX
PF   17-MAY-2002; 2002WO-EP05448.
XX
XX
PR   21-MAY-2001; 2001AT-0000805.
XX
XX
PA   (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX
PI   Lingnau K, Schellack C, Schmidt W;
XX
XX
WPI; 2003-183880/18.
XX
XX
PT   New oligodeoxynucleic acid molecules useful for the preparation of
PT   vaccine -
XX
XX
PS   Example 4; Page 25; 57pp; English.
XX
XX
CC   The present sequence is that of peptide CSP, which was used as an
CC   'irrelevant' peptide in an example from the invention describing
CC   the generation of specific immune responses against a
CC   mastocytoma-derived peptide (see ABP58361) using deoxyuridine
CC   monophosphate-modified oligonucleotide U-ODN 13 (see AB224776).
CC   U-ODN 13 is an example of new oligodeoxynucleic acid (ODN)
CC   molecules useful in the preparation of vaccines. The invention is
CC   based on the discovery that ODNs containing deoxyuridine residues
CC   have an immunostimulatory effect comparable to, or greater than, ODNs
CC   containing CpG motifs. Combining the ODN with an antigen strongly
CC   increases the potential of the antigen to raise the protection/immune
CC   response of a vaccinated individual.
XX
XX
SQ   Sequence 9 AA;

Query Match      44.4%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      1 SYVP 4
|||||

RESULT 46
AAR79143
ID   AAR79143 standard; Peptide; 10 AA.
XX
XX
AC   AAR79143;
XX
XX
DT   25-MAR-2003 (updated)
DT   05-DEC-1995 (first entry)
XX
XX
DE   Fructosyltransferase N-terminal peptide.
XX
XX
KW   Fructosyltransferase; FTase; fructooligosaccharide; sweetener;
KW   fructan.
XX
XX
OS   Acetobacter diazotrophicus.
XX
XX
PA   EP663442-A1.

```



```

CC peptide.
XX
SQ Sequence 10 AA;

Query Match 44.4%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
    ||||
Db 6 SYVP 9

RESULT 49
ABR06228
ID ABR06228 standard; Peptide; 10 AA.
XX
AC ABR06228;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 109P1D4 HLA peptide #163.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 174; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 10 AA;

Query Match 44.4%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
    ||||
Db 1 PLFP 4

RESULT 51
ABR06590
ID ABR06590 standard; Peptide; 10 AA.
XX
AC ABR06590;
XX
DT 19-MAY-2003 (first entry)

```

XX Human cancer-related protein 109PID4 HLA peptide #525.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX Human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283921-A2.  
 XX PA  
 XX 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 XX PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX PA  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 DR New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 178; 1021pp; English.  
 PS The present invention relates to novel human cancer-related genes and  
 XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX Sequence 10 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PLFP 9  
 DB 1 PLFP 4  
 RESULT 52  
 ABR07254  
 ID ABR07254 standard; Peptide; 10 AA.  
 XX AC  
 XX ABR07254;  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 109PID4 HLA peptide #1189.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283921-A2.  
 XX PA

PD 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX PA  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 DR New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 184; 1021pp; English.  
 PS The present invention relates to novel human cancer-related genes and  
 XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX Sequence 10 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PLFP 9  
 DB 3 PLFP 6  
 RESULT 53  
 ABR07442  
 ID ABR07442 standard; Peptide; 10 AA.  
 XX AC  
 XX ABR07442;  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 109PID4 HLA peptide #1377.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283921-A2.  
 XX PA  
 XX 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 XX PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX PA  
 XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX  
XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients -  
XX  
XX Claim 13; Page 186; 1021pp; English.  
XX  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC inhibiting the expression of the protein, as tools for modulating or  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 44.4%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PLFP 9  
Db |||||  
2 PLFP 5  
RESULT 54  
AAR72659  
ID AAR72659 standard; peptide; 11 AA.  
XX  
AC AAR72659;  
XX  
XX 25-MAR-2003 (updated)  
DT 25-OCT-1995 (first entry)  
XX  
DE Cladosporium herbarum allergen Clah22 B-cell epitope (141-151).  
XX  
XX Fungal spore; allergen; Clah22; allergy; yeast protein YCP4;  
KW B-cell epitope; antigenic region.  
XX  
XX Cladosporium herbarum.  
OS  
XX WO9506121-A2.  
PN  
XX 02-MAR-1995.  
PD  
XX 24-AUG-1994; 94WO-AT00120.  
PF  
XX 27-AUG-1993; 93AT-0001725.  
PR  
XX (BIOM-) BIOMAY PROD. & HANDELSGES MBH.  
PA  
XX Achatz G, Breitenbach M, Ebner C, Hirschwehr R;  
PI Kraft D, Lechenauer E, Oberkofler H, Prillinger H;  
PI Simon B, Unger A;  
XX  
XX WPI; 1995-106850/14.  
DR  
XX Allergens derived from Cladosporium herbarum spores - also  
PT recombinant DNA for expressing the allergens, useful for in vitro  
PT allergy detection  
XX  
XX Claim 1; Page 23; 35pp; German.

XX Spores of Cladosporium herbarum are the most common fungal spores  
CC found in the air; they can cause allergic reactions. Various Clah  
CC allergens and sequences encoding them have now been isolated. The  
CC mature Clah22 allergen has mol. wt. 22 kD and is encoded by cDNA  
CC sequence AAQ87845. The allergen has homology to the yeast protein  
CC YCP4. Potential epitopic subfragments were identified by computer  
CC analysis of the amino acid sequence. See AAR72653-R72661 for potential  
CC B-cell epitopes and AAR72662-R72668 for potential T-cell epitopes.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 11 AA;  
SQ  
Query Match 44.4%; Score 4; DB 16; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 YVPL 7  
Db |||||  
2 YVPL 5  
RESULT 55  
AAE11116  
ID AAE11116 standard; peptide; 11 AA.  
XX  
AC AAE11116;  
XX  
XX 18-DEC-2001 (first entry)  
DT  
XX  
DE Tryptic peptide #18 of phhAB fusion protein.  
XX  
XX Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; phhB;  
KW aromatic aminotransferase; phhC; milk protein; animal protein; casein;  
KW proteinaceous food product; globulin; whey protein; phenylketonuria;  
KW PKU; inherited metabolic disorder; impaired brain function; nootropic;  
KW cell therapy; tryptic peptide.  
XX  
XX Unidentified.  
OS  
XX WO200168822-A2.  
PN  
XX 20-SEP-2001.  
PD  
XX 14-MAR-2001; 2001WO-DK00172.  
PF  
XX 14-MAR-2000; 2000US-0525116.  
PR  
XX (NILA-) NILAB APS.  
PA  
XX Johnsen M, Ravn P, Madsen SM, Vrang A, Israelsen H, Bredmose L;  
PI Arnau J, Jensen SH, Gjetting T, Nielsen E;  
XX  
XX WPI; 2001-590055/66.  
DR  
XX Novel recombinant cells comprising a nucleic acid encoding a gene  
PT product having phenylalanine hydroxylase activity, that is derived from  
PT a prokaryotic organism, is useful for treating phenylketonuria in  
PT mammals -  
XX  
XX Example 8; Page 47; 91pp; English.  
XX  
XX The patent discloses novel cells comprising a nucleic acid encoding  
CC a gene product having phenylalanine hydroxylase (PAH) activity such  
CC as phenylalanine hydroxylase (phhA), 4a-carbinolamine dehydratase  
CC (phhB) and aromatic aminotransferase (phhC), which are derived  
CC from a prokaryotic organism. The patent also relates to fusion  
CC proteins comprising a protein enhancing and/or stabilising the  
CC PAH activity in addition to PAH activity. The cells are useful  
CC for producing PAH. The sequences of the invention are also useful  
CC for preparing a proteinaceous food product (animal protein such  
CC as a milk protein derived from casein, globulin or a whey protein)  
CC having reduced content of phenylalanine. The method involves contacting



CC	disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,
CC	allergy, graft rejection, infection, hormonal disorders and central
CC	nervous system diseases), also, where (I) is a MHC ligand (Ia), in
CC	vaccines for treatment or prevention of: (i) viral, bacterial, parasitic
CC	or fungal infections; or (ii) of cancers. A particular application is in
CC	anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of
CC	diseases associated with interactions between MHC and (I), e.g. melanoma
CC	and human immunodeficiency virus infection. AAM9898 to AAM99592
CC	represent peptides which can be used in pharmaceutical compounds from
CC	the present invention.
XX	
XX	Sequence 11 AA;
SQ	
	Query Match 44.4%; Score 4; DB 22; Length 11;
	Best Local Similarity 100.0%; Pred. No. 2.7e-02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3 SYVP 6
Db	3 SYVP 6
RESULT 57	
AAG63527	
ID	AAG63527 standard; peptide; 11 AA.
XX	
AC	AAG63527;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	An epitope which may be conjugated to pseudopeptides.
XX	
KW	Pseudopeptide; immunomodulation; adjuvant; antigen presenting cell;
KW	macrophage; dendritic cell; cytokine production; immunocompetent cell;
KW	autoimmune disease.
XX	
OS	Synthetic.
XX	
PN	WO200146126-A1.
XX	
PD	28-JUN-2001.
XX	
PF	21-DEC-2000; 2000WO-FR03650.
XX	
PR	22-DEC-1999; 99WO-IB02038.
XX	
PA	(OMPH-) OM-PHARMA.
XX	
PI	Bauer J, Martin OR, Rodriguez S;
XX	
DR	WPI; 2001-496651/54.
XX	
PT	New amphiphilic acylated pseudopeptides having a functionalized
PT	auxiliary spacer, useful as immunomodulators, e.g. as adjuvants in
PT	vaccines -
XX	
PS	Example 3.9; Fig 67; 267pp; French.
XX	
CC	The specification describes N-Acylated pseudopeptides, which have
CC	a neutral or charged acidic group at one terminal and a functionalized
CC	auxiliary spacer at the other. The pseudopeptides show immunomodulatory
CC	and adjuvant action, based on activation of antigen presenting cells
CC	(e.g. macrophages or dendritic cells), induction of differentiation of
CC	dendritic cells, induction of cytokine production and induction of
CC	maturatation of immunocompetent cell strains originating from hematopoietic
CC	and lymphoid organs. They reinforce humoral and cellular immunity. They
CC	can be grafted onto antigens (to modulate immune response) or onto
CC	drugs (to improve the therapeutic activity or targeting). The
CC	pseudopeptides are thus useful in human or veterinary medicine as
CC	immunizing or diagnostic agents. Typically, the pseudopeptides are used
CC	as adjuvants together with (or covalently bonded to) antigens for
CC	vaccination against viral, parasitic/protozoal, microbial or fungal
CC	infections; incubated with blood cells ex vivo, to render the cells

CC immunocompetent before reintroduction in vivo; or used in therapy of  
 CC certain autoimmune diseases. The present sequence represents an  
 CC epitope which may be conjugated to pseudopeptides of the invention.

SQ Sequence 11 AA;

Query Match 44.4%; Score 4; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6  
 |||||  
 Db 3 SYVP 6

RESULT 58  
 ABP99426  
 ID ABP99426 standard; Peptide; 11 AA.

XX AC ABP99426;

DT 24-MAR-2003 (first entry)

XX Beta-amyloid binding D-form peptide 13.

XX Alzheimer's disease; beta amyloid; nootropic; neuroprotective;  
 KW plaque.

XX Unidentified.

XX Key Location/Qualifiers

PH Misc-difference 1..11

PT Note= "D-form residue"

XX WO200281505-A2.

XX 17-OCT-2002.

XX 08-APR-2002; 2002WO-EP03862.

XX 06-APR-2001; 2001DE-1017281.

XX (IMBM-) IMB INST MOLEKULARE BIOTECHNOLOGIE EV.

XX Willbold D, Wiesehan K;

XX WPI; 2003-103321/09.

XX New D-amino acid peptide specific for beta-amyloid peptide, useful in  
 PT diagnosis, prevention and treatment of Alzheimer's disease -

XX Example; Fig 1; 28pp; German.

XX The invention relates to peptides (I) consisting essentially of D-amino  
 CC acids and able to bind to monomeric, oligomeric and/or fibrils of  
 CC beta-amyloid peptide (bAP) with dissociation constant (Kd) at most 10,  
 CC preferably 4 micro M. (I) act by inhibiting the aggregation of bAP to  
 CC plaques and dissolution of existing plaques. (I) or other peptides with  
 CC high binding affinity for bAP, are used for diagnosis of Alzheimer's  
 CC disease (AD) in living subjects, as contrast agents for detection of  
 CC amyloid plaque, for prevention or treatment of AD and for investigating  
 CC the relationship between pathological conditions and AD symptoms. (I)  
 CC have no significant side effects, are more resistant to proteases than  
 CC L-peptides, have low immunogenicity and are highly specific. The present  
 CC sequence is that of a peptide of the invention.

SQ Sequence 11 AA;

Query Match 44.4%; Score 4; DB 24; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6

Db |||||  
 6 SYVP 9

RESULT 59

AAV67307

ID AAV67307 standard; peptide; 12 AA.

XX AC AAV67307;

XX 05-APR-2000 (first entry)

XX Malarial epitope of Plasmodium yoelii, used to alter viral proteins.

XX Malarial epitope; ME1; reduced lethal dose; attenuated influenza virus;  
 KW nonstructural gene segment; NS1; tumour antigen expression; vaccine;  
 KW HIV; HBV; herpes virus; polio virus; interferon.

XX Plasmodium yoelii.

XX WO9964571-A1.

XX 16-DEC-1999.

XX 11-JUN-1999; 99WO-US13139.

XX 12-JUN-1998; 98US-0089103.

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

PA (EGOR/) EGOROV A.

PA (MUST/) MUSTER T.

PI Egorov A, Muster T, Garcia-Sastre A, Palese P;

XX WPI; 2000-105886/09.

XX Novel interferon inducing genetically engineered attenuated viruses  
 PT used. e.g. against polioviruses -

XX Disclosure; Page 23; 48pp; English.

XX This peptide represents the malarial epitope (ME 1) of Plasmodium yoelii,  
 CC which can be introduced into the antigenic site E of the haemagglutinin  
 CC of the influenza virus. The resulting chimeric virus has a reduced lethal  
 CC dose when compared to the wild type virus. The invention relates to novel  
 CC genetically engineered attenuated viruses, which contain a modified viral  
 CC nonstructural (NS) gene segment, which affects the ability of the virus  
 CC to grow in interferon deficient substrates. The attenuated virus is  
 CC genetically engineered Influenza A virus with an IFN-inducing phenotype  
 CC containing a knockout of the NS1 segment. The attenuated virus can be  
 CC used in a vaccine. The attenuated virus of the invention may also be used  
 CC to express heterologous proteins, including tumour and viral antigens.  
 CC Especially, the attenuated viruses are used as vaccines against a broad  
 CC range of viruses and antigens from different species, e.g. epitopes of  
 CC HIV such as gp120, HBV surface antigen; Herpes virus glycoproteins, VP1  
 CC of polioviruses, etc. The attenuated viruses can also be used for the  
 CC prophylaxis or treatment of infection (viral or nonviral pathogens) or  
 CC tumour formation.

XX Sequence 12 AA;

Query Match 44.4%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6  
 |||||  
 Db 4 SYVP 7

RESULT 60

AAW99153

ID AAW99153 standard; Peptide; 12 AA.



XX Epitope, from allergens Aln g I, Cor a I and Bet v I.  
 DE T-cell response; Fagales; birch; alder; hazel; tree pollen; IgE.  
 XX Fagales.  
 OS WO9202621-A.  
 PN 20-FEB-1992.  
 PD  
 XX 06-MAY-1991; 91WO-EP01479.  
 XX 08-AUG-1990; 90AT-0001668.  
 PR 11-APR-1991; 91US-0683931.  
 XX (BIOM-) BIOMAY BIOTECHN PRO.  
 PA Breiteneder H, Reikerstorfer A, Valenta R, Hoffmann-Sommergruber K;  
 PI Breitenbach M, Kraft D, Rumpold H, Scheiner O;  
 XX WPI; 1992-080075/10.  
 DR Aln g I, Cor a I and Bet v I allergens - and DNA from alder,  
 PT hazel and birch, useful in diagnosis or therapy of allergic  
 PT diseases  
 XX Claim 3; Page 44; 54pp; English.  
 XX The epitope was derived from one of the allergens Aln g I, Cor a I,  
 CC or Bet v I, from alder, hazel or birch respectively (AAR21791-6).  
 CC The epitope has the ability to bind IgE from the serum of tree  
 CC pollen allergic individuals and alters the individuals T-cell  
 CC response. The epitope sequence allows mammals to be tested for  
 CC allergic reactions to specific tree allergens. The peptide  
 CC may be used to challenge the mammal to elicit bronchial,  
 CC conjunctival, dermal, nasal or oral provocation. The peptide  
 CC may be used to treat a mammal afflicted with a pollen allergy.  
 CC It is administered in an amount sufficient to hypersensitize the  
 CC mammal to any of the allergens.  
 CC See also AAR21791-801.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX Sequence 13 AA;  
 SQ  
 Query Match 44.4%; Score 4; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VESY 4  
 Db |||||  
 5 VESY 8  
 RESULT 63  
 AAU17675  
 ID AAU17675 standard; Protein; 13 AA.  
 XX  
 AC AAU17675;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Novel signal transduction pathway protein, Seq ID 1240.  
 XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
 XX anti-inflammatory; anti-HIV; antibacterial; anti-inflammatory; cancer;  
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;  
 KW organ transplant rejection; infection; hepatitis C; blood disorder;  
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
 KW reproductive system; gastrointestinal; liver disorder; AIDS;  
 XX acquired immune deficiency syndrome.  
 XX Homo sapiens.  
 XX WO200154733-A1.  
 XX 02-AUG-2001.  
 XX 17-JAN-2001; 2001WO-US01312.  
 XX 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.  
 PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.

PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239335.  
PR 13-OCT-2000; 2000US-0239337.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0241826.  
PR 08-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246529.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0251990.  
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465460/50.  
XX Novel polypeptides useful for diagnosing, treating, preventing and/or  
XX prognosing disorders related to the proteins, including cancers, immune  
XX disorders and neuronal disorders -  
XX Claim 1; SEQ ID No 1240; 880pp; English.  
XX The invention relates to novel isolated polypeptides (I), and  
XX polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
XX diagnosing, preventing and treating diseases including immune system  
XX disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
XX disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
XX transplant rejections and graft versus host disease, infectious diseases  
XX (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
XX other blood-related disorders (sickle cell anaemia), myeloproliferative  
XX disorders, primary haematopoietic disorders, hyperproliferative  
XX disorders (e.g. Gaucher's disease and cancer), neurodegenerative  
XX disorders (e.g. Alzheimer's disease and Parkinson's disease), chromosomal  
XX abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal  
XX disorders (e.g. glomerulonephritis), cardiovascular disorders  
XX (e.g. arrhythmia), respiratory disorders, dermatological disorders, in  
XX wound healing, epithelial cell proliferation, endocrine disorders (e.g.  
XX Addison's disease), reproductive system disorders, gastrointestinal  
XX disorder (inflammatory disorders), liver disorders (cirrhosis),  
XX as stimulators of B-cell responsiveness to pathogens, activators of  
XX T-cells, to induce higher affinity antibodies, and as a means to induce  
XX tumour proliferation in pathologies e.g. acquired immune deficiency  
XX syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction  
XX pathway protein, amino acid sequences of the invention.  
XX Sequence 13 AA;  
Query Match 44.4%; Score 4; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SYVP 6  
Db 1 SYVP 4  
RESULT 64  
AAB68132  
ID AAB68132 standard; peptide; 13 AA.  
XX AAB68132;  
XX AAB68132;  
DT 09-JUL-2001 (first entry)  
XX Peptide derived from the beta4 part of alpha6beta4 integrin.  
XX Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;  
XX tumour-associated antigen; metastatic disease; malignant disease;  
XX tumour typing; tumour screening; tumour.  
XX Homo sapiens.  
XX WO200130854-A2.  
XX 03-MAY-2001.  
XX 26-OCT-2000; 2000WO-SE02082.  
XX 28-OCT-1999; 99SE-0003895.  
XX (ACTI-) ACTIVE BIOTECH AB.  
XX

PI Brodin TN, Karlstroem PJ, Ohlsson LG, Tordsson MJ, Kearney PP;  
 PI Nilsson BHK;  
 XX WPI; 2001-308619/32.  
 XX  
 PT Novel antibody for diagnosis, treatment of human metastatic and  
 PT malignant diseases, has binding structure for target structure  
 PT displayed on cell surface of human gastrointestinal epithelial tumour  
 PT and normal cells -  
 XX  
 XX Claim 27; Page 27; 75pp; English.  
 XX  
 CC The present sequence is derived from the beta4 part of alpha6beta4  
 CC integrin. The specification describes antibodies which bind to this  
 CC protein. Alpha6beta4 integrin is displayed in and on the cell surface of  
 CC human gastrointestinal epithelial tumour cells and in a subpopulation of  
 CC normal human gastrointestinal epithelial cells. Alpha6beta4 integrin is  
 CC a tumour-associated antigen. The antibody, and its fragments, are  
 CC useful for treating conditions based on anti-angiogenic mechanism in  
 CC humans. They are useful for treating human metastatic and malignant  
 CC disease, for in vitro, in vivo diagnosis and prognosis of human malignant  
 CC disease, comprising tumour typing, tumour screening, tumour diagnosis and  
 CC prognosis and monitoring premalignant conditions. Quantitative in vivo  
 CC diagnosis is carried out by determining the localization of antibody to  
 CC tumour deposits in humans.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VPLF 8  
 DB 1 VPLF 4  
 RESULT 65  
 ID ABP53814 standard; Peptide; 13 AA.  
 XX  
 AC ABP53814;  
 XX  
 DT 06-JAN-2003 (first entry)  
 XX  
 DE Human CNTF potential MHC class II binding activity peptide #4.  
 XX  
 KW Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;  
 KW immune response; major histocompatibility complex; MHC class II;  
 KW T cell epitope; immunogenic.  
 OS Homo sapiens.  
 XX  
 XX WO200270698-A2.  
 FN  
 XX 12-SEP-2002.  
 PD  
 XX 27-FEB-2002; 2002WO-EP02084.  
 PF  
 XX 02-MAR-2001; 2001EP-0105089.  
 PR  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Carr FJ, Carter G;  
 PI  
 XX WPI; 2003-018694/01.  
 DR  
 XX New modified human ciliary neurotrophic factor which is substantially  
 PT non-immunogenic or less immunogenic than any non-modified molecule,  
 PT useful for treating conditions in a mammal -  
 XX  
 XX Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the  
 CC biological activity of human ciliary neurotrophic factor (CNTF) which is  
 CC substantially non-immunogenic or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. Also  
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical  
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;  
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with  
 CC a potential MHC Class II binding activity and created from a non-modified  
 CC CNTF selected from the 81 peptide sequences given in ABP53811 to  
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9  
 CC consecutive amino acid residues of (IV). The modified CNTF molecule can  
 CC be administered to humans for therapeutic purposes. The 13-mer T cell  
 CC epitope peptide and the peptide sequence is useful in the manufacture of  
 CC CNTF with substantially no or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. The  
 CC modified human CNTF can be substantially non-immunogenic or less  
 CC immunogenic than any non-modified counterpart. The sequence given in  
 CC ABP53810 represents the primary sequence of human CNTF, which is given  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ESYV 5  
 DB 3 ESYV 6  
 RESULT 66  
 ID ABP53834 standard; Peptide; 13 AA.  
 XX  
 AC ABP53834;  
 XX  
 DT 06-JAN-2003 (first entry)  
 XX  
 DE Human CNTF potential MHC class II binding activity peptide #24.  
 XX  
 KW Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;  
 KW immune response; major histocompatibility complex; MHC class II;  
 KW T cell epitope; immunogenic.  
 OS Homo sapiens.  
 XX  
 XX WO200270698-A2.  
 FN  
 XX 12-SEP-2002.  
 PD  
 XX 27-FEB-2002; 2002WO-EP02084.  
 PF  
 XX 02-MAR-2001; 2001EP-0105089.  
 PR  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Carr FJ, Carter G;  
 PI  
 XX WPI; 2003-018694/01.  
 DR  
 XX New modified human ciliary neurotrophic factor which is substantially  
 PT non-immunogenic or less immunogenic than any non-modified molecule,  
 PT useful for treating conditions in a mammal -  
 XX  
 XX Claim 6; Page 11; 33pp; English.  
 PS  
 XX The present invention describes a modified molecule (I) with the  
 CC biological activity of human ciliary neurotrophic factor (CNTF) which is  
 CC substantially non-immunogenic or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. Also  
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical  
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;

CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with  
 CC a potential MHC Class II binding activity and created from a non-modified  
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to  
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9  
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can  
 CC be administered to humans for therapeutic purposes. The 13-mer T cell  
 CC epitope peptide and the peptide sequence is useful in the manufacture of  
 CC CNTP with substantially no or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. The  
 CC modified human CNTP can be substantially non-immunogenic or less  
 CC immunogenic than any non-modified counterpart. The sequence given in  
 CC ABP53810 represents the primary sequence of human CNTP, which is given  
 CC in the exemplification of the present invention.

XX  
 SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5  
 Db |||||  
 9 ESYV 12

RESULT 67  
 ABP53835  
 ID ABP53835 standard; Peptide; 13 AA.  
 XX  
 AC ABP53835;  
 XX  
 DT 06-JAN-2003 (first entry)  
 XX  
 DE Human CNTP potential MHC class II binding activity peptide #25.  
 XX  
 KW Human; ciliary neurotrophic factor; CNTP; reduced immunogenicity;  
 KW immune response; major histocompatibility complex; MHC class II;  
 KW T cell epitope; immunogenic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270698-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002WO-EP02084.  
 XX  
 PR 02-MAR-2001; 2001EP-0105089.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Carr FJ, Carter G;  
 XX  
 DR WPI; 2003-018694/01.  
 XX  
 PT New modified human ciliary neurotrophic factor which is substantially  
 PT non-immunogenic or less immunogenic than any non-modified molecule,  
 PT useful for treating conditions in a mammal -  
 XX  
 PS Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the  
 CC biological activity of human ciliary neurotrophic factor (CNTP) which is  
 CC substantially non-immunogenic or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. Also  
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical  
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;  
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with  
 CC a potential MHC Class II binding activity and created from a non-modified  
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to  
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9  
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can  
 CC be administered to humans for therapeutic purposes. The 13-mer T cell  
 CC epitope peptide and the peptide sequence is useful in the manufacture of  
 CC CNTP with substantially no or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. The  
 CC modified human CNTP can be substantially non-immunogenic or less  
 CC immunogenic than any non-modified counterpart. The sequence given in  
 CC ABP53810 represents the primary sequence of human CNTP, which is given  
 CC in the exemplification of the present invention.

CC epitope peptide and the peptide sequence is useful in the manufacture of  
 CC CNTP with substantially no or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. The  
 CC modified human CNTP can be substantially non-immunogenic or less  
 CC immunogenic than any non-modified counterpart. The sequence given in  
 CC ABP53810 represents the primary sequence of human CNTP, which is given  
 CC in the exemplification of the present invention.

XX  
 SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5  
 Db |||||  
 1 ESYV 4

RESULT 68  
 ABP53854  
 ID ABP53854 standard; Peptide; 13 AA.  
 XX  
 AC ABP53854;  
 XX  
 DT 06-JAN-2003 (first entry)  
 XX  
 DE Human CNTP potential MHC class II binding activity peptide #44.  
 XX  
 KW Human; ciliary neurotrophic factor; CNTP; reduced immunogenicity;  
 KW immune response; major histocompatibility complex; MHC class II;  
 KW T cell epitope; immunogenic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270698-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002WO-EP02084.  
 XX  
 PR 02-MAR-2001; 2001EP-0105089.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Carr FJ, Carter G;  
 XX  
 DR WPI; 2003-018694/01.  
 XX  
 PT New modified human ciliary neurotrophic factor which is substantially  
 PT non-immunogenic or less immunogenic than any non-modified molecule,  
 PT useful for treating conditions in a mammal -  
 XX  
 PS Claim 6; Page 11; 33pp; English.

CC The present invention describes a modified molecule (I) with the  
 CC biological activity of human ciliary neurotrophic factor (CNTP) which is  
 CC substantially non-immunogenic or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. Also  
 CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical  
 CC carrier (III) comprising (I) and a carrier, diluent or excipient;  
 CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with  
 CC a potential MHC Class II binding activity and created from a non-modified  
 CC CNTP selected from the 81 peptide sequences given in ABP53811 to  
 CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9  
 CC consecutive amino acid residues of (IV). The modified CNTP molecule can  
 CC be administered to humans for therapeutic purposes. The 13-mer T cell  
 CC epitope peptide and the peptide sequence is useful in the manufacture of  
 CC CNTP with substantially no or less immunogenic than any non-modified  
 CC molecule with the same biological activity when used in vivo. The  
 CC modified human CNTP can be substantially non-immunogenic or less  
 CC immunogenic than any non-modified counterpart. The sequence given in  
 CC ABP53810 represents the primary sequence of human CNTP, which is given  
 CC in the exemplification of the present invention.

CC in the exemplification of the present invention.

XX  
SQ Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5  
Db 8 ESYV 11

RESULT 69

ABP53874  
ID ABP53874 standard; Peptide; 13 AA.

XX  
AC ABP53874;

DT 06-JAN-2003 (first entry)

XX Human CNTF potential MHC class II binding activity peptide #64.

XX Human; ciliary neurotrophic factor; CNTF; reduced immunogenicity;  
KW immune response; major histocompatibility complex; MHC class II;  
KW T cell epitope; immunogenic.

XX Homo sapiens.

XX WO200270698-A2.

PN 12-SEP-2002.

XX 27-FEB-2002; 2002WO-EP02084.

XX 02-MAR-2001; 2001EP-0105089.

XX (MERE ) MERCK PATENT GMBH.

XX Carr FJ, Carter G;

XX WPI; 2003-019694/01.

XX New modified human ciliary neurotrophic factor which is substantially  
PT non-immunogenic or less immunogenic than any non-modified molecule,  
PT useful for treating conditions in a mammal

XX Claim 6; Page 11; 33pp; English.

XX The present invention describes a modified molecule (I) with the  
CC biological activity of human ciliary neurotrophic factor (CNTF) which is  
CC substantially non-immunogenic or less immunogenic than any non-modified  
CC molecule with the same biological activity when used in vivo. Also  
CC described: (1) a DNA sequence (II) coding for (I); (2) a pharmaceutical  
CC carrier (III) comprising (I) and a carrier, diluent or excipient;  
CC (3) manufacturing (M1) (I); (4) a 13mer T cell epitope peptide (IV) with  
CC a potential MHC Class II binding activity and created from a non-modified  
CC CNTF selected from the 81 peptide sequences given in ABP53811 to  
CC ABP53891; and (5) a peptide sequence (V) consisting of at least 9  
CC consecutive amino acid residues of (IV). The modified CNTF molecule can  
CC be administered to humans for therapeutic purposes. The 13-mer T cell  
CC epitope peptide and the peptide sequence is useful in the manufacture of  
CC CNTF with substantially no or less immunogenic than any non-modified  
CC molecule with the same biological activity when used in vivo. The  
CC modified human CNTF can be substantially non-immunogenic or less  
CC immunogenic than any non-modified counterpart. The sequence given in  
CC ABP53810 represents the primary sequence of human CNTF, which is given  
CC in the exemplification of the present invention.

XX Sequence 13 AA;

Query Match 44.4%; Score 4; DB 24; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5  
Db 5 ESYV 8

RESULT 70

AA83142  
ID AA83142 standard; peptide; 14 AA.

XX  
AC AA83142;

DT 14-DEC-1995 (first entry)

XX [4-Leu, 12-D-Arg, 13-Leu] motilin-(1-14) peptide (porcine).

XX motilin; gastrointestinal; diabetic gastroparesis; paralytic ileus.  
XX Synthetic.

XX Key Location/Qualifiers  
FT Misc-difference 12 /note= "D-Arg"

FT Modified-site 14

FT /note= "Gln-OH or Gln-NH2"

XX AU9455967-A.

XX 16-FEB-1995.

XX 24-JUN-1994; 94AU-0065967.

XX 06-AUG-1993; 93US-0103490.

XX (OHME-) OHMEDA PHARM PROD DIV INC.

XX Dharanipragada R, Florance JR, Galdes A, Macielag MJ;  
PI Marvin MS;

XX WPI; 1995-107112/15.

XX New motilin-like polypeptide(s) - with gastrointestinal motor  
PT stimulating activity

XX Disclosure; Page 14; 50pp; English.

XX New motilin-like polypeptides are disclosed which have gastrointestinal  
CC motor stimulating activity and which bind with high affinity to the  
CC motilin receptor and mimic the peristaltic effects of motilin on  
CC gastrointestinal tissue. The peptides are 12-22 amino acids in length  
CC and (with reference to motilin) contain one or more of (a) Leu instead  
CC of Met at position 13 for greater chemical stability, (b) D-Arg instead  
CC of L-Arg at position 12 for greater potency and (c) an N-alkylated Phe  
CC at position 1 for increased stability to biodegradation. The peptides  
CC are useful clinically for the treatment of diabetic gastroparesis,  
CC paralytic ileus and post-operative ileus.  
CC The present sequence is a specific example of the new peptides.

XX Sequence 14 AA;

Query Match 44.4%; Score 4; DB 16; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8  
Db 2 VPLF 5

RESULT 71

ABB56665  
ID ABB56665 standard; Peptide; 14 AA.



XX ABB56665;  
 XX 05-MAR-2002 (first entry)  
 XX Human SNP related amino acid sequence SEQ ID NO:1230.  
 XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 KW autoimmune disease; inflammation; cancer; nervous system disease;  
 KW infection; polymorphic protein.  
 XX  
 XX Homo sapiens.  
 XX WO200138586-A2.  
 XX 31-MAY-2001.  
 XX 22-NOV-2000; 2000WO-US32311.  
 XX 24-NOV-1999; 99US-0167383.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 XX WPI; 2001-355949/37.  
 XX Isolated human nucleic acids comprising one or more single nucleotide  
 PT polymorphisms, useful for treating a subject suffering from a  
 PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
 PT sequence polymorphism -  
 XX  
 PS Claim 1; Page 616; 674pp; English.  
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB56903 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterised  
 CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the  
 CC polymorphic protein within appropriate physiological samples).  
 XX  
 SQ Sequence 14 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 YVPL 7  
 Db 6 YVPL 9  
 RESULT 72  
 AAM97755  
 ID AAM97755 standard; Peptide; 14 AA.  
 XX AAM97755;  
 AC AAM97755;  
 XX 24-JAN-2002 (first entry)  
 XX Human peptide #1030 encoded by a SNP oligonucleotide.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX  
 XX Homo sapiens.  
 XX WO200147944-A2.  
 XX 05-JUL-2001.  
 XX 28-DEC-2000; 2000WO-US35498.  
 XX 28-DEC-1999; 99US-0173419.  
 XX 27-DEC-2000; 2000US-0173419.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 XX WPI; 2001-465210/50.  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Disclosure; Page 3893; 4143pp; English.  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VPLF 8  
 Db 1 VPLF 4  
 RESULT 73  
 AAM99155  
 ID AAM99155 standard; Peptide; 14 AA.  
 XX AAM99155;  
 AC AAM99155;  
 XX 07-DEC-2001 (first entry)  
 XX Vaccine related MHC ligand peptide SEQ ID NO:258.  
 KW Glutamic acid; glutamine; vaccine; major histocompatibility complex;  
 KW MHC; immunomodulator; antiallergic; endocrine; neuroprotectant;  
 KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;

KW medicine; pharmaceutical; immune disorder; immune deficiency;  
 KW autoimmunity; hypersensitivity; allergy; graft rejection; infection;  
 KW hormonal disorder; central nervous system disease; cancer; melanoma;  
 KW anti-melanoma vaccine; human immunodeficiency virus.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200170772-A2.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 22-MAR-2001; 2001WO-FR00872.  
 XX  
 XX 23-MAR-2000; 2000FR-0003711.  
 XX  
 XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX  
 XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;  
 XX  
 XX WPI; 2001-611470/70.  
 XX  
 XX Stabilized pharmaceutical containing N-terminal glutamic acid or  
 XX glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
 XX with strong acid -  
 XX  
 XX Claim 9; Page 75; 149pp; French.  
 XX  
 XX The present invention describes a pharmaceutical compound (I) that  
 XX contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue  
 XX in the form of an addition salt with a strong, physiologically  
 XX acceptable acid (II). Also described are: (a) a pharmaceutical  
 XX composition containing at least one (I); (b) a vaccine containing at  
 XX least one (I) where this is a major histocompatibility complex (MHC)  
 XX ligand (Ia); (c) a method for in vitro diagnosis of diseases associated  
 XX with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);  
 XX and (e) a process for preparing (I). (I) has immunomodulator, endocrine,  
 XX antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic,  
 XX fungicidal and cytostatic activities. (I) are useful in human or  
 XX veterinary medicine, in pharmaceutical compositions (for treating immune  
 XX disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,  
 XX allergy, graft rejection, infection, hormonal disorders and central  
 XX nervous system diseases), also, where (I) is a MHC ligand (Ia), in  
 XX vaccines for treatment or prevention of: (i) viral, bacterial, parasitic  
 XX or fungal infections; or (ii) of cancers. A particular application is in  
 XX anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of  
 XX diseases associated with interactions between MHC and (I), e.g. melanoma  
 XX and human immunodeficiency virus infection. AAM98898 to AAM99592  
 XX represent peptides which can be used in pharmaceutical compounds from  
 XX the present invention.  
 XX  
 XX SQ Sequence 14 AA;  
 XX  
 XX Query Match 44.4%; Score 4; DB 22; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 XX QY 1 VESY 4  
 XX |||||  
 XX 7 VESY 10  
 XX  
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 XX RESULT 74  
 XX AAB70401  
 XX ID AAB70401 standard; Peptide; 14 AA.  
 XX  
 XX AC AAB70401;  
 XX  
 XX 02-MAY-2001 (first entry)  
 XX  
 XX DE Rabies matrix protein derived peptide SEQ ID NO:35.  
 XX  
 XX KW Identification; antiviral; viral protein; viral replication; NP;  
 XX viral infection; nucleoprotein.

XX Rabies virus.  
 XX  
 XX WO200111335-A2.  
 XX  
 XX 15-FEB-2001.  
 XX  
 XX 11-AUG-2000; 2000WO-US222257.  
 XX  
 XX 11-AUG-1999; 99US-0148263.  
 XX  
 XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX  
 XX O'Neill R, Harty R, Palese PM;  
 XX  
 XX WPI; 2001-168816/17.  
 XX  
 XX Identifying a substance that inhibits the interaction between a viral  
 XX protein and a host cell protein, useful for the discovery of new  
 XX antiviral compounds -  
 XX  
 XX Example; Page 77; 147pp; English.  
 XX  
 XX The present invention describes a method (M1) for identifying a  
 XX substance that inhibits the interaction of a viral protein (VP) with a  
 XX host cell protein (HP). The method comprises: (a) contacting HP with VP  
 XX in the presence of a test substance; and (b) detecting complex formation,  
 XX where the ability of the test substance to inhibit HP/VP interaction is  
 XX indicated by a decrease in complex formation. The antiviral compounds  
 XX that inhibit the interaction between a host protein (NS1-BP or NPI-1)  
 XX and a viral protein (NS1) are useful for treating or inhibiting viral  
 XX infection, preferably influenza and rhinovirus infection, in humans.  
 XX Antiviral compounds include peptides and antibodies. In particular  
 XX compositions comprising a polypeptide containing an amino acid sequence  
 XX corresponding to the NP-NLS domain of the influenza virus NP protein,  
 XX which inhibits the specific interaction of the NPI-1 protein with the  
 XX influenza virus NP protein are useful for treating or inhibiting  
 XX influenza viral infection in humans. The present sequence represents  
 XX a peptide, which is used in an example from the present invention.  
 XX  
 XX SQ Sequence 14 AA;  
 XX  
 XX Query Match 44.4%; Score 4; DB 22; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 4 YVPL 7  
 XX |||||  
 XX 9 YVPL 12  
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 XX Db  
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 XX RESULT 75  
 XX ABP46338  
 XX ID ABP46338 standard; peptide; 14 AA.  
 XX  
 XX AC ABP46338;  
 XX  
 XX 19-AUG-2002 (first entry)  
 XX  
 XX DE Human BlyS binding scFv VH CDR3 SEQ ID 2349.  
 XX  
 XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
 XX immunosuppressive; immunostimulant; immunomodulatory; antitumorigenic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX WO200202641-A1.  
 XX  
 XX 10-JAN-2002.

```

XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
XX
XX 17-OCT-2000; 2000US-240816P.
XX
XX 16-MAR-2001; 2001US-276248P.
XX
XX 21-MAR-2001; 2001US-277379P.
XX
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 2; Page 2975; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
XX Sequence 14 AA;
XX
Query Match 44.4%; Score 4; DB 23; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PLFP 9
Db 11 PLFP 14

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 Job time : 24.9709 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 14.4419 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLPFP 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	5	55.6	15	11	US-09-880-748-2310
3	5	55.6	16	11	US-09-880-748-2263
4	4	44.4	7	9	US-09-833-067-26
5	4	44.4	7	10	US-09-758-128-45
6	4	44.4	7	10	US-09-758-426-45
7	4	44.4	7	10	US-09-758-198-45
8	4	44.4	7	11	US-09-861-661-45
9	4	44.4	7	12	US-10-052-578-286
10	4	44.4	7	12	US-10-053-520-286
11	4	44.4	7	12	US-10-286-457-308
12	4	44.4	7	12	US-10-053-498B-286
13	4	44.4	8	11	US-09-865-548A-195
14	4	44.4	8	12	US-10-052-578-82
15	4	44.4	8	12	US-10-053-520-82

4	44.4	16	8	12	US-10-053-498B-82	Sequence 82, Appl
4	44.4	17	8	16	US-10-305-346-10	Sequence 10, Appl
4	44.4	18	9	12	US-10-206-155-2	Sequence 2, Appl
4	44.4	19	9	12	US-10-360-836-1	Sequence 1, Appl
4	44.4	20	9	12	US-10-275-707-9	Sequence 9, Appl
4	44.4	21	9	14	US-10-205-150-3	Sequence 3, Appl
4	44.4	22	10	10	US-09-950-313-40	Sequence 40, Appl
4	44.4	23	10	12	US-10-360-836-81	Sequence 81, Appl
4	44.4	24	10	15	US-10-062-710-208	Sequence 208, App
4	44.4	25	11	12	US-10-239-313A-268	Sequence 268, App
4	44.4	26	12	12	US-10-239-313A-256	Sequence 256, App
4	44.4	27	13	10	US-09-764-868-1240	Sequence 1240, Ap
4	44.4	28	13	11	US-09-955-999-120	Sequence 120, App
4	44.4	29	14	11	US-09-880-748-2349	Sequence 2349, Ap
4	44.4	30	14	11	US-09-880-748-2388	Sequence 2388, Ap
4	44.4	31	14	11	US-09-880-748-2423	Sequence 2423, Ap
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4	44.4	37	14	11	US-09-880-748-2689	Sequence 2689, Ap
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4	44.4	40	15	11	US-09-880-748-2269	Sequence 2269, Ap
4	44.4	41	15	11	US-09-880-748-2270	Sequence 2270, Ap
4	44.4	42	15	11	US-09-880-748-2286	Sequence 2286, Ap
4	44.4	43	15	11	US-09-880-748-2292	Sequence 2292, Ap
4	44.4	44	15	12	US-10-161-791-379	Sequence 379, App
4	44.4	45	15	12	US-10-275-707-16	Sequence 16, Appl
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4	44.4	48	16	11	US-09-880-748-2261	Sequence 2261, Ap
4	44.4	49	16	11	US-09-880-748-2266	Sequence 2266, Ap
4	44.4	50	16	12	US-10-239-313A-259	Sequence 259, App
4	44.4	51	18	9	US-09-789-561-189	Sequence 189, App
4	44.4	52	18	14	US-10-038-612-76	Sequence 76, Appl
4	44.4	53	19	9	US-09-823-936-18	Sequence 18, Appl
4	44.4	54	19	10	US-09-755-836-23	Sequence 23, Appl
4	44.4	55	19	11	US-09-880-748-2793	Sequence 2793, Ap
4	44.4	56	19	12	US-10-236-508-28	Sequence 28, Appl
4	44.4	57	19	15	US-10-072-438-42	Sequence 42, Appl
4	44.4	58	19	15	US-10-137-765-41	Sequence 41, Appl
4	44.4	59	19	15	US-10-146-337-41	Sequence 41, Appl
4	44.4	60	19	15	US-10-286-140-18	Sequence 18, Appl
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3	33.3	62	4	8	US-08-424-550B-343	Sequence 343, App
3	33.3	63	4	9	US-09-834-765-735	Sequence 735, App
3	33.3	64	4	10	US-09-922-261-399	Sequence 399, App
3	33.3	65	4	10	US-09-742-096-26	Sequence 26, Appl
3	33.3	66	4	12	US-10-293-086-39	Sequence 39, Appl
3	33.3	67	4	12	US-10-331-907-48	Sequence 48, Appl
3	33.3	68	4	15	US-10-006-869-157	Sequence 157, App
3	33.3	69	5	10	US-09-185-908-35	Sequence 35, Appl
3	33.3	70	5	10	US-09-185-908-156	Sequence 156, App
3	33.3	71	5	12	US-10-281-479A-25	Sequence 25, Appl
3	33.3	72	5	12	US-10-275-180A-25	Sequence 25, Appl
3	33.3	73	5	12	US-10-286-132A-25	Sequence 25, Appl
3	33.3	74	5	15	US-10-006-869-160	Sequence 160, App
3	33.3	75	5	15	US-10-006-869-1282	Sequence 1282, Ap
3	33.3	76	5	15	US-10-235-483-28	Sequence 28, Appl
3	33.3	77	5	15	US-10-235-483-29	Sequence 29, Appl
3	33.3	78	5	15	US-10-283-349-40	Sequence 40, Appl
3	33.3	79	5	15	US-10-288-986-12	Sequence 12, Appl
3	33.3	80	6	8	US-08-859-699-23	Sequence 23, Appl
3	33.3	81	6	9	US-09-761-636A-12	Sequence 12, Appl
3	33.3	82	6	10	US-09-953-657-1	Sequence 1, Appl
3	33.3	83	6	10	US-09-953-657-2	Sequence 2, Appl
3	33.3	84	6	10	US-09-953-657-3	Sequence 3, Appl
3	33.3	85	6	10	US-09-953-657-6	Sequence 6, Appl
3	33.3	86	6	10	US-09-953-657-7	Sequence 7, Appl
3	33.3	87	6	10	US-09-953-657-8	Sequence 8, Appl
3	33.3	88	6	10	US-09-727-963A-85	Sequence 85, Appl

89 3 33.3 6 10 US-09-185-908-36 Sequence 36, Appl  
90 3 33.3 6 10 US-09-185-908-38 Sequence 38, Appl  
91 3 33.3 6 10 US-09-185-908-157 Sequence 157, App  
92 3 33.3 6 10 US-09-185-908-159 Sequence 159, App  
93 3 33.3 6 12 US-09-969-748C-21 Sequence 21, Appl  
94 3 33.3 6 12 US-09-949-039-17 Sequence 17, Appl  
95 3 33.3 6 12 US-10-272-497-47 Sequence 47, Appl  
96 3 33.3 6 12 US-10-272-497-51 Sequence 51, Appl  
97 3 33.3 6 12 US-10-315-515-143 Sequence 143, App  
98 3 33.3 6 12 US-10-031-874A-60 Sequence 60, Appl  
99 3 33.3 6 12 US-10-277-292-697 Sequence 697, App  
100 3 33.3 6 12 US-10-280-340-697 Sequence 697, App

## ALIGNMENTS

RESULT 1  
US-10-281-652-31  
; Sequence 31, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-31

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Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 VESYVPLFP 9  
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Db 1 VESYVPLFP 9

RESULT 2  
US-09-880-748-2310  
; Sequence 2310, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2310  
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QY 3 SYVPL 7  
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US-09-880-748-2263  
; Sequence 2263, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
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US-09-880-748-2263

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Db 8 SYVPL 12

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US-09-833-067-26  
; Sequence 26, Application US/09833067  
; Patent No. US2002005488A1  
; GENERAL INFORMATION:  
; APPLICANT: O'HANLEY, PETER  
; APPLICANT: DENICH, KENNETH  
; TITLE OF INVENTION: DISSOCIATED PILI, THEIR PRODUCTION AND USE  
; FILE REFERENCE: 050939/0102  
; CURRENT APPLICATION NUMBER: US/09/833,067  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/196,493  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Unknown Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Sequence: highly hydrophobic region  
; OTHER INFORMATION: of amino acids  
US-09-833-067-26

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Qy 5 VPLF 8  
Db 2 VPLF 5

RESULT 5  
US-09-758-128-45  
; Sequence 45, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-128-45

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Qy 6 PLPF 9  
Db 3 PLPF 6

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US-09-758-426-45  
; Sequence 45, Application US/09758426  
; Patent No. US20020169116A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020169116A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,426  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-426-45

Query Match 44.4%; Score 4; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPF 9  
Db 3 PLPF 6

RESULT 7  
US-09-758-198-45  
; Sequence 45, Application US/09758198  
; Publication No. US20020187925A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020187925A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,198  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-198-45

Query Match 44.4%; Score 4; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLPF 9  
Db 3 PLPF 6

RESULT 8  
US-09-861-661-45  
; Sequence 45, Application US/09861661  
; Publication No. US20030045676A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, DAVID J.  
; APPLICANT: GERRATY, NORMAN L.  
; APPLICANT: WESTBROOK, SIMON L.  
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF  
; FILE REFERENCE: 054270/0135  
; CURRENT APPLICATION NUMBER: US/09/861,661  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-861-661-45

Query Match 44.4%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
|||  
Db 3 PLFP 6

## RESULT 9

US-10-052-578-286  
; Sequence 286, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46003  
; CURRENT APPLICATION NUMBER: US/10/052,578  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-052-578-286

Query Match 44.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
|||  
Db 2 YVPL 5

## RESULT 10

US-10-053-520-286  
; Sequence 286, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-520-286

Query Match 44.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
|||  
Db 2 YVPL 5

## RESULT 11

US-10-286-457-308  
; Sequence 308, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 308  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, bas  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-308

Query Match 44.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8  
|||  
Db 4 VPLF 7

## RESULT 12

US-10-053-498B-286  
; Sequence 286, Application US/10053498B  
; Publication No. US20030194409A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46002  
; CURRENT APPLICATION NUMBER: US/10/053,498B  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-498B-286

Query Match 44.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|  
|  
|  
|  
Db 2 YVPL 5

## RESULT 13

US-09-865-548A-195  
; Sequence 82, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 195  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-195

Query Match 44.4%; Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|  
|  
|  
|  
Db 4 YVPL 7

## RESULT 14

US-10-052-578-82  
; Sequence 82, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46003  
; CURRENT APPLICATION NUMBER: US/10/052,578  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 82  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-052-578-82

Query Match 44.4%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|  
|  
|  
|  
Db 2 YVPL 5

## RESULT 15

US-10-053-520-82  
; Sequence 82, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 82  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-520-82

Query Match 44.4%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7  
|  
|  
|  
|  
Db 2 YVPL 5

## RESULT 16

US-10-053-498B-82  
; Sequence 82, Application US/10053498B  
; Publication No. US20030194409A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46002  
; CURRENT APPLICATION NUMBER: US/10/053,498B  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 82  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-498B-82



Query Match 44.4%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
Db 2 YVPL 5

## RESULT 17

US-10-305-346-10  
; Sequence 10, Application US/10305346  
; Publication No. US20030130195A1  
; GENERAL INFORMATION:  
; APPLICANT: AMIOT, Jean  
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS  
; FILE REFERENCE: 6013-57/US-1  
; CURRENT APPLICATION NUMBER: US/10/305,346  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins  
US-10-305-346-10

Query Match 44.4%; Score 4; DB 16; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7  
Db 1 YVPL 4

## RESULT 18

US-10-206-155-2  
; Sequence 2, Application US/10206155  
; Publication No. US20030157135A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Moriya  
; APPLICANT: Gonzalez-Asguinolaza, Gloria  
; APPLICANT: Nussenzweig, Ruth S.  
; APPLICANT: Koezuka, Yasuhiko  
; TITLE OF INVENTION: USE OF GLYCOSYLCERAMIDES AS ADJUVANTS  
; TITLE OF INVENTION: FOR VACCINES AGAINST INFECTIONS AND CANCER  
; FILE REFERENCE: 5986/1H958US1  
; CURRENT APPLICATION NUMBER: US/10/206,155  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/308,056  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: P. yoelii  
US-10-206-155-2

Query Match 44.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

## RESULT 19

US-10-360-836-1  
; Sequence 1, Application US/10360836  
; Publication No. US20030185854A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavala, Fidel  
; APPLICANT: Birkett, Ashley  
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE  
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS  
; TITLE OF INVENTION: AND MALIGNANCIES  
; FILE REFERENCE: 5986/1J876  
; CURRENT APPLICATION NUMBER: US/10/360,836  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/354,963  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Plasmodium  
US-10-360-836-1

Query Match 44.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

## RESULT 20

US-10-275-707-9  
; Sequence 9, Application US/10275707  
; Publication No. US20030194801A1  
; GENERAL INFORMATION:  
; APPLICANT: BONALDO, MIRNA C.  
; APPLICANT: GALLER, RICARDO  
; APPLICANT: FREIRE, MARCOS DA SILVA  
; APPLICANT: GARRAT, RICHARD C.  
; TITLE OF INVENTION: USE OF FLAVIVIRUS FOR THE EXPRESSION OF PROTEIN EPITOPES  
; TITLE OF INVENTION: AND DEVELOPMENT OF NEW LIVE ATTENUATED VACCINE VIRUS TO  
; TITLE OF INVENTION: IMMUNE AGAINST FLAVIVIRUS AND OTHER INFECTIOUS AGENTS  
; FILE REFERENCE: 3673-21  
; CURRENT APPLICATION NUMBER: US/10/275,707  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/BR02/00036  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: GB 0105877.5  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Plasmodium yoelii  
US-10-275-707-9

Query Match 44.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

## RESULT 21

US-10-205-150-3  
; Sequence 3, Application US/10205150  
; Publication No. US20020197269A1  
; GENERAL INFORMATION:

```
; APPLICANT: LINGNAU, KAREN ET AL.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR IMMUNOMODULATION AND PREPARATION
; TITLE OF INVENTION: OF VACCINES COMPRISING AN ANTIGEN AND AN IMMUNOGENIC OLIGODEOXYN
; TITLE OF INVENTION: AND A POLYCATIONIC POLYMER AS ADJUVANTS
; FILE REFERENCE: SONN:0180US
; CURRENT APPLICATION NUMBER: US/10/205,150
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: PCT/EP01/00087
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-205-150-3

Query Match      44.4%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      1 SYVP 4

RESULT 22
US-09-950-313-40
; Sequence 40, Application US/09950313
; Patent No. US20020102610A1
; GENERAL INFORMATION:
; APPLICANT: TOWNSEND, ROBERT
; APPLICANT: ROBINSON, ANDREW
; TITLE OF INVENTION: AUTOMATED IDENTIFICATION OF PEPTIDES
; FILE REFERENCE: 9195-064
; CURRENT APPLICATION NUMBER: US/09/950,313
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: UK 0022,136.6
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,273
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-313-40

Query Match      44.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      6 SYVP 9

RESULT 23
US-10-360-836-81
; Sequence 81, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/IJ876
; CURRENT APPLICATION NUMBER: US/10/360,836
```

```
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmidial CS T cell epitope sequence inserted
; OTHER INFORMATION: into V7 constructs
US-10-360-836-81

Query Match      44.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      2 SYVP 5

RESULT 24
US-10-062-710-208
; Sequence 208, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B
US-10-062-710-208

Query Match      44.4%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYVP 6
Db      6 SYVP 9

RESULT 25
US-10-239-313A-268
; Sequence 268, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Lilliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
```

; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 268  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Plasmodium yoelii  
US-10-239-313A-268

Query Match 44.4%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
|||  
Db 3 SYVP 6

RESULT 26  
US-10-239-313A-256  
; Sequence 256, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 256  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-256

Query Match 44.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESY 4  
|||  
Db 7 VESY 10

RESULT 27  
US-09-764-868-1240  
; Sequence 1240, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ32  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1240  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-868-1240

Query Match 44.4%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
|||  
Db 1 SYVP 4

RESULT 28  
US-09-955-999-120  
; Sequence 120, Application US/09955999  
; Publication No. US20030036505A1  
; GENERAL INFORMATION:  
; APPLICANT: Barash et al.  
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypept  
; FILE REFERENCE: PT086Pi  
; CURRENT APPLICATION NUMBER: US/09/955,999  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-999-120

Query Match 44.4%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
|||  
Db 1 SYVP 4

RESULT 29  
US-09-880-748-2349  
; Sequence 2349, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2349  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2349

Query Match 44.4%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9

```
Db          11 PLFP 14
|||||
RESULT 30
US-09-880-748-2388
; Sequence 2388, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2388
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2388

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14
|||||
US-09-880-748-2423
; Sequence 2423, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2423
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2423

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14
|||||
US-09-880-748-2467
; Sequence 2467, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2467
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2467

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14
|||||
US-09-880-748-2447
; Sequence 2447, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2447
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2447

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 PLFP 9
|||||
Db          11 PLFP 14
|||||
US-09-880-748-2467
; Sequence 2467, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2467
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2467

Query Match          44.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
|||  
Db 11 PLFP 14

RESULT 36  
US-09-880-748-2657  
; Sequence 2657, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2657  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2657

Query Match 44.4%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
|||  
Db 11 PLFP 14

RESULT 37  
US-09-880-748-2689  
; Sequence 2689, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2689  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2689

Query Match 44.4%; Score 4; DB 11; Length 14;

QY 6 PLFP 9  
|||  
Db 11 PLFP 14

RESULT 34  
US-09-880-748-2533  
; Sequence 2533, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2533  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2533

Query Match 44.4%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
|||  
Db 11 PLFP 14

RESULT 35  
US-09-880-748-2640  
; Sequence 2640, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2640  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2640

Query Match 44.4%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;

```
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db 11 PLFP 14
|||||

RESULT 38
US-10-239-313A-258
; Sequence 258, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIRA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2000-03-23
; PRIOR FILING DATE: 2000-03-23
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-239-313A-258

Query Match 44.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESY 4
Db 7 VESY 10
|||||

RESULT 39
US-09-880-748-2267
; Sequence 2267, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2267
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2267

Query Match 44.4%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 8 SYVP 11
|||||

RESULT 40
US-09-880-748-2269
; Sequence 2269, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2269
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2269

Query Match 44.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 8 SYVP 11
|||||

RESULT 41
US-09-880-748-2270
; Sequence 2270, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2270
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-2270
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Query Match 44.4%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
| | | |  
Db 8 SYVP 11

## RESULT 42

US-09-880-748-2286  
; Sequence 2286, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2286  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2286

Query Match 44.4%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
| | | |  
Db 8 SYVP 11

## RESULT 43

US-09-880-748-2292  
; Sequence 2292, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2292  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2292

Query Match 44.4%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
| | | |  
Db 8 SYVP 11

## RESULT 44

US-10-161-791-379  
; Sequence 379, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLER, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 379:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-379

Query Match 44.4%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
| | | |  
Db 8 PLFP 11

## RESULT 45

US-10-275-707-16  
; Sequence 16, Application US/10275707  
; Publication No. US20030194801A1

```
; GENERAL INFORMATION:
; APPLICANT: BONALDO, MIRNA C.
; APPLICANT: GALLER, RICARDO
; APPLICANT: FREIRE, MARCOS DA SILVA
; APPLICANT: GARRAT, RICHARD C.
; TITLE OF INVENTION: USE OF FLAVIVIRUS FOR THE EXPRESSION OF PROTEIN EPITOPES
; TITLE OF INVENTION: AND DEVELOPMENT OF NEW LIVE ATTENUATED VACCINE VIRUS TO
; TITLE OF INVENTION: IMMUNIZE AGAINST FLAVIVIRUS AND OTHER INFECTIOUS AGENTS
; FILE REFERENCE: 3673-21
; CURRENT APPLICATION NUMBER: US/10/275,707
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/BR02/00036
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: GB 0105877.5
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-275-707-16

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYVP 6
      ||||
Db      4 SYVP 7

RESULT 46
US-09-947-258-1
; Sequence 1, Application US/09947258
; Patent No. US20020102248A1
; GENERAL INFORMATION:
; APPLICANT: Chung, J.H.
; TITLE OF INVENTION: Modulating Response to Genotoxic Stress
; FILE REFERENCE: 4239-61084
; CURRENT APPLICATION NUMBER: US/09/947,258
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-258-1

Query Match      44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
      ||||
Db      5 PLFP 8

RESULT 47
US-09-947-258-4
; Sequence 4, Application US/09947258
; Patent No. US20020102248A1
; GENERAL INFORMATION:
; APPLICANT: Chung, J.H.
; TITLE OF INVENTION: Modulating Response to Genotoxic Stress
; FILE REFERENCE: 4239-61084
; CURRENT APPLICATION NUMBER: US/09/947,258
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
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```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-947-258-4

Query Match      44.4%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PLFP 9
      ||||
Db      5 PLFP 8

RESULT 48
US-09-880-748-2261
; Sequence 2261, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2261
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2261

Query Match      44.4%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYVP 6
      ||||
Db      8 SYVP 11

RESULT 49
US-09-880-748-2266
; Sequence 2266, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2266
```



```
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2266

Query Match          44.4%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
    ||||
Db 8 SYVP 11

RESULT 50
US-10-239-313A-259
; Sequence 259, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: BECK, Alain
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-259

Query Match          44.4%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESY 4
    ||||
Db 7 VESY 10

RESULT 51
US-09-789-561-189
; Sequence 189, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-189

Query Match          44.4%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9
    ||||
Db 6 PLFP 9

RESULT 52
US-10-038-612-76
; Sequence 76, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 18
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Tyk2
US-10-038-612-76

Query Match          44.4%; Score 4; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
    ||||
Db 3 YVPL 6

RESULT 53
US-09-823-936-18
; Sequence 18, Application US/09823936
; Patent No. US20020061309A1
; GENERAL INFORMATION:
; APPLICANT: GARGER, Stephen J.
; APPLICANT: GROSS, Cynthia
; APPLICANT: LINDBO, John A.
; APPLICANT: FOGUE, Gregory P.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS
; TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: 008010087CPUS05
; CURRENT APPLICATION NUMBER: US/09/823,936
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 09/ 520,967
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Tobacco mosaic virus
US-09-823-936-18

Query Match          44.4%; Score 4; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6
    ||||
Db 1 SYVP 4
```

RESULT 54  
US-09-755-836-23  
; Sequence 23, Application US/09755836  
; Patent No. US20020107387A1  
; GENERAL INFORMATION:  
; APPLICANT: Turpen, Thomas H.  
; Reinl, Stephen  
; Grill, Laurence K.  
; TITLE OF INVENTION: Production of Peptides in Plants as  
; Viral Coat Protein Fusions  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/755,836  
; FILING DATE: 05-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/324,003  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8129-087  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-755-836-23

Query Match 44.4%; Score 4; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 55  
US-09-880-748-2793  
; Sequence 2793, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2793  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2793

Query Match 44.4%; Score 4; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
Db 6 PLFP 9

RESULT 56  
US-10-236-508-28  
; Sequence 28, Application US/10236508  
; Publication No. US20030167512A1  
; GENERAL INFORMATION:  
; APPLICANT: Monto H. Kumagai  
; APPLICANT: Guy R. della-Cioppa  
; APPLICANT: Robert L. Erwin  
; APPLICANT: David R. McGee  
; TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY  
; TITLE OF INVENTION: TRANSPECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A  
; FILE OF INVENTION: DIFFERENT HOST PLANT IN A POSITIVE ORIENTATION  
; FILE REFERENCE: 008010137US05  
; CURRENT APPLICATION NUMBER: US/10/236,508  
; CURRENT FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: P. yoelii  
US-10-236-508-28

Query Match 44.4%; Score 4; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 57  
US-10-072-438-42  
; Sequence 42, Application US/10072438  
; Publication No. US20030027173A1  
; GENERAL INFORMATION:  
; APPLICANT: della-Cioppa, Guy  
; APPLICANT: Erwin, Robert L.  
; APPLICANT: Fitzmaurice, Wayne P.  
; APPLICANT: Hanley, Kathleen M.  
; APPLICANT: Kumagai, Monto H.  
; APPLICANT: Lindbo, John A.  
; APPLICANT: McGee, David R.  
; APPLICANT: Padgett, Hal S.  
; APPLICANT: Pogue, Gregory P.  
; TITLE OF INVENTION: METHOD OF DETERMINING THE FUNCTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND THE PROTEINS THEY ENCODE BY  
; TITLE OF INVENTION: TRANSPECTING THE SAME INTO A HOST  
; FILE REFERENCE: 08010137US01

; CURRENT APPLICATION NUMBER: US/10/072,438  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US/09/232,170  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: VIRAL  
US-10-072-438-42

Query Match 44.4%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 58  
US-10-137-765-41  
; Sequence 41, Application US/10137765  
; Publication No. US20030028926A1  
; GENERAL INFORMATION:  
; APPLICANT: KUMAGAI, Monto H.  
; APPLICANT: DELLA-CIOPPA, Guy R.  
; APPLICANT: ERWIN, Robert L.  
; APPLICANT: MCGEE, David R.  
; TITLE OF INVENTION: METHOD OF COMPILING A FUNCTIONAL GENE PROFILE BY  
; TITLE OF INVENTION: TRANSFECTING A NUCLEIC  
; TITLE OF INVENTION: ACID SEQUENCE OF A NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE  
; TITLE OF INVENTION: ORIENTATION  
; FILE REFERENCE: 008010137US07  
; CURRENT APPLICATION NUMBER: US/10/137,765  
; CURRENT FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: US/09/359,300A  
; PRIOR FILING DATE: 2002-04-29  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 41  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: P yoelii  
US-10-137-765-41

Query Match 44.4%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 59  
US-10-146-337-41  
; Sequence 41, Application US/10146337  
; Publication No. US20030041355A1  
; GENERAL INFORMATION:  
; APPLICANT: KUMAGAI, Monto H.  
; APPLICANT: DELLA-CIOPPA, Guy R.  
; APPLICANT: ERWIN, Robert L.  
; APPLICANT: MCGEE, David R.  
; TITLE OF INVENTION: METHOD OF COMPILING A FUNCTIONAL GENE PROFILE BY  
; TITLE OF INVENTION: TRANSFECTING A NUCLEIC  
; TITLE OF INVENTION: ACID SEQUENCE OF A NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE  
; TITLE OF INVENTION: ORIENTATION  
; FILE REFERENCE: 008010137US07  
; CURRENT APPLICATION NUMBER: US/10/146,337  
; CURRENT FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: US/09/359,300

; PRIOR FILING DATE: 2002-04-29  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 41  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: P yoelii  
US-10-146-337-41

Query Match 44.4%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 60  
US-10-286-140-18  
; Sequence 18, Application US/10286140  
; Publication No. US20030108557A1  
; GENERAL INFORMATION:  
; APPLICANT: GARGER, Stephen J.  
; APPLICANT: GROSS, Cynthia  
; APPLICANT: LINDBO, John A.  
; APPLICANT: FOGUE, Gregory P.  
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS  
; TITLE OF INVENTION: N-TERMINAL VIRAL COAT PROTEIN FUSIONS  
; FILE REFERENCE: 008010087CPUS05  
; CURRENT APPLICATION NUMBER: US/10/286,140  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US/09/823,936  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 09/ 520,967  
; PRIOR FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Tobacco mosaic virus  
US-10-286-140-18

Query Match 44.4%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6  
Db 1 SYVP 4

RESULT 61  
US-10-225-567A-1293  
; Sequence 1293, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTO  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1293  
; LENGTH: 20  
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-10-225-567A-1293

Query Match      44.4%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPLF 8
DB      9 VPLF 12

RESULT 62
US-08-424-550B-343
; Sequence 343, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-343

Query Match      33.3%; Score 3; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
DB      1 VES 3

RESULT 63
US-09-834-765-735
; Sequence 735, Application US/09834765

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LFP 9
DB      2 LFP 4

RESULT 65
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US20020155441A1

; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Paris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 735
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-735

Query Match      33.3%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SYV 5
DB      1 SYV 3

RESULT 64
US-09-922-261-399
; Sequence 399, Application US/0992261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-399

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 LFP 9
DB      2 LFP 4

RESULT 65
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US20020155441A1
```

```

; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USODIV
; CURRENT APPLICATION NUMBER: US/09/742,096
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-742-096-26

Query Match      33.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VES 3
      |||
Db      2 VES 4

RESULT 66
US-10-293-086-39
; Sequence 39, Application US/10293086
; Publication No. US20030134310A1
; GENERAL INFORMATION:
; APPLICANT: Cujec, Thomas P.
; TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors,
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 50036/048002
; CURRENT APPLICATION NUMBER: US/10/293,086
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/337,990
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-086-39

Query Match      33.3%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YVP 6
      |||
Db      2 YVP 4

RESULT 67
US-10-331-907-48
; Sequence 48, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly

```

```

; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4091
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-331-907-48

Query Match      33.3%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 VPL 7
      |||
Db      1 VPL 3

RESULT 68
US-10-006-869-157
; Sequence 157, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence

```

; FEATURE:  
; OTHER INFORMATION: Representative linear modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-157

Query Match 33.3%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
|||  
Db 1 VES 3

RESULT 69  
US-09-185-908-35  
; Sequence 35, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence  
US-09-185-908-35

Query Match 33.3%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5  
|||  
Db 3 SYV 5

RESULT 70  
US-09-185-908-156  
; Sequence 156, Application US/09185908A  
; Publication No. US20020193294A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
; TITLE OF INVENTION: FUNCTIONS  
; FILE REFERENCE: 100086.409  
; CURRENT APPLICATION NUMBER: US/09/185,908A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 156  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-185-908-156

Query Match 33.3%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SYV 5  
|||  
Db 3 SYV 5

RESULT 71  
US-10-281-479A-25  
; Sequence 25, Application US/10281479A  
; Publication No. US20030133932A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Koopman, Robert P.  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Oshumi, Jun  
; APPLICANT: LoBuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THI  
; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: 21085.0029U6  
; CURRENT APPLICATION NUMBER: US/10/281,479A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/391,478  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030133932A1e = Synt  
US-10-281-479A-25

Query Match 33.3%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYV 5  
|||  
Db 1 SYV 3

RESULT 72  
US-10-275-180A-25  
; Sequence 25, Application US/10275180A  
; Publication No. US20030190687A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Koopman, Robert P.  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPT  
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.0029U5  
; CURRENT APPLICATION NUMBER: US/10/275,180A  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 5  
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-25

```

```

Query Match      33.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SYV 5
      |||
Db      1 SYV 3

```

```

RESULT 73
US-10-286-132A-25
; Sequence 25, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Loeuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286.132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-25

```

```

Query Match      33.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 SYV 5
      |||
Db      1 SYV 3

```

```

RESULT 74
US-10-006-869-160
; Sequence 160, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-160

```

```

Query Match      33.3%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VES 3
      |||
Db      2 VES 4

```

```

RESULT 75
US-10-006-869-1282
; Sequence 1282, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1282
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-10-006-869-1282

```

```

Query Match      33.3%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VES 3
      |||
Db      2 VES 4

```

```

Search completed: November 25, 2003, 20:37:07
Job time : 14.4419 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 7.27326 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-31

Perfect score: 9

Sequence: 1 VESYVLP 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 32817 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata1/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata1/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata1/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata1/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata1/1/iaa/PCITUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata1/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	4	US-09-641-803-31
2	4	44.4	7	2	US-08-837-593-13
3	4	44.4	8	4	US-09-492-766-10
4	4	44.4	9	1	US-08-146-145-11
5	4	44.4	9	3	US-08-481-985B-137
6	4	44.4	9	4	US-09-266-764-16
7	4	44.4	10	1	US-08-362-232-3
8	4	44.4	10	1	US-08-814-196-3
9	4	44.4	11	3	US-08-652-877-72
10	4	44.4	11	3	US-08-476-515A-72
11	4	44.4	12	3	US-08-318-794-1
12	4	44.4	12	4	US-08-470-106-1
13	4	44.4	14	1	US-08-103-490A-23
14	4	44.4	14	1	US-08-103-490A-40
15	4	44.4	14	4	US-09-636-791A-35
16	4	44.4	15	3	US-08-602-999A-379
17	4	44.4	15	3	US-08-743-168B-26
18	4	44.4	15	3	US-08-743-168B-27
19	4	44.4	15	4	US-09-117-860-11
20	4	44.4	15	4	US-09-500-124-379
21	4	44.4	15	5	PCT-US96-10435-26
22	4	44.4	15	5	PCT-US96-10435-27
23	4	44.4	16	1	US-08-002-466-2
24	4	44.4	17	1	US-08-002-466-3
25	4	44.4	17	3	US-08-318-794-23
26	4	44.4	17	4	US-08-470-106-23
27	4	44.4	19	2	US-08-324-003A-23
					Sequence 31, Appl
					Sequence 13, Appl
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 137, App
					Sequence 16, Appl
					Sequence 3, Appl
					Sequence 3, Appl
					Sequence 72, Appl
					Sequence 72, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 23, Appl
					Sequence 40, Appl
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					Sequence 379, App
					Sequence 26, Appl
					Sequence 27, Appl
					Sequence 11, Appl
					Sequence 379, App
					Sequence 26, Appl
					Sequence 27, Appl
					Sequence 2, Appl
					Sequence 3, Appl
					Sequence 23, Appl
					Sequence 23, Appl

28	4	44.4	19	2	US-09-174-060-20	Sequence 20, Appl
29	4	44.4	19	3	US-08-338-382-20	Sequence 20, Appl
30	4	44.4	20	1	US-07-798-776-10	Sequence 10, Appl
31	4	44.4	20	1	US-07-798-776-11	Sequence 11, Appl
32	4	44.4	20	3	US-08-251-288A-10	Sequence 10, Appl
33	4	44.4	20	3	US-08-251-288A-11	Sequence 11, Appl
34	4	44.4	20	3	US-09-298-819A-10	Sequence 10, Appl
35	4	44.4	20	3	US-09-298-819A-11	Sequence 11, Appl
36	4	44.4	20	4	US-09-586-563C-10	Sequence 10, Appl
37	4	44.4	20	4	US-09-586-563C-11	Sequence 11, Appl
38	4	44.4	20	4	US-09-586-562C-10	Sequence 10, Appl
39	4	44.4	20	4	US-09-586-562C-11	Sequence 11, Appl
40	3	33.3	4	2	US-08-459-568-33	Sequence 33, Appl
41	3	33.3	4	2	US-08-399-411-33	Sequence 33, Appl
42	3	33.3	4	2	US-08-803-899-22	Sequence 22, Appl
43	3	33.3	4	2	US-08-789-347A-16	Sequence 16, Appl
44	3	33.3	4	2	US-08-789-347A-17	Sequence 17, Appl
45	3	33.3	4	3	US-08-516-859A-33	Sequence 33, Appl
46	3	33.3	4	3	US-08-973-462-26	Sequence 26, Appl
47	3	33.3	4	3	US-09-461-697-339	Sequence 399, App
48	3	33.3	4	4	US-09-586-472-33	Sequence 33, Appl
49	3	33.3	4	4	US-09-187-859-157	Sequence 157, App
50	3	33.3	4	4	US-08-469-260A-343	Sequence 343, App
51	3	33.3	4	4	US-09-528-706-33	Sequence 33, Appl
52	3	33.3	4	4	US-09-060-299-48	Sequence 48, Appl
53	3	33.3	4	4	US-09-402-923A-48	Sequence 48, Appl
54	3	33.3	4	4	US-08-488-446-343	Sequence 343, App
55	3	33.3	4	4	US-09-839-542B-157	Sequence 157, App
56	3	33.3	4	4	US-08-467-344A-343	Sequence 343, App
57	3	33.3	5	1	US-08-170-360-14	Sequence 14, Appl
58	3	33.3	5	1	US-08-358-160-195	Sequence 195, App
59	3	33.3	5	1	US-08-358-160-199	Sequence 199, App
60	3	33.3	5	2	US-08-747-137-168	Sequence 168, App
61	3	33.3	5	3	US-08-836-561-40	Sequence 40, Appl
62	3	33.3	5	3	US-09-171-554-12	Sequence 12, Appl
63	3	33.3	5	4	US-09-187-859-1282	Sequence 1282, Ap
64	3	33.3	5	4	US-09-187-859-1282	Sequence 1282, Ap
65	3	33.3	5	4	US-09-646-154-11	Sequence 11, Appl
66	3	33.3	5	4	US-08-766-596A-28	Sequence 28, Appl
67	3	33.3	5	4	US-08-766-596A-29	Sequence 29, Appl
68	3	33.3	5	4	US-09-434-122-40	Sequence 40, Appl
69	3	33.3	5	4	US-09-839-542B-160	Sequence 160, App
70	3	33.3	5	4	US-08-205-938A-3	Sequence 3, Appl
71	3	33.3	6	1	US-08-282-758B-40	Sequence 40, Appl
72	3	33.3	6	1	US-08-405-230-2	Sequence 2, Appl
73	3	33.3	6	1	US-08-595-718A-1	Sequence 1, Appl
74	3	33.3	6	1	US-08-595-718A-2	Sequence 2, Appl
75	3	33.3	6	1	US-08-595-718A-3	Sequence 3, Appl
76	3	33.3	6	1	US-08-595-718A-6	Sequence 6, Appl
77	3	33.3	6	1	US-08-595-718A-7	Sequence 7, Appl
78	3	33.3	6	1	US-08-595-718A-8	Sequence 8, Appl
79	3	33.3	6	1	US-08-468-543-12	Sequence 12, Appl
80	3	33.3	6	1	US-08-403-378B-11	Sequence 11, Appl
81	3	33.3	6	2	US-08-910-990-2	Sequence 2, Appl
82	3	33.3	6	2	US-08-376-967-6	Sequence 6, Appl
83	3	33.3	6	2	US-08-376-967-6	Sequence 6, Appl
84	3	33.3	6	2	US-08-317-310A-42	Sequence 42, Appl
85	3	33.3	6	2	US-08-286-819A-34	Sequence 34, Appl
86	3	33.3	6	2	US-08-469-692-12	Sequence 12, Appl
87	3	33.3	6	2	US-08-398-046-12	Sequence 12, Appl
88	3	33.3	6	3	US-08-980-357-34	Sequence 34, Appl
89	3	33.3	6	4	US-09-187-859-159	Sequence 159, App
90	3	33.3	6	4	US-09-187-859-161	Sequence 161, App
91	3	33.3	6	4	US-09-187-859-163	Sequence 163, App
92	3	33.3	6	4	US-09-187-859-1111	Sequence 1111, Ap
93	3	33.3	6	4	US-09-187-859-1111	Sequence 1111, Ap
94	3	33.3	6	4	US-09-187-859-1155	Sequence 1155, Ap
95	3	33.3	6	4	US-09-187-859-1157	Sequence 1157, Ap
96	3	33.3	6	4	US-09-187-859-1242	Sequence 1242, Ap
97	3	33.3	6	4	US-09-187-859-1281	Sequence 1281, Ap
98	3	33.3	6	4	US-09-187-859-1283	Sequence 1283, Ap
99	3	33.3	6	4	US-09-187-859-1285	Sequence 1285, Ap
100	3	33.3	6	4	US-09-187-859-1285	Sequence 1285, Ap



ALIGNMENTS

RESULT 1  
US-09-641-803-31  
; Sequence 31, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-31  
  
Query Match 100.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VESYVPLFP 9  
| | | | | | | | | |  
Db 1 VESYVPLFP 9  
  
RESULT 2  
US-08-837-593-13  
; Sequence 13, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhuqun  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252

; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-837-593-13  
  
Query Match 44.4%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PLFP 9  
| | | | |  
Db 2 PLFP 5  
  
RESULT 3  
US-09-492-766-10  
; Sequence 10, Application US/09492766  
; Patent No. 6506732  
; GENERAL INFORMATION:  
; APPLICANT: AMTOT, Jean  
; TITLE OF INVENTION: ENZYMTIC HYDROLYSATE OF MILK PROTEINS  
; FILE REFERENCE: 6013-57"US"  
; CURRENT APPLICATION NUMBER: US/09/492,766  
; CURRENT FILING DATE: 2000-01-27  
; EARLIER APPLICATION NUMBER: 60/117,661  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
; OTHER INFORMATION: proteins  
US-09-492-766-10  
  
Query Match 44.4%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 YVPL 7  
| | | |  
Db 1 YVPL 4  
  
RESULT 4  
US-08-146-145-11  
; Sequence 11, Application US/08146145  
; Patent No. 5747269  
; GENERAL INFORMATION:  
; APPLICANT: Rammensee, Hans-Georg  
; APPLICANT: Falk, Kirsten  
; APPLICANT: R tzsckke, Olaf  
; APPLICANT: Scevanovic, Stefan  
; APPLICANT: Jung, G nther  
; TITLE OF INVENTION: DETERMINATION OF PEPTIDE MOTIFS ON MHC  
; TITLE OF INVENTION: MOLECULES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,145
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-146-145-11

Query Match 44.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 5
US-08-481-985B-137
; Sequence 137, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-137

Query Match 44.4%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 6
US-09-266-764-16
; Sequence 16, Application US/09266764
; Patent No. 6545139
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: Compositions and Methods For the Treatment and
; TITLE OF INVENTION: Prevention of Metastatic Disorders
; FILE REFERENCE: 00A146.0122
; CURRENT APPLICATION NUMBER: US/09/266,764
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/077,934
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-266-764-16

Query Match 44.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9
Db 6 PLFP 9

RESULT 7
US-08-362-232-3
; Sequence 3, Application US/08362232
; Patent No. 5641667
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method
; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.0 for DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,232  
; FILING DATE: 22-December-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CU 125/93  
; FILING DATE: 23-December-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baron, Ronald J.  
; REGISTRATION NUMBER: 29,281  
; REFERENCE/DOCKET NUMBER: 294-29  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-362-232-3

Query Match 44.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
Db 3 PLFP 6

## RESULT 8

US-08-814-196-3  
; Sequence 3, Application US/08814196  
; Patent No. 5731173  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Fructosyltransferase Enzyme, Method  
; TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11758  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 6.0 for DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,196  
; FILING DATE: 10-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,232  
; FILING DATE: 22-December-1994  
; APPLICATION NUMBER: CU 125/93  
; FILING DATE: 23-December-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baron, Ronald J.  
; REGISTRATION NUMBER: 29,281  
; REFERENCE/DOCKET NUMBER: 294-29  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-814-196-3

Query Match 44.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
Db 3 PLFP 6

## RESULT 9

US-08-652-877-72  
; Sequence 72, Application US/08652877  
; Patent No. 6187548  
; GENERAL INFORMATION:  
; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjaln, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rofer Inc.  
; STREET: 500 Arcola Rd., 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.5.1  
; SOFTWARE: Word 6.0 (patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,877  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15203  
; FILING DATE: 22-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,314  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355E-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal  
US-08-652-877-72

Query Match 44.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VESY 4  
Db 3 VESY 6

## RESULT 10

US-08-476-515A-72  
; Sequence 72, Application US/08476515A  
; Patent No. 6239270  
; GENERAL INFORMATION:  
; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjaln, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Martin Savitzky  
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
; STREET: 3C43,  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Compaq PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 7.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/SE94/00483  
; FILING DATE: 24-MAY-1994

; APPLICATION NUMBER: SE 9301764-8  
; FILING DATE: 24-MAY-1993  
; TELECOMMUNICATION INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355D  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-476-515A-72

Query Match 44.4%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VESY 4  
Db 3 VESY 6

## RESULT 11

US-08-318-794-1  
; Sequence 1, Application US/08318794  
; Patent No. 6022726  
; GENERAL INFORMATION:  
; APPLICANT: Palese, Peter  
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED  
; TITLE OF INVENTION: VIRUSES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,794  
; FILING DATE: 20-DEC-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7682-019  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-318-794-1

Query Match 44.4%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYVP 6  
Db 4 SYVP 7

## RESULT 12

US-08-470-106-1  
; Sequence 1, Application US/08470106  
; Patent No. 6316243  
; GENERAL INFORMATION:  
; APPLICANT: Palese, Peter  
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED  
; VIRUSES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/470,106
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-470-106-1

Query Match 44.4%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
DB 4 SYVP 7

RESULT 13
US-08-103-490A-23
; Sequence 23, Application US/08103490A
; Patent No. 5422341
; GENERAL INFORMATION:
; APPLICANT: Macielag, Mark J.
; TITLE OF INVENTION: Motilin-Like Polypeptides With
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc.
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H817
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-771-6292
; TELEFAX: 908-771-6159
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-103-490A-40

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 14
US-08-103-490A-40
; Sequence 40, Application US/08103490A
; Patent No. 5422341
; GENERAL INFORMATION:
; APPLICANT: Macielag, Mark J.
; TITLE OF INVENTION: Motilin-Like Polypeptides With
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc.
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H817
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-771-6292
; TELEFAX: 908-771-6159
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-103-490A-40

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 15
US-09-636-791A-35
; Sequence 35, Application US/09636791A
; Patent No. 6503703
; GENERAL INFORMATION:
; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; TITLE OF INVENTION: PROTEINS REQUIRED FOR VIRAL REPLICATION
; FILE REFERENCE: 6923-077-999
; CURRENT APPLICATION NUMBER: US/09/636,791A
```

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MOLECULE TYPE: peptide
US-08-103-490A-23

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 14
US-08-103-490A-40
; Sequence 40, Application US/08103490A
; Patent No. 5422341
; GENERAL INFORMATION:
; APPLICANT: Macielag, Mark J.
; TITLE OF INVENTION: Motilin-Like Polypeptides With
; TITLE OF INVENTION: Gastrointestinal Motor Stimulating Activity
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The BOC Group, Inc.
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24,864
; REFERENCE/DOCKET NUMBER: 92H817
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-771-6292
; TELEFAX: 908-771-6159
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-103-490A-40

Query Match 44.4%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLF 8
DB 2 VPLF 5

RESULT 15
US-09-636-791A-35
; Sequence 35, Application US/09636791A
; Patent No. 6503703
; GENERAL INFORMATION:
; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; TITLE OF INVENTION: PROTEINS REQUIRED FOR VIRAL REPLICATION
; FILE REFERENCE: 6923-077-999
; CURRENT APPLICATION NUMBER: US/09/636,791A
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; CURRENT FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/148,263  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Rabies virus  
US-09-636-791A-35

Query Match 44.4%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 YVPL 7  
|||  
DB 9 YVPL 12

RESULT 16  
US-08-602-999A-379  
; Sequence 379, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PSNNT  
; INFORMATION FOR SEQ ID NO: 379:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-379

Query Match 44.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 PLFP 9  
|||

DB 8 PLFP 11

RESULT 17  
US-08-743-168B-26  
; Sequence 26, Application US/08743168B  
; Patent No. 6271015  
; GENERAL INFORMATION:  
; APPLICANT: Gilula, No. 6271015ton B  
; APPLICANT: Cravatt, Benjamin F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute  
; STREET: 10550 No. 6271015th Torrey Pines Road  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/743,168B  
; FILING DATE: 04-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/489,535  
; FILING DATE: 12-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSRI 485.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 784-2937  
; TELEFAX: (619) 784-9399  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-743-168B-26

Query Match 44.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLFP 9  
|||  
DB 12 PLFP 15

RESULT 18  
US-08-743-168B-27  
; Sequence 27, Application US/08743168B  
; Patent No. 6271015  
; GENERAL INFORMATION:  
; APPLICANT: Gilula, No. 6271015ton B  
; APPLICANT: Cravatt, Benjamin F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute  
; STREET: 10550 No. 6271015th Torrey Pines Road  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/743,168B  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/489,535  
FILING DATE: 12-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 485.2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-743-168B-27

Query Match 44.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 PLFP 9  
DB 2 PLFP 5

RESULT 19  
US-09-117-860-11  
Sequence 11, Application US/09117860A  
Patent No. 6338955  
GENERAL INFORMATION:  
APPLICANT: OGURI, Suguru  
APPLICANT: MINOWA, Mari  
APPLICANT: YOSHIDA, Aruto  
APPLICANT: TANIGUCHI, Naoyuki  
APPLICANT: TAKEUCHI, Nakoto  
TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTTRANSFERASE AND GENE  
FILE REFERENCE: 081356/0119  
CURRENT APPLICATION NUMBER: US/09/117,860A  
CURRENT FILING DATE: 1998-08-12  
EARLIER APPLICATION NUMBER: WO PCT/JP97/04546  
EARLIER FILING DATE: 1997-12-10  
EARLIER APPLICATION NUMBER: JP 161462/1997  
EARLIER FILING DATE: 1997-06-18  
EARLIER APPLICATION NUMBER: JP 332411/1996  
EARLIER FILING DATE: 1996-12-12  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Bovine  
US-09-117-860-11

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 VESY 4  
||||

DB 6 VESY 9  
RESULT 20  
US-09-500-124-379  
Sequence 379, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 379:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-379

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 PLFP 9  
DB 8 PLFP 11

RESULT 21  
PCT-US96-10435-26  
Sequence 26, Application PC/TUS9610435  
GENERAL INFORMATION:  
APPLICANT: The Scripps Research Institute  
TITLE OF INVENTION: CIS-9, 10-OCTADECENAMIDASE  
NUMBER OF SEQUENCES: 32  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10435  
; FILING DATE: 12-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/489,535  
; APPLICATION NUMBER: 12-JUN-1995  
; FILING DATE: 12-JUN-1995  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
PCT-US96-10435-26

Query Match 44.4%; Score 4; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
Db 12 PLFP 15

RESULT 22  
PCT-US96-10435-27  
; Sequence 27, Application PC/TUS9610435  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; TITLE OF INVENTION: CIS-9, 10-OCTADECENAMIDASE  
; NUMBER OF SEQUENCES: 32  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10435  
; FILING DATE: 12-JUN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/489,535  
; FILING DATE: 12-JUN-1995  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
PCT-US96-10435-27

Query Match 44.4%; Score 4; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLFP 9  
Db 2 PLFP 5

RESULT 23  
US-08-002-466-2  
; Sequence 2, Application US/08002466  
; Patent No. 5580561  
; GENERAL INFORMATION:  
; APPLICANT: Cercek, Boris  
; TITLE OF INVENTION: Inhibition of Suppression of Immune  
; Defense Caused by Peptides Active in the Structuredness of  
; the Cytoplasmic Matrix (SCM) Assay

; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/002,466  
; APPLICATION NUMBER: 19930108  
; FILING DATE: 19930108  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/539,686  
; FILING DATE: 18-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/167/007  
; FILING DATE: 03-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/022,759  
; FILING DATE: 06-MAR-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farber, Michael B  
; REGISTRATION NUMBER: 32,612  
; REFERENCE/DOCKET NUMBER: 8941  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-002-466-2

Query Match 44.4%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPLF 8  
Db 10 VPLF 13

RESULT 24  
US-08-002-466-3  
; Sequence 3, Application US/08002466  
; Patent No. 5580561  
; GENERAL INFORMATION:  
; APPLICANT: Cercek, Boris  
; TITLE OF INVENTION: Inhibition of Suppression of Immune  
; Defense Caused by Peptides Active in the Structuredness of  
; the Cytoplasmic Matrix (SCM) Assay  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:



;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 19930108  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION NUMBER: US/08/002,466  
;; FILING DATE: 18-JUN-1990  
;; APPLICATION NUMBER: US 07/539,686  
;; FILING DATE: 03-MAR-1988  
;; APPLICATION NUMBER: US 07/167/007  
;; FILING DATE: 06-MAR-1987  
;; APPLICATION NUMBER: US 07/022,759  
;; FILING DATE: 06-MAR-1987  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Farber, Michael B  
;; REGISTRATION NUMBER: 32,612  
;; REFERENCE/DOCKET NUMBER: 8941  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (818) 796-4000  
;; TELEFAX: (818) 795-6321  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;;  
US-08-002-466-3  
  
Query Match 44.4%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 5 VPLF 8  
Db 10 VPLF 13  
  
RESULT 25  
US-08-318-794-23  
; Sequence 23, Application US/08318794  
; Patent No. 6022726  
; GENERAL INFORMATION:  
; APPLICANT: Palese, Peter  
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED  
; TITLE OF INVENTION: VIRUSES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-DEC-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 7682-019  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;;  
US-08-318-794-23  
  
Query Match 44.4%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 3 SYVP 6  
Db 5 SYVP 8  
  
RESULT 26  
US-08-470-106-23  
; Sequence 23, Application US/08470106  
; Patent No. 6316243  
; GENERAL INFORMATION:  
; APPLICANT: Palese, Peter  
; TITLE OF INVENTION: GENETICALLY ENGINEERED ATTENUATED  
; TITLE OF INVENTION: VIRUSES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: US/08/470,106  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7682-025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
; US-08-470-106-23  
  
Query Match 44.4%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 3 SYVP 6  
Db 5 SYVP 8

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RESULT 27
US-08-324-003A-23
; Sequence 23, Application US/08324003A
; Patent No. 5977438
; GENERAL INFORMATION:
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Reini, Stephen
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: Production of Peptides in Plants as
; TITLE OF INVENTION: Viral Coat Protein Fusions
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,003A
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8129-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-324-003A-23
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYVP 6
Db 1 SYVP 4

RESULT 28
US-09-174-060-20
; Sequence 20, Application US/09174060
; Patent No. 5989554
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA

QY 4 YVPL 7
Db 6 YVPL 9

RESULT 29
US-08-338-382-20
; Sequence 20, Application US/08338382
; Patent No. 6069230
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,382
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-174-060-20
Query Match 44.4%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVPL 7
Db 6 YVPL 9
```

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; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-382-20

Query Match 44.4%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVPL 7
Db 6 YVPL 9

RESULT 30
US-07-798-776-10
; Sequence 10, Application US/07798776
; Patent No. 5434074
; GENERAL INFORMATION:
; APPLICANT: GIBSON, D. WADE
; APPLICANT: WELCH, ANTHONY R.
; TITLE OF INVENTION: HERPES VIRUS PROTEINASE AND METHOD OF
; TITLE OF INVENTION: ASSAYING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/798,776
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOULKE, CYNTHIA L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 1107.07080
; TELEPHONE: (202) 508-9100
; TELEFAX: (202) 508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Simian cytomegalovirus
US-07-798-776-10

Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYV 5
Db 5 ESYV 8

RESULT 31
US-07-798-776-11
; Sequence 11, Application US/07798776
; Patent No. 5434074
; GENERAL INFORMATION:
; APPLICANT: GIBSON, D. WADE
; APPLICANT: WELCH, ANTHONY R.
; TITLE OF INVENTION: HERPES VIRUS PROTEINASE AND METHOD OF
; TITLE OF INVENTION: ASSAYING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/798,776
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOULKE, CYNTHIA L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 1107.07080
; TELEPHONE: (202) 508-9100
; TELEFAX: (202) 508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Human cytomegalovirus
US-07-798-776-11

Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESYV 5
Db 5 ESYV 8

RESULT 32
US-08-251-288A-10
; Sequence 10, Application US/08251288A
; Patent No. 6001967
; GENERAL INFORMATION:
; APPLICANT: Gibson, Wade
; APPLICANT: Welch, Anthony
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD
; TITLE OF INVENTION: OF ASSAYING
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; STRAIN: Colburn
US-07-798-776-10

Query Match 44.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

;; ADDRESSEE: Banner & Witcoff  
;; STREET: 1001 G Street, NW  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20001  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/251,288A  
;; FILING DATE: 31-MAY-1994  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kagan, Sarah A  
;; REGISTRATION NUMBER: 32141  
;; REFERENCE/DOCKET NUMBER: 01107.46284  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: No. 6001967e  
;; US-08-251-288A-10  
;;  
Query Match 44.4%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Qy 2 ESYV 5  
Db 5 ESYV 8  
|||||  
RESULT 33  
US-08-251-288A-11  
; Sequence 11, Application US/08251288A  
; Patent No. 6001967  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD  
; TITLE OF INVENTION: OF ASSAYING  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/251,288A  
; FILING DATE: 31-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kagan, Sarah A  
;; REGISTRATION NUMBER: 32141  
;; REFERENCE/DOCKET NUMBER: 01107.46284  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-508-9100  
;; TELEFAX: 202-508-9299  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: No. 6001967e  
;; US-08-251-288A-11  
;;  
Query Match 44.4%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Qy 2 ESYV 5  
Db 5 ESYV 8  
|||||  
RESULT 34  
US-09-298-819A-10  
; Sequence 10, Application US/09298819A  
; Patent No. 6077679  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD  
; TITLE OF INVENTION: OF ASSAYING  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/298,819A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/251,288  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A  
; REGISTRATION NUMBER: 32141  
; REFERENCE/DOCKET NUMBER: 01107.46284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6077679e  
; US-09-298-819A-10  
; Query Match 44.4%; Score 4; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 2 ESYV 5  
Db 5 ESYV 8

RESULT 35  
US-09-298-819A-11  
; Sequence 11, Application US/09298819A  
; Patent No. 6077679  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: HERPES PROTEINASE AND METHOD  
; TITLE OF INVENTION: OF ASSAYING  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/298,819A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/251,288  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A  
; REGISTRATION NUMBER: 32141  
; REFERENCE/DOCKET NUMBER: 01107.46284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6077679e  
US-09-298-819A-11

Query Match 44.4%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 2 ESYV 5  
Db 5 ESYV 8

RESULT 36  
US-09-586-563C-10  
; Sequence 10, Application US/09586563C  
; Patent No. 6406902  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying  
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003  
; CURRENT APPLICATION NUMBER: US/09/586,563C

; CURRENT FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/298,819  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian cytomegalovirus  
US-09-586-563C-10

Query Match 44.4%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 2 ESYV 5  
Db 5 ESYV 8

RESULT 37  
US-09-586-563C-11  
; Sequence 11, Application US/09586563C  
; Patent No. 6406902  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying  
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003  
; CURRENT APPLICATION NUMBER: US/09/586,563C  
; CURRENT FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/298,819  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian cytomegalovirus  
US-09-586-563C-11

Query Match 44.4%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 2 ESYV 5  
Db 5 ESYV 8

RESULT 38  
US-09-586-562C-10  
; Sequence 10, Application US/09586562C  
; Patent No. 6410296  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying  
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003  
; CURRENT APPLICATION NUMBER: US/09/586,562C  
; CURRENT FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/298,819  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian cytomegalovirus  
US-09-586-562C-10

Query Match 44.4%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESYV 5  
|||  
Db 5 ESYV 8

RESULT 39  
US-09-586-562C-11  
; Sequence 11, Application US/09586562C  
; Patent No. 6410296  
; GENERAL INFORMATION:  
; APPLICANT: Gibson, Wade  
; APPLICANT: Welch, Anthony  
; TITLE OF INVENTION: Herpes Proteinase and Method of Assaying  
; FILE REFERENCE: Gibson Herpes Proteinase Matter 00003  
; CURRENT APPLICATION NUMBER: US/09/586,562C  
; CURRENT FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/298,819  
; PRIOR FILING DATE: 1998-04-26  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian cytomegalovirus  
US-09-586-562C-11

Query Match 44.4%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 ESYV 5  
|||  
Db 5 ESYV 8

RESULT 40  
US-08-459-568-33  
; Sequence 33, Application US/08459568  
; Patent No. 5811304  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; TITLE OF INVENTION: Zinc Finger Proteins  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,568  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER:  
; FILING DATE: 06-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1264  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-459-568-33

Query Match 33.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6  
|||  
Db 1 YVP 3

RESULT 41  
US-08-399-411-33  
; Sequence 33, Application US/08399411  
; Patent No. 5831008  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; TITLE OF INVENTION: Zinc Finger Proteins  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/399,411  
; FILING DATE: 06-MAR-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1264  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-399-411-33

Query Match 33.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6  
|||  
Db 1 YVP 3

RESULT 42  
US-08-803-899-22  
; Sequence 22, Application US/08803899  
; Patent No. 5912224  
; GENERAL INFORMATION:  
; APPLICANT: DONAHOE, PATRICIA K.  
; APPLICANT: WANG, TONGWEN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING  
; TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS  
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,899  
; FILING DATE: 02/21/1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/012,054  
; FILING DATE: 02/22/1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 35,688  
; REFERENCE/DOCKET NUMBER: 0609.4240001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-803-899-22

Query Match 33.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
|||  
Db 2 PLF 4

RESULT 43  
US-08-789-347A-16  
; Sequence 16, Application US/08789347A  
; Patent No. 5922837  
; GENERAL INFORMATION:  
; APPLICANT: MEINKE, PETER T.  
; APPLICANT: RATTRAY, SANDRA J.  
; APPLICANT: SCHMATZ, DENNIS M.  
; TITLE OF INVENTION: ANTIPROTOZOAL CYCLIC TETR  
; TITLE OF INVENTION: APEPTIDES  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,347A  
; FILING DATE: 27-JAN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/010,931  
; FILING DATE: 31-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yang, Mollie M  
; REGISTRATION NUMBER: 32,718  
; REFERENCE/DOCKET NUMBER: 19628  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-6343  
; TELEFAX: 908-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
US-08-789-347A-16

Query Match 33.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLF 8  
|||  
Db 1 PLF 3

RESULT 44  
US-08-789-347A-17  
; Sequence 17, Application US/08789347A  
; Patent No. 5922837  
; GENERAL INFORMATION:  
; APPLICANT: MEINKE, PETER T.  
; APPLICANT: RATTRAY, SANDRA J.  
; APPLICANT: SCHMATZ, DENNIS M.  
; TITLE OF INVENTION: ANTIPROTOZOAL CYCLIC TETR  
; TITLE OF INVENTION: APEPTIDES  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,347A  
; FILING DATE: 27-JAN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/010,931  
; FILING DATE: 31-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yang, Mollie M  
; REGISTRATION NUMBER: 32,718  
; REFERENCE/DOCKET NUMBER: 19628  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-6343  
; TELEFAX: 908-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide

US-08-789-347A-17

Query Match 33.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8  
|||  
Db 1 PLF 3  
|||

RESULT 45

US-08-516-859A-33  
; Sequence 33, Application US/08516859A  
; Patent No. 6069231  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; TITLE OF INVENTION: Zinc Finger Proteins  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/516,859A  
; FILING DATE: 18-AUG-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/399,411  
; FILING DATE: 06-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/292,683  
; FILING DATE: 18-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1776  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-516-859A-33

Query Match 33.3%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6  
|||  
Db 1 YVP 3  
|||

RESULT 46

US-08-973-462-26  
; Sequence 26, Application US/08973462B  
; Patent No. 6191270  
; GENERAL INFORMATION:  
; APPLICANT: DRUILHE, PIERRE  
; APPLICANT: DAUBERSTES, PIERRE  
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 0660-0125-0 PCT  
; CURRENT APPLICATION NUMBER: US/08/973,462B  
; CURRENT FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: PCT/FR96/00894  
; EARLIER FILING DATE: 1996-06-12  
; EARLIER APPLICATION NUMBER: FR 95/07007  
; EARLIER FILING DATE: 1995-06-13  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide  
US-08-973-462-26

Query Match 33.3%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3  
|||  
Db 2 VES 4  
|||

RESULT 47

US-09-461-697-399  
; Sequence 399, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; TITLE OF INVENTION: CELL DEATH  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 399  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-461-697-399

Query Match 33.3%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFP 9  
|||  
Db 2 LFP 4  
|||

RESULT 48

US-09-586-472-33  
; Sequence 33, Application US/09586472  
; Patent No. 6323335  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; Zinc Finger Proteins  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700



CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/586,472  
FILING DATE: 01-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/528,706  
FILING DATE: 17-MAR-2000  
APPLICATION NUMBER: US 08/516,859  
FILING DATE: 18-AUG-1995  
APPLICATION NUMBER: US 08/399,411  
FILING DATE: 06-MAR-1995  
APPLICATION NUMBER: US 08/292,683  
FILING DATE: 18-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 4130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-586-472-33

Query Match 33.3%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6  
Db 1 YVP 3

RESULT 49  
US-09-187-859-157  
Sequence 157, Application US/09187859A  
Patent No. 6358920  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407C1  
CURRENT APPLICATION NUMBER: US/09/187,859A  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 157  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative linear modulating agent based on  
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-157

Query Match 33.3%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
Db 1 VES 3  
RESULT 50  
US-08-469-260A-343  
Sequence 343, Application US/08469260A  
Patent No. 6451578  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: ISAK K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 343:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-260A-343

Query Match 33.3%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
Db 1 VES 3

RESULT 51  
US-09-528-706-33  
Sequence 33, Application US/09528706  
Patent No. 648985  
GENERAL INFORMATION:  
APPLICANT: Huang, Shi  
TITLE OF INVENTION: Retinoblastoma Protein - Interacting

```

; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; CLASSIFICATION:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-528-706-33

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YVP 6
Db 1 YVP 3

RESULT 52
US-09-060-299-48
; Sequence 48, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE: 14-Feb-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4091
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-060-299-48

Query Match 33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 1 VPL 3

RESULT 53
US-09-402-923A-48
; Sequence 48, Application US/09402923A
; Patent No. 6555654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6555654el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740

```

```
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-402-923A-48

Query Match      33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPL 7
      |||
Db      1 VPL 3

RESULT 54
US-08-488-446-343
; Sequence 343, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAM J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
;
; FILING DATE: 05-JUN-1997
; MOLECULE TYPE: protein
US-08-488-446-343

Query Match      33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
      |||
Db      1 VES 3

RESULT 55
US-09-839-542B-157
; Sequence 157, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-157

Query Match      33.3%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VES 3
      |||
Db      1 VES 3

RESULT 56
US-08-467-344A-343
; Sequence 343, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAM J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMBSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 343:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 343:  
US-08-467-344A-343  
  
Query Match 33.3%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 1 VES 3  
|||  
Db 1 VES 3  
  
RESULT 57  
US-08-170-360-14  
; Sequence 14, Application US/08170360  
; Patent No. 5656602  
; GENERAL INFORMATION:  
; APPLICANT: Tseng, Albert P. S.  
; APPLICANT: Inglis, Adam  
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/170,360  
; FILING DATE: 03-MAR-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PCT/AU92/00333  
; FILING DATE: 06-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PK 7058  
; FILING DATE: 04-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1871-104A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-170-360-14  
  
Query Match 33.3%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 2 ESY 4  
|||  
Db 2 ESY 4  
  
RESULT 58  
US-08-358-160-195  
; Sequence 195, Application US/08358160  
; Patent No. 5663143  
; GENERAL INFORMATION:  
; APPLICANT: LEY, Arthur C.  
; APPLICANT: LADNER, Robert C.  
; APPLICANT: GUTERMAN, Sonia K.  
; APPLICANT: ROBERTS, Bruce L.  
; APPLICANT: MARKLAND, William  
; APPLICANT: KENT, Rachel B.  
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ  
; DOMAIN THAT INHIBIT HUMAN NEUTROPHIL ELASTASE  
; NUMBER OF SEQUENCES: 234  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W. Suite 300  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,160  
; FILING DATE: 16-DEC-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,031  
; FILING DATE: 13-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/009,319  
; FILING DATE: 26-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/664,989  
; FILING DATE: 01-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/487,063  
; FILING DATE: 02-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/240,160  
; FILING DATE: 02-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cooper, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: LEY=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528



```
Db          1 VES 3
[[[
; CURRENT APPLICATION NUMBER: US/09/171,554
; CURRENT FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: 60/034,041
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: 60/052,860
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059,806
; PRIOR FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: N-terminal is capped with acetyl
; NAME/KEY: PEPTIDE
; LOCATION: (5)
; OTHER INFORMATION: C-terminal is modified with activated carbonyl:
; OTHER INFORMATION: C(O)-NH-CH2-phenyl
; OTHER INFORMATION: Description of Artificial Sequence:peptidomimetic
; OTHER INFORMATION: inhibitor
; US-09-171-554-12

Query Match          33.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 SYV 5
          |||
Db          1 SYV 3
          |||

RESULT 63
US-09-187-859-160
; Sequence 160, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
; US-09-187-859-160

Query Match          33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 VES 3
          |||
Db          2 VES 4
          |||

RESULT 64
US-09-187-859-1282
; Sequence 1282, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

; US-08-836-561-40
; Sequence 40, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; TITLE OF INVENTION: Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-561-40

Query Match          33.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 SYV 5
          |||
Db          1 SYV 3
          |||

RESULT 62
US-09-171-554-12
; Sequence 12, Application US/09171554
; Patent No. 6291640
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: PEPTIDOMIMETIC INHIBITORS OF THE HUMAN CYTOMEGALOVIRUS
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: Response of OA
```

APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407C1  
CURRENT APPLICATION NUMBER: US/09/187,859A  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1282  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-1282

Query Match 33.3%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
Db 2 VES 4  
|||

RESULT 65  
US-09-646-154-11  
Sequence 11, Application US/09646154  
Patent No. 6429024  
GENERAL INFORMATION:  
APPLICANT: KOKUBO, TOHRU  
APPLICANT: ARAI, KENJI  
TITLE OF INVENTION: TEST METHOD FOR IGA NEPHROPATHY  
FILE REFERENCE: KP-8821  
CURRENT APPLICATION NUMBER: US/09/646,154  
CURRENT FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: PCT/JP99/01525  
PRIOR FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Bovine sp.  
US-09-646-154-11

Query Match 33.3%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3  
Db 3 VES 5  
|||

RESULT 66  
US-08-766-596A-28  
Sequence 28, Application US/08766596A  
Patent No. 6462171  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-28

Query Match 33.3%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFP 9  
Db 1 LFP 3  
|||

RESULT 67  
US-08-766-596A-29  
Sequence 29, Application US/08766596A  
Patent No. 6462171  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FRANGIONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-29

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLF 8
Db 1 PLF 3

RESULT 68
US-09-434-122-40
; Sequence 40, Application US/09434122
; Patent No. 6538111
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, No. 6538111uo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-NO. 6538111-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-434-122-40

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 1 SYV 3

TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-434-122-40

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 1 SYV 3

RESULT 69
US-09-839-542B-160
; Sequence 160, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-160

Query Match 33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VES 3
Db 2 VES 4

RESULT 70
US-09-839-542B-1282
; Sequence 1282, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1282
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```



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; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-1282

Query Match          33.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VES 3
Db 2 VES 4

RESULT 71
US-08-205-938A-3
; Sequence 3, Application US/08205938A
; Patent No. 5466671
; GENERAL INFORMATION:
; APPLICANT: TEMPST, PAUL
; APPLICANT: CASTEELS, PETER
; TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH
; TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
; TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205,938A
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-205-938A-3

Query Match          33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
Db 4 YVP 6

RESULT 72
US-08-282-758B-40
; Sequence 40, Application US/08282758B
; Patent No. 5670310
; GENERAL INFORMATION:
; APPLICANT: Fields, Howard A.
; APPLICANT: Khudyakov, Yuri E.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Differential Diagnosis of Chronic and Acute Hepatitis C
```

```
; TITLE OF INVENTION: Virus Infection
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,758B
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Jamie L.
; REGISTRATION NUMBER: 32,467
; REFERENCE/DOCKET NUMBER: 03063-0100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-282-758B-40

Query Match          33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YVP 6
Db 2 YVP 4

RESULT 73
US-08-405-230-2
; Sequence 2, Application US/08405230
; Patent No. 5707846
; GENERAL INFORMATION:
; APPLICANT: TANIGUCHI, Naoyuki
; APPLICANT: NISHIKAWA, Atsushi
; APPLICANT: YAMAGUCHI, No. 5707846om1
; TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,230
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/110,736
; FILING DATE: 23-AUG-1993
; APPLICATION NUMBER: JP 4-245950
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-237118
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 001560-215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-230-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 4 SYV 6

RESULT 74
US-08-595-718A-1
; Sequence 1, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6

APPLICATION NUMBER: US 08/110,736
FILING DATE: 23-AUG-1993
APPLICATION NUMBER: JP 4-245950
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-237118
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 001560-215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-405-230-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYV 5
Db 4 SYV 6

RESULT 74
US-08-595-718A-1
; Sequence 1, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
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; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
US-08-595-718A-1

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 4 VPL 6

RESULT 75
US-08-595-718A-2
; Sequence 2, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
US-08-595-718A-2

Query Match 33.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VPL 7
Db 4 VPL 6
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Job time : 8.27326 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 8.9186 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR\_76:\*

1: Pirl1.\*

2: Pirl2.\*

3: Pirl3.\*

4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	46.2	18	2	S49026
2	5	38.5	14	2	A60737
3	4	30.8	17	2	S50742
4	4	30.8	20	2	B44581
5	3	23.1	3	3	A33802
6	3	23.1	6	2	PT0560
7	3	23.1	7	2	S70335
8	3	23.1	7	2	A33098
9	3	23.1	7	2	PT0246
10	3	23.1	7	2	A39690
11	3	23.1	7	2	S29735
12	3	23.1	8	2	A39308
13	3	23.1	8	4	I54017
14	3	23.1	10	2	B33710
15	3	23.1	10	2	PX0030
16	3	23.1	10	2	PH1345
17	3	23.1	10	2	B45482
18	3	23.1	11	2	C33652
19	3	23.1	11	2	F58501
20	3	23.1	11	2	B41835
21	3	23.1	11	2	A55149
22	3	23.1	11	2	C51497
23	3	23.1	11	2	C37196
24	3	23.1	11	2	I52980
25	3	23.1	11	2	PH1583
26	3	23.1	12	2	S01749
27	3	23.1	12	2	S65629
28	3	23.1	12	2	PN0162
29	3	23.1	12	2	A60528

30	23.1	12	2	C20907	Ig kappa-1 chain J
31	23.1	12	2	A33520	inhibitory diffusi
32	23.1	12	2	A32734	enkephalin precurs
33	23.1	13	2	S70723	lipamide dehydrog
34	23.1	13	2	PH1316	Ig heavy chain DJ
35	23.1	13	2	B47415	mannose-1-phosphat
36	23.1	13	2	S03063	Ig lambda chain J
37	23.1	13	4	I70075	glycophorin B (mis
38	23.1	14	2	S22336	lipoygenase (EC 1
39	23.1	14	2	S27140	hypothetical prote
40	23.1	14	2	PA0111	protein QA100054 -
41	23.1	14	2	S33802	chaperone, TCP1-re
42	23.1	14	2	A28018	very late antigen-
43	23.1	14	2	B61597	cytochrome P450 AL
44	23.1	14	2	C59137	protein Pfl3 - gold
45	23.1	15	1	LFTWL	leu leader peptide
46	23.1	15	2	PW0004	chlorophyll a/b-bi
47	23.1	15	2	C37765	hypothetical prote
48	23.1	15	2	PA0079	malate dehydrogena
49	23.1	15	2	FA0088	Ig heavy chain DJ
50	23.1	15	2	PH1342	acidic fibroblast
51	23.1	15	2	S03955	collagen alpha 2(X
52	23.1	15	2	E56978	thyrotropin-releas
53	23.1	15	2	A45096	thyrotropin-releas
54	23.1	15	2	B59137	protein Pfl1 - gold
55	23.1	16	2	E41425	cytochrome P450 IF
56	23.1	16	2	S03405	hydrogenase (EC 1.
57	23.1	16	2	I57530	gene c-fms protein
58	23.1	16	2	S65520	phospholipase A2 (
59	23.1	16	2	A39109	hypothetical prote
60	23.1	16	2	S66613	protein p12E - Fri
61	23.1	16	2	I40065	shikimate 5-dehydr
62	23.1	16	2	S09732	photosystem I prot
63	23.1	16	2	C61414	chymotrypsin (EC 3
64	23.1	16	2	PT0224	Ig heavy chain CDR
65	23.1	16	2	PH1302	Ig heavy chain DJ
66	23.1	16	2	E49855	T-cell-receptor be
67	23.1	16	2	S68730	bleomycin-binding
68	23.1	16	2	S65430	pyrogallol hydroxy
69	23.1	16	2	T14224	NADH2 dehydrogenas
70	23.1	17	2	S05917	chorion class A pr
71	23.1	17	2	S05913	chorion class A pr
72	23.1	17	2	S05919	chorion class A pr
73	23.1	17	2	S05921	chorion class A pr
74	23.1	17	2	F58502	41K stone protein
75	23.1	17	2	S41207	41K stone protein
76	23.1	17	2	S71327	hypothetical prote
77	23.1	17	2	A61557	major merozoite su
78	23.1	17	2	D22595	bombolitin IV - Am
79	23.1	17	2	E22595	bombolitin V - Ame
80	23.1	17	2	B61414	chymotrypsin (EC 3
81	23.1	17	2	A60570	Ig mu heavy chain
82	23.1	17	2	I55612	thyroid hormone re
83	23.1	17	2	E23734	insulin-like growt
84	23.1	18	2	E24735	glutathione transfr
85	23.1	18	2	S74195	epoxide hydrolase
86	23.1	18	2	S09086	proteasome chain 5
87	23.1	18	2	D56049	kidney stone prote
88	23.1	18	2	S46418	NTL1 protein - cur
89	23.1	18	2	S48863	cyclin C - mouse (
90	23.1	18	2	A60277	pinin - Vibrio par
91	23.1	18	2	S23950	45K protein - pig
92	23.1	18	2	I50389	myosin heavy chain
93	23.1	18	2	S09026	carboxylesterase (
94	23.1	18	2	PH1350	Ig heavy chain DJ
95	23.1	18	2	A42016	mammary-derived gr
96	23.1	18	2	S71592	serine proteinase
97	23.1	19	2	S32548	glutathione transfr
98	23.1	19	2	S13046	calreticulin - rab
99	23.1	19	2	I40063	shikimate 5-dehydr
100	23.1	19	2	B33708	thionin, soluble -

## ALIGNMENTS

RESULT 1  
S49026  
ribosomal protein HS25 [validated] - Haloarcula marismortui (fragment)  
C:Species: Haloarcula marismortui  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: S49026; S63967  
R:Engemann, S.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold, B.  
submitted to the Protein Sequence Database, November 1994  
A:Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic  
A:Reference number: S49023  
A:Accession: S49026  
A:Molecule type: protein  
A:Residues: 1-18 <ENG>  
R:Engemann, S.; Noelle, R.; Herfurth, E.; Briesemeister, U.; Grelle, G.; Wittmann-Liebold  
Eur. J. Biochem. 234, 24-31, 1995  
A:Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic Haloar  
A:Reference number: S63964; MUID:96096717; PMID:8529646  
A:Accession: S63967  
A:Molecule type: protein  
A:Residues: 1-18 <ENW>  
C:Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match 46.2%; Score 6; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGPVR 13  
Db 12 VLGPVR 17  
|||||

RESULT 2  
A60737  
pollen allergen Lol p IV - perennial ryegrass (fragments)  
C:Species: Lolium perenne (perennial ryegrass)  
C>Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 17-Mar-1999  
C:Accession: A60737  
R:Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kisil, F.T.  
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1989  
A:Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.  
A:Reference number: A60737; MUID:90007726; PMID:2793222  
A:Accession: A60737  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <JAG>  
C:Keywords: pollen

Query Match 38.5%; Score 5; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVLG 10  
Db 3 EPVLG 7  
|||||

RESULT 3  
S50742  
proteinase inhibitor (Kunitz-type) 1-related protein - potato (fragment)  
N:Alternate names: PKPI minor protein  
C:Species: Solanum tuberosum (potato)  
C>Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C:Accession: S50742  
R:Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
Plant Mol. Biol. 26, 961-969, 1994  
A:Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibito  
A:Reference number: S50741; MUID:95093035; PMID:8000008  
A:Accession: S50742  
A:Molecule type: protein  
A:Residues: 1-17 <MIT>

Query Match 30.8%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
Db 7 PVLG 10  
|||||

RESULT 4  
B44581  
bombinin H Met-8 - yellow-bellied toad  
C:Species: Bombina variegata (yellow-bellied toad)  
C>Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 11-Jan-2000  
C:Accession: B44581  
R:Mignogna, G.; Simmaco, M.; Kreil, G.; Barra, D.  
EMBO J. 12, 4829-4832, 1993  
A:Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the s  
A:Reference number: S39612; MUID:94038967; PMID:8223491  
A:Accession: B44581  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <MIG>  
C:Superfamily: bombinin H precursor  
C:Keywords: amidated carboxyl end; D-amino acid  
F:2/Modified site: D-allo-isoleucine (Ile) #status experimental  
F:20/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match 30.8%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
Db 4 PVLG 7  
|||||

RESULT 5  
A33802  
thyrotropin-releasing hormone-like peptide - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A33802  
R:Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.  
J. Biol. Chem. 264, 7788-7791, 1989  
A:Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate c  
A:Reference number: A33802; MUID:89255196; PMID:2498305  
A:Accession: A33802  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <COC>  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F:1/Modified site: pyrolidone carboxylic acid (Gln) #status experimental  
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 23.1%; Score 3; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7  
Db 1 QEP 3  
|||||

RESULT 6  
PT0560  
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0560  
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0560  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-6 <PEE>  
 A;Experimental source: day 18 fetal thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 23.1%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 ||||  
 Db 3 VLG 5

## RESULT 7

S70335  
 endosperm protein, 40K - rye (fragment)

C;Species: Secale cereale (rye)  
 C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C;Accession: S70335  
 R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.  
 Biochim. Biophys. Acta 1295, 13-22, 1996  
 A;Title: Identification of major rye scalins as coeliac immunoreactive proteins.  
 A;Reference number: S70327; MUID:96283789; PMID:8679669  
 A;Accession: S70335  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <ROC>

Query Match 23.1%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 ||||  
 Db 2 VLG 4

## RESULT 8

A33098  
 244K exantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum  
 C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C;Accession: A33098  
 R;Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A;Reference number: A33098  
 A;Accession: A33098  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <NIC>

Query Match 23.1%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11  
 ||||  
 Db 2 LGP 4

## RESULT 9

PT0246

Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0246  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0246  
 A;Molecule type: DNA  
 A;Residues: 1-7 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 ||||  
 Db 3 VLG 5

## RESULT 10

A39690

neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C;Accession: A39690  
 R;Reyes, A.A.; Small, S.J.; Akesson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule  
 A;Reference number: A39690; MUID:91141516; PMID:1996115  
 A;Accession: A39690  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-7 <REY>  
 A;Cross-references: GB:M63970  
 C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 23.1%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PVR 13  
 ||||  
 Db 2 PVR 4

## RESULT 11

S29735

polysphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichii  
 C;Species: Propionibacterium freudenreichii subsp. shermanii  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
 C;Accession: S29735  
 R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
 Arch. Biochem. Biophys. 300, 309-319, 1993  
 A;Title: The polysphosphate- and ATP-dependent glucokinase from Propionibacterium shermanii  
 A;Reference number: S29735; MUID:93143332; PMID:8380966  
 A;Accession: S29735  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <PHI>  
 C;Keywords: phosphotransferase

Query Match 23.1%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 ||||  
 Db 3 VLG 5

## RESULT 12

A39308

glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklandii  
 C;Species: Clostridium sticklandii

C>Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997

C/Accession: A39308

R/Stadtman, T.C.; Davis, J.N.

J. Biol. Chem. 266, 22147-22153, 1991

A/Title: Glycine reductase protein C. Properties and characterization of its role in the

A/Reference number: A39308; MUID:92042141; PMID:1939235

C/Accession: A39308

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-8 <STA>

C/Function:

A/Description: glycine reductase complex catalyzes the reductive deamination of glycine

C/Keywords: ATP; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9

|||

Db 3 PVL 5

RESULT 13

I54017

C/Species: synthetic

A/Note: human gene engineered and expressed in *Echerichia coli*

C/Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000

C/Accession: I54017

R/Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.

Gene 65, 13-22, 1988

A/Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac

i.

A/Reference number: I54017; MUID:88284374; PMID:2456256

A/Accession: I54017

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-8 <DEV>

A/Cross-references: GB:M20922; NID:9806638; PIDN:AAA66353.1; PID:G183043

Query Match

Best Local Similarity 23.1%; Score 3; DB 4; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11

|||

Db 4 LGP 6

RESULT 14

B33710

C/Species: *Rattus norvegicus* - rat

C/Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999

C/Accession: B33710

R/Wen, L.; Huang, J.K.; Blackshear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A/Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory ele

A/Reference number: A33710; MUID:89255378; PMID:2722815

C/Accession: B33710

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: mRNA

A/Residues: 1-10 <WEN>

A/Cross-references: GB:J04791; NID:9205807; PIDN:AAA66163.1; PID:G806309

C/Superfamily: unassigned leader peptides

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9

|||

Db 8 PVL 10

RESULT 15

PX0030

C/Species: *Geotrichum candidum* (fragments)

C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 30-Sep-1993

C/Accession: PX0030

R/Sugihara, A.; Shimada, Y.; Tominaga, Y.

J. Biochem. 107, 426-430, 1990

A/Title: Separation and characterization of two molecular forms of *Geotrichum candidu*

A/Reference number: PX0030; MUID:90256718; PMID:2341377

C/Accession: PX0030

A/Molecule type: protein

A/Residues: 1-10 <SUG>

C/Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains

C/Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4

|||

Db 7 LLY 9

RESULT 16

PH1345

C/Species: *Homo sapiens* (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C/Accession: PH1345

R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor ly

A/Reference number: PH1302; MUID:93094761; PMID:1460419

C/Accession: PH1345

A/Molecule type: DNA

A/Residues: 1-10 <WAS>

A/Note: the authors translated the stop codon for residue 4 as X

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11

|||

Db 6 LGP 8

RESULT 17

B45482

C/Species: *Homo sapiens* (man)

C/Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 05-May-1995

C/Accession: B45482

R/Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.

J. Biol. Chem. 268, 3857-3865, 1993

A/Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Puri

A/Reference number: A45482; MUID:93179380; PMID:8440681

C/Accession: B45482

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <STA>

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10

Db 7 VLG 9  
|||  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLL 3  
|||  
Db 7 FLL 9  
|||  
RESULT 18  
C53652  
rhlR protein - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998  
C;Accession: C53652  
R;Ochsner, U.A.; Flechter, A.; Reiser, J.  
J. Biol. Chem. 269, 19787-19795, 1994  
A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas  
A;Reference number: A53652; MUID:94327521; PMID:8051059  
A;Accession: C53652  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <OCH>  
A;Cross-references: GB:L28170  
C;Superfamily: sdhA regulatory protein  
Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLL 3  
|||  
Db 7 FLL 9  
|||  
RESULT 19  
F58501  
43.5K bile stone protein - unidentified bacterium (fragment)  
C;Species: unidentified bacterium  
C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C;Accession: F58501  
R;Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A;Description: The proteins of kidney and gallbladder stones.  
A;Reference number: F58501  
A;Accession: F58501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <BIN>  
A;Experimental source: human bile with stones  
A;Note: 6-Asn and 8-Ala were also found  
Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 GPV 12  
|||  
Db 8 GPV 10  
|||  
RESULT 20  
B41835  
translation elongation factor EF-G homolog - Bacillus subtilis (fragment)  
C;Species: Bacillus subtilis  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Dec-1997  
C;Accession: B41835  
R;Mitchell, C.; Morris, P.W.; Vary, J.C.  
J. Bacteriol. 174, 2474-2477, 1992  
A;Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus  
A;Reference number: A41835; MUID:92210489; PMID:1556067  
A;Accession: B41835  
A;Molecule type: protein  
A;Residues: 1-11 <MIT>  
A;Note: this protein is phosphorylated during stationary phase but not during exponential  
C;Keywords: phosphoprotein  
Query Match 23.1%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLL 3  
|||  
Db 1 FLL 3  
|||  
RESULT 21  
A55149  
tetracenomycin A2 oxygenase (BC 1.-.-.-) - Streptomyces glaucescens (fragment)  
N;Alternate names: tcmA2 oxygenase; tcmG  
C;Species: Streptomyces glaucescens  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Mar-1996  
C;Accession: A55149  
R;Shen, B.; Hutchinson, C.R.  
J. Biol. Chem. 269, 30726-30733, 1994  
A;Title: Triple hydroxylation of tetracenomycin A2 to tetracenomycin C in Streptomyces  
A2 oxygenase.  
A;Reference number: A55149; MUID:95074090; PMID:7982994  
A;Accession: A55149  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <SHE>  
C;Genetics:  
A;Start codon: TTG  
C;Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase  
Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PVL 9  
|||  
Db 7 PVL 9  
|||  
RESULT 22  
C61497  
seed protein ws-18 - winged bean (fragment)  
C;Species: Psophocarpus tetragonolobus (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: C61497  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-c  
A;Reference number: A61491; MUID:89351606; PMID:2765119  
A;Accession: C61497  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <HIR>  
C;Keywords: glycoprotein; seed  
Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PVL 9  
|||  
Db 7 PVL 9  
|||  
RESULT 23  
C37196  
bradykinin-potentiating peptide 3 - island jataraca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C;Accession: C37196  
R;Gintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides  
A;Reference number: A37196; MUID:90351557; PMID:2386615  
A;Accession: C37196



A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <CIN>  
C:Keywords: pyroglycolic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental

Query Match 23.1%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 2 LGP 4

## RESULT 24

I52980

glucocerebrosidase - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

A:Accession: I52980; I65971

R:Reiner, O.; Wigderson, M.; Horowitz, M.

DNA 7, 107-116, 1988

A&gt;Title: Structural analysis of the human glucocerebrosidase genes.

A:Reference number: I52980; MUID:88195776; PMID:3359914

A:Accession: I52980

A&gt;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-11 &lt;RES&gt;

A:Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A:Accession: I65971

A&gt;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-11 &lt;RE2&gt;

A:Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

## Query Match

23.1%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13  
|||  
Db 6 PVR 8

## RESULT 25

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

A:Accession: PH1583

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A&gt;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1583

A:Molecule type: DNA

A:Residues: 1-11 &lt;LEV&gt;

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

## Query Match

23.1%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 5 LGP 7

## RESULT 26

S01749

collagen alpha 1(I) chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 13-Aug-1999

A:Accession: S01749; S21415

R:Mooslehner, K.; Harbers, K.

Nucleic Acids Res. 16, 773, 1988

A&gt;Title: Two mRNAs of mouse pro alpha-1(I) collagen gene differ in the size of the 3'

A:Reference number: S01749; MUID:88124276; PMID:3340560

A:Accession: S01749

A&gt;Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-12 &lt;MOO&gt;

A:Cross-references: EMBL:X06753; NID:g50499; PIDN:CXA29927.1; PID:g50500

R:Mooslehner, K.; Harbers, K.

Submitted to the EMBL Data Library, July 1989

A:Reference number: S21415

A:Accession: S21415

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-12 &lt;MO2&gt;

A:Cross-references: EMBL:X15896; NID:g50497; PIDN:CAA33904.1; PID:g50498

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

## Query Match

23.1%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.7e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
|||  
Db 7 GPV 9

## RESULT 27

S65629

protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-May-2000

A:Accession: S65629

R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohnno, H.; Tokunaga, R.; Nishimura, K.;

Eur. J. Biochem. 230, 760-765, 1995

A&gt;Title: Induction of terminal enzymes for heme biosynthesis during differentiation o

A:Reference number: S65629; MUID:95331315; PMID:7607249

A:Accession: S65629

A:Molecule type: protein

A:Residues: 1-12 &lt;TAK&gt;

C:Genetics:

C:Genome: nuclear

C:Function:

A:Pathway: heme biosynthesis; porphyrin biosynthesis

C:Superfamily: phytoene dehydrogenase

C:Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

## Query Match

23.1%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.7e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
|||  
Db 6 VLG 8

## RESULT 28

PN0162

malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C&gt;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 11-Nov-1994

A:Accession: PN0162

R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr

A:Reference number: PN0160

A:Accession: PN0162

A:Molecule type: protein

A:Residues: 1-12 &lt;FUK&gt;

## C;Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 |||  
 Db 5 VLG 7

## RESULT 29

A60528  
 insulin-like growth factor-binding protein, serum - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
 C;Accession: A60528

R;Walton, P.E.; Baxter, R.C.; Bursleigh, B.D.; Ethernton, T.D.  
 Comp. Biochem. Physiol. B 92, 561-567, 1989

A;Title: Purification of the serum acid-stable insulin-like growth factor binding protein  
 A;Reference number: A60528; MUID:89209787; PMID:2469442

A;Accession: A60528

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <WAL>

Query Match 23.1%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12  
 |||  
 Db 8 GPV 10

## RESULT 30

C20907

Ig kappa-1 chain J3 region - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996  
 C;Accession: C20907

R;Emorine, L.; Max, E.E.

Nucleic Acids Res. 11, 8877-8890, 1983

A;Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple  
 A;Reference number: A20907; MUID:84169523; PMID:6324107

A;Accession: C20907

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <EMO>

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11  
 |||  
 Db 3 LGP 5

## RESULT 31

A33520

inhibitory diffusible factor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 30-Sep-1993  
 C;Accession: A33520

R;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.

J. Biol. Chem. 264, 6021-6024, 1989

A;Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inhibitory diffusible factor)  
 A;Reference number: A33520; MUID:89197888; PMID:2703477

A;Accession: A33520

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <BLA>

Query Match 23.1%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12  
 |||  
 Db 8 GPV 10

## RESULT 32

A32734

enkephalin precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 21-Jan-2000  
 C;Accession: A32734

R;Micancovic, R.; Ray, P.; Kruggel, W.; Lewis, R.V.

Biochem. Biophys. Res. Commun. 118, 299-303, 1984  
 A;Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin  
 A;Reference number: A32734; MUID:84128045; PMID:6546517

A;Accession: A32734

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <MIC>

C;Superfamily: proenkephalin

C;Keywords: neuropeptide; opioid peptide

Query Match 23.1%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 |||  
 Db 4 VLG 6

## RESULT 33

S70723

lipamide dehydrogenase homolog - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C;Accession: S70723

R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A;Reference number: S70719; MUID:96100451; PMID:8559071

A;Accession: S70723

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <QIS>

A;Experimental source: strain SL1344

Query Match 23.1%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 |||  
 Db 10 VLG 12

## RESULT 34

PH1316

Ig heavy chain DJ region (clone C388-107) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1316

R;Wasserman, R.; Gaili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1316

A:Molecule type: DNA  
A:Residues: 1-13 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 8 LGP 10

## RESULT 35

B47415  
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)  
N;Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 25-Feb-1994 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C;Accession: B47415  
R;Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.  
J. Biol. Chem. 268, 17943-17950, 1993  
A;Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and utility  
A;Reference number: A47415; MUID:93352609; PMID:7688733  
A;Accession: B47415  
A:Molecule type: protein  
A:Residues: 1-13 <SZU>  
A;Experimental source: liver  
A;Complex: The enzyme appears to be a heterodimer of alpha and beta chains.  
C;Function:  
A;Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP  
A;Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ad  
C;Keywords: blocked amino end; nucleotidyltransferase

Query Match 23.1%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3  
|||  
Db 11 FLL 13

## RESULT 36

S03063  
Ig lambda chain J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 11-Jan-2002  
C;Accession: S03063  
R;Udey, J.A.; Blomberg, B.B.  
Nucleic Acids Res. 16, 2959-2969, 1988  
A;Title: Intergenic exchange maintains identity between two human lambda light chain imm  
A;Reference number: S03063; MUID:88217512; PMID:3130611  
A;Accession: S03063  
A:Molecule type: DNA  
A:Residues: 1-13 <UDE>  
A;Cross-references: EMBL:X06877; NID:G33357; PIDN:CAA29996.1; PID:G1335162  
C;Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
|||  
Db 11 VLG 13

## RESULT 37

I70075  
Glycophorin B (mistranslated) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Feb-1997 #sequence\_revision 14-Aug-1997 #text\_change 20-Apr-2000

C;Accession: I70075  
R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.  
J. Biol. Chem. 265, 9259-9263, 1990  
A;Title: Identification of the crossing-over point of a hybrid gene encoding human g1  
A;Reference number: I55334; MUID:90264417; PMID:1971625  
A;Accession: I70075  
A;Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-13 <REA>  
A;Cross-references: GB:M33505; GB:J05465; NID:G183726; PIDN:AAA53152.1; PID:G442425  
A;Note: this sequence was not determined in this report; the translation is from an i  
C;Genetics:  
A;Gene: GDB:GYPB  
A;Cross-references: GDB:118891  
A;Map position: 4q28-4q31

Query Match 23.1%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5  
|||  
Db 11 LYQ 13

## RESULT 38

S22236  
Lipoxygenase (EC 1.13.11.12) 1 - barley (fragment)  
C;Species: Hordeum vulgare (barley)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
A;Accession: S22236  
R;Dodrerer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.  
Biochim. Biophys. Acta 1120, 97-104, 1992  
A;Title: Purification and characterization of two lipoxygenase isoenzymes from germin  
A;Reference number: S21772; MUID:92207997; PMID:1554746  
A;Accession: S22236  
A:Molecule type: protein  
A:Residues: 1-14 <BOD>  
A;Experimental source: var. Triumph, seed  
C;Function:  
A;Description: catalyzes the peroxidation of polyunsaturated fatty acids to their cor  
C;Superfamily: lipoxygenase  
C;Keywords: monomer; oxidoreductase; seed

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4  
|||  
Db 5 LLY 7

## RESULT 39

S27140  
hypotheical protein 1 estrogen receptor 5'-region - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 18-Aug-2000  
C;Accession: S27140  
R;Keaveney, M.; Klug, J.; Gannon, F.  
DNA Seq. 2, 347-359, 1992  
A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor 9  
A;Reference number: S27140; MUID:93075998; PMID:1476547  
A;Accession: S27140  
A;Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-14 <KEA>  
A;Cross-references: EMBL:X62462; NID:G31201; PIDN:CAA44319.1; PID:G31202  
C;Superfamily: unassigned leader peptides

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11  
|||  
Db 12 LGP 14

## RESULT 40

PA0111  
protein QAI00054 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 06-Jun-1997  
C:Accession: PA0111  
R:Kano, M.; Kawakami, T.; Tsugita, A.  
submitted to JIPID, March 1995  
A:Reference number: PA0109  
A:Accession: PA0111  
A:Molecule type: protein  
A:Residues: 1-14 <KAM>  
A:Experimental source: root

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12  
|||  
Db 2 GPV 4

## RESULT 41

S33802  
Chaperone, TCPI-related - oat  
C:Species: Avena sativa (oat)  
C>Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999  
C:Accession: S33802  
R:Mummet, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer  
Nature 363, 644-648, 1993  
A:Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo  
A:Reference number: S33800; MUID:93288140; PMID:8099715  
A:Accession: S33802  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <MDM>

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11  
|||  
Db 7 LGP 9

## RESULT 42

A28018  
very late antigen-1 alpha chain - human (fragment)  
N:Alternate names: VLA-1 alpha chain  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994  
C:Accession: A28018  
R:Takada, Y.; Strominger, J.L.; Henler, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987  
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu  
A:Reference number: A94151; MUID:87204112; PMID:3033641  
A:Accession: A28018  
A:Molecule type: protein  
A:Residues: 1-14 <RAK>  
C:Keywords: duplication; heterodimer; membrane protein

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11  
|||  
Db 12 LGP 14

## RESULT 43

B61597  
cytochrome P450 AL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: B61597  
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.  
Drug Metab. Dispos. 19, 291-297, 1991  
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto  
A:Reference number: A61597; MUID:91292910; PMID:1676625  
A:Accession: B61597  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SHI>

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3  
|||  
Db 9 FLL 11

## RESULT 44

C59137  
protein Pf3 - golden needle mushroom (fragment)  
C:Species: Flammulina velutipes (golden needle mushroom)  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: C59137  
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non  
A:Reference number: A59137  
A:Accession: C59137  
A:Molecule type: protein  
A:Residues: 1-14 <SAK>

Query Match 23.1%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
|||  
Db 3 VLG 5

## RESULT 45

LFTWL  
leu leader peptide - Thermus aquaticus  
C:Species: Thermus aquaticus  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999  
C:Accession: S00901  
R:Croft, J.E.; Love, D.R.; Bergquist, P.L.  
Mol. Gen. Genet. 210, 490-497, 1987  
A:Title: Expression of leucine genes from an extremely thermophilic bacterium in Eschi  
A:Reference number: S00901; MUID:88121725; PMID:3323845  
A:Accession: S00901  
A:Molecule type: DNA  
A:Residues: 1-15 <CRO>  
A:Cross-references: EMBL:X06604; NID:948244; PIDN:CAA29823.1; PID:948245  
A:Note: the source is designated as Thermus thermophilus  
C:Superfamily: Thermus aquaticus leu leader peptide

Query Match 23.1%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
|||  
Db 13 GPV 15

## RESULT 46

PM0004  
Chlorophyll a/b-binding protein 24.5K - green alga (*Dunaliella tertiolecta*) (fragment)  
N:Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein  
C:Species: *Dunaliella tertiolecta*  
C:Date: 04-Sep-1998 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C:Accession: PM0004  
R:Chow, L.P.; Bennett, J.; Falkowski, P.G.  
Gene 95, 165-171, 1990  
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the  
A:Reference number: JW0040; PMID:9106528; PMID:2249775  
A:Accession: PM0004  
A:Molecule type: protein  
A:Residues: 1-15 <LAR>  
C:Superfamily: chlorophyll a/b-binding protein  
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane ph

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 12 LGP 14

## RESULT 47

C37765  
Hypothetical protein (csma 3' region) - *Chloroflexus aurantiacus* (fragment)  
C:Species: *Chloroflexus aurantiacus*  
C:Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
C:Accession: C37765  
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
J. Bacteriol. 172, 4497-4504, 1990  
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of *Chloroflexus aurantiacus*  
A:Reference number: A37765; PMID:90330558; PMID:2376566  
A:Accession: C37765  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <THE>  
A:Cross-references: GB:M33964

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4  
|||  
Db 4 LLY 6

## RESULT 48

PA0079  
Malate dehydrogenase (EC 1.1.1.37) II - fungus (*Fusarium sporotrichioides*) (fragment)  
C:Species: *Fusarium sporotrichioides*  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0079  
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
A:Reference number: PA0051  
A:Accession: PA0079  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
C:Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 8 VLG 10

|||  
Db 5 VLG 7

## RESULT 49

PA0088  
Protein QP200051 - fungus (*Fusarium sporotrichioides*) (fragment)  
C:Species: *Fusarium sporotrichioides*  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0088  
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
A:Reference number: PA0051  
A:Accession: PA0088  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9  
|||  
Db 13 PVL 15

## RESULT 50

PHI342  
Ig heavy chain DJ region (clone C507-95) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PHI342  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PHI302; PMID:93094761; PMID:1460419  
A:Accession: PHI342  
A:Molecule type: DNA  
A:Residues: 1-15 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 10 LGP 12

## RESULT 51

S03955  
acidic fibroblast growth factor - dog (fragment)  
N:Alternate names: alpha-endothelial cell growth factor  
C:Species: *Canis lupus familiaris* (dog)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C:Accession: S03955  
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schur, J. Biochem. 181, 67-73, 1989  
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine  
A:Reference number: S03953; PMID:89231704; PMID:2714282  
A:Accession: S03955  
A:Molecule type: protein  
A:Residues: 1-15 <QUI>  
C:Keywords: growth factor

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLY 4  
|||  
Db 7 LLY 9

## RESULT 52

E56978

collagen alpha 2(XI) chain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Oct-1995

C:Accession: B56978

R:Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins

A:Reference number: A56978; MUID:95370194; PMID:7642541

A:Accession: B56978

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 &lt;WUA&gt;

A&gt;Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in FS

## Query Match

23.1%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12

|||

Db 10 GPV 12

## RESULT 53

A45096

thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C:Accession: A45096

R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.

J. Biol. Chem. 267, 25703-25708, 1992

A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alterna

A:Reference number: A45096; MUID:93100278; PMID:1334485

A:Accession: A45096

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-15 &lt;DEL&gt;

A:Cross-references: GB:S51512; NID:g261982; PIDN:AAR24549.1; PID:g261983

A:Experimental source: GH3 anterior pituitary cells

A&gt;Note: sequence extracted from NCBI backbone (NCBIP:120927)

## Query Match

23.1%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9

|||

Db 7 PVL 9

## RESULT 54

B59137

Protein Pfl - golden needle mushroom (fragment)

C:Species: Flammulina velutipes (golden needle mushroom)

C&gt;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: B59137

R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

submitted to the Protein Sequence Database, November 1999

A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr

A:Reference number: A59137

A:Accession: B59137

A:Molecule type: protein

A:Residues: 1-15 &lt;SAK&gt;

A:Experimental source: strain FV-4

A:Status: preliminary; translated from GB/EMBL/DDBJ

Query Match 23.1%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10

. |||

Db 3 VLG 5

## RESULT 55

E41425

cytochrome P450 1F-6 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 10-Apr-1992 #sequence\_revision 10-Apr-1992 #text\_change 05-Mar-1999

C:Accession: E41425

R:Imaoka, S.; Kamataki, T.; Funae, Y.

J. Biochem. 102, 843-851, 1987

A:Title: Purification and characterization of six cytochromes P-450 from hepatic micro

A:Reference number: A41425; MUID:88139237; PMID:3436956

A:Accession: E41425

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 &lt;IMA&gt;

C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C:Keywords: heme

## Query Match

23.1%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGP 11

|||

Db 7 LGP 9

## RESULT 56

S03405

hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)

C:Species: Alcaligenes eutrophus

C&gt;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998

C:Accession: S03405

R:Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.

Biochim. Biophys. Acta 995, 1-9, 1989

A:Title: Immunological comparison of subunits isolated from various hydrogenases of a

A:Reference number: S03404; MUID:89166625; PMID:2493816

A:Accession: S03405

A:Molecule type: protein

A:Residues: 1-16 &lt;LOR&gt;

A:Experimental source: strain H16, DMS 541

A:Superfamily: hydrogenase (NiFe) small chain

C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein;

## Query Match

23.1%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9

|||

Db 8 PVL 10

## RESULT 57

I57530

gene c-fms protein - mouse (fragment)

C:Species: Mus sp. (mouse)

C&gt;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-May-1997

C:Accession: I57530

R:Yue, X.; Favot, P.; Dunn, T.L.; Cassidy, A.I.; Hume, D.A.

Mol. Cell. Biol. 13, 3191-3201, 1993

A:Title: Expression of mRNA encoding the macrophage colony-stimulating factor recepto

A:Reference number: I57530; MUID:93268269; PMID:8497248

A:Accession: I57530

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA  
A:Residues: 1-16 <RES>  
A:Cross-references: GB:S62219; NID:G986001  
C:Genetics:  
A:Gene: C-fms  
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
|||  
Db 3 LGP 5

RESULT 58  
S65520  
phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)  
N:Contains: muscarinic acetylcholine receptor inhibitor  
C:Species: Naja naja sputatrix (Malayan spitting cobra)  
C>Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 17-Mar-2000  
C:Accession: S65520  
R:Miyoishi, S.; Tu, A.T.  
Arch. Biochem. Biophys. 328, 17-25, 1996  
A:Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine  
A:Reference number: S65520; MUID:9619575; PMID:8638927  
A:Accession: S65520  
A:Molecule type: protein  
A:Residues: 1-16 <MIY>  
C:Superfamily: phospholipase A2  
C:Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5  
|||  
Db 2 LYQ 4

RESULT 59  
A39109  
Hypothetical protein 1 - hepatitis C virus  
C:Species: hepatitis C virus  
C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 18-Jun-1993  
C:Accession: A39109  
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identificati  
A:Reference number: A39109; MUID:91156678; PMID:1705704  
A:Accession: A39109  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-16 <HAN>  
A:Cross-references: GB:M58406

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13  
|||  
Db 5 PVR 7

RESULT 60  
S66613  
protein p12E - Friend murine leukemia virus (fragments)  
C:Species: Friend murine leukemia virus  
C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S66613

R:Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.  
Eur. J. Biochem. 232, 373-380, 1995  
A:Title: Localization of the palmitoylation site in the transmembrane protein p12E of  
A:Reference number: S66613; MUID:96035869; PMID:7556184  
A:Accession: S66613  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9;10-16 <HEN>

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8  
|||  
Db 1 EPV 3

RESULT 61  
I40065  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C:Species: Buchnera aphidicola  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C:Accession: I40065  
R:Roubakish, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en  
A:Reference number: I40061; MUID:95212914; PMID:7535281  
A:Accession: I40065  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <RES>  
A:Cross-references: EMBL:U10499; NID:G854717; PIDN:AAA79128.1; PID:G854718  
C:Genetics:  
A:Gene: aroE  
C:Keywords: oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8  
|||  
Db 13 EPV 15

RESULT 62  
S03732  
Photosystem I protein psaJ - spinach chloroplast (fragment)  
C:Species: chloroplast Spinacia oleracea (spinach)  
C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Feb-1997  
C:Accession: S03732  
R:Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.  
FEBS Lett. 263, 274-278, 1990  
A:Title: Polypeptide composition of higher plant photosystem I complex. Identificati  
A:Reference number: S03730; MUID:90242987; PMID:2185953  
A:Accession: S03732  
A:Molecule type: protein  
A:Residues: 1-16 <IKE>  
C:Genetics:  
A:Gene: psaJ  
C:Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 23.1%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9  
|||  
Db 12 PVL 14

```

RESULT 63
C61414
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
C:Species: Pseudemys scripta (slider)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: C61414
R:Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence deter
A:Reference number: A61414; PMID:76146602; PMID:4807189
C:Accession: C61414
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BHA>
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 8 PVL 10

RESULT 64
PT0224
Ig heavy chain CDR3 region (clone 1-91) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0224
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; PMID:91108337; PMID:1899102
C:Accession: PT0224
A:Molecule type: DNA
A:Residues: 1-16 <YAM>
A:Experimental source: B lymphocyte
A:Note: the authors translated the stop codon for residue 9 as X
C:Keywords: heterotetramer; immunoglobulin

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
DB 11 LGP 13

RESULT 65
PH1302
Ig heavy chain DJ region (clone C76-105) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1302
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; PMID:93094761; PMID:1460419
C:Accession: PH1302
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
DB 11 LGP 13

RESULT 66
E49655
T-cell-receptor beta chain variable region, TCR V beta (clone 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: E49655
R:Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juv
A:Reference number: E49655; MUID:94068553; PMID:8248215
C:Accession: E49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <GRO>
A:Experimental source: peripheral blood lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIP:140450)
C:Keywords: T-cell receptor

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13
DB 5 PVR 7

RESULT 67
S68730
bleomycin-binding protein - Streptomyces verticillius (fragment)
C:Species: Streptomyces verticillius
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: S68730
R: Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
RBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St
al characterisation.
A:Reference number: S68730; MUID:95212588; PMID:7535252
C:Accession: S68730
A:Molecule type: protein
A:Residues: 1-16 <SUG>
A:Experimental source: ATCC 15003
C:Keywords: antibiotic resistance

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 9 PVL 11

RESULT 68
S65430
pyrogallol hydroxyltransferase (EC 1.97.1.2) large chain - Pelobacter acidigallici (f
C:Species: Pelobacter acidigallici
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
C:Accession: S65430
R:Reichenbecher, W.; Ruediger, A.; Kroneck, P.M.H.; Schink, B.
Eur. J. Biochem. 237, 406-413, 1996
A:Title: One molecule of molybdopterin guanine dinucleotide is associated with each s
and mass spectrometry.
A:Reference number: S65429; MUID:96215436; PMID:8647079
C:Accession: S65430
A:Molecule type: protein
A:Residues: 1-16 <REI>
C:Keywords: oxidoreductase

Query Match      23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;

```



Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12

Db 13 GPV 15

# RESULT 69

Tl4224 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Euhadra herklotsi mitochondrion

C:Species: mitochondrion Euhadra herklotsi

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C:Accession: Tl4224

R;Yamazaki, N.; Ueshima, R.; Terrett, J.A.; Yokobori, S.; Kaifu, M.; Segawa, R.; Kobayashi

submitted to the EMBL Data Library, May 1996

A;Description: Evolution of pulmonate gastropod mitochondrial genomes: Comparisons of co

.

A;Reference number: Z17932

A;Accession: Tl4224

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <YAM>

A;Cross-references: EMBL:Z171694; NID:e912660; PID:e244560; PIDN:CAA96364.1

A;Experimental source: adult; hepatopancreas

C;Genetics:

A;Genome: mitochondrion

C;Keywords: mitochondrion; NAD; oxidoreductase

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 16;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3

Db 10 FLL 12

# RESULT 70

S05917

chorion class A protein L4 precursor - silkworm (fragment)

C:Species: Bombyx mori (silkworm)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999

C:Accession: S05917

R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.

J. Mol. Biol. 209, 1-19, 1989

A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridizat

A;Reference number: S05913; MUID:90040707; PMID:2810362

A;Accession: S05917

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-17 <SPO>

A;Cross-references: EMBL:X15560; NID:g5781; PIDN:CAA33571.1; PID:g5782

A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989

C;Genetics:

A;Map position: 2

C;Superfamily: chorion class A protein pc292

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3

Db 6 FLL 8

# RESULT 71

S05913

chorion class A protein L2 precursor - silkworm (fragment)

C:Species: Bombyx mori (silkworm)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999

C:Accession: S05913

R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

J. Mol. Biol. 209, 1-19, 1989

A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridizat

A;Reference number: S05913; MUID:90040707; PMID:2810362

A;Accession: S05913

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-17 <SPO>

A;Cross-references: EMBL:X15558; NID:g5771; PIDN:CAA33567.1; PID:g5772

A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989

C;Genetics:

A;Map position: 2

C;Superfamily: chorion class A protein pc292

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3

Db 7 FLL 9

# RESULT 72

S05919

chorion class A protein L5 precursor - silkworm (fragment)

C:Species: Bombyx mori (silkworm)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999

C:Accession: S05919

R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.

J. Mol. Biol. 209, 1-19, 1989

A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridizat

A;Reference number: S05913; MUID:90040707; PMID:2810362

A;Accession: S05919

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-17 <SPO>

A;Cross-references: EMBL:X15561; NID:g5786; PIDN:CAA33573.1; PID:g5787

A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989

C;Genetics:

A;Map position: 2

C;Superfamily: chorion class A protein pc292

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3

Db 6 FLL 8

# RESULT 73

S05921

chorion class A protein L6 precursor - silkworm (fragment)

C:Species: Bombyx mori (silkworm)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999

C:Accession: S05921

R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.

J. Mol. Biol. 209, 1-19, 1989

A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridizat

A;Reference number: S05913; MUID:90040707; PMID:2810362

A;Accession: S05921

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-17 <SPO>

A;Cross-references: EMBL:X15562; NID:g5791; PIDN:CAA33575.1; PID:g5792

A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989

C;Genetics:

A;Map position: 2

C;Superfamily: chorion class A protein pc292

Query Match

Best Local Similarity 23.1%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3  
|||  
Db 6 FLL 8

## RESULT 74

F58502

41K stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C:Accession: F58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: F58502

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 &lt;BIN&gt;

A&gt;Note: a secondary sequence SVFALNEQXM was also found

Query Match 23.1%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12  
|||  
Db 8 GPV 10

## RESULT 75

S41207

F420-non-reducing-hydrogenase (EC 1.12.99.-) 51K chain - Methanobacterium thermoautotroph

C:Species: Methanobacterium thermoautotrophicum

A:Variety: strain Marburg

C:Date: 06-Feb-1995 #sequence\_revision 17-Jul-1998 #text\_change 07-May-1999

C:Accession: S41207

R:Seitzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.

Eur. J. Biochem. 220, 139-148, 1994

A:Title: H(2): heterodisulfide oxidoreductase complex from Methanobacterium thermoautotroph

A:Reference number: S41204; MUID:94164153; PMID:8119281

A:Accession: S41207

A:Molecule type: protein

A:Residues: 1-17 &lt;SET&gt;

A:Experimental source: strain Marburg

C:Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidore

ducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2)

C:Function:

A:Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreonine phosphate heterodis

ulfide (EC 1.12.99.2)

C:Keywords: membrane-associated complex; oxidoreductase

Query Match 23.1%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPV 8  
|||  
Db 6 EPV 8

Search completed: November 25, 2003, 19:36:14

Job time : 9.9186 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 4.61047 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLXQEPVLGVR 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	30.8	12	1	TM2A_METWA
2	4	30.8	20	1	MAX6_BOMMX
3	4	30.8	20	1	MAX7_BOMMX
4	4	30.8	20	1	MAX8_BOMMX
5	3	23.1	9	1	FAR9_ASCSU
6	3	23.1	11	1	BPP3_BOTIN
7	3	23.1	13	1	CRBL_ICASP
8	3	23.1	13	1	VC16_BACSU
9	3	23.1	15	1	APF3_MALPA
10	3	23.1	15	1	FGF1_CANFA
11	3	23.1	15	1	LPL_TRETH
12	3	23.1	16	1	HBD_CLOPA
13	3	23.1	16	1	PA2_NAJSP
14	3	23.1	16	1	BGLT_PELAC
15	3	23.1	17	1	BOL4_MEGPE
16	3	23.1	17	1	BOL5_MEGPE
17	3	23.1	17	1	EPG_THEAQ
18	3	23.1	17	1	MDH_ACIDE
19	3	23.1	18	1	PG6_PACGO
20	3	23.1	19	1	FLA3_SPIAU
21	3	23.1	19	1	OXLA_OPHHA
22	3	23.1	19	1	PCG7_PACGO
23	3	23.1	19	1	UKA1_HUMAN
24	3	23.1	19	1	UP25_UPEIN
25	3	23.1	19	1	UP27_UPEMJ
26	3	23.1	19	1	UP28_UPEMJ
27	3	23.1	20	1	AF2L_MALPA
28	3	23.1	20	1	BIP_PHAUV
29	3	23.1	20	1	CD4_SHEEP
30	3	23.1	20	1	FRE3_LITIN
31	2	15.4	4	1	FLRF_HIRME
32	2	15.4	4	1	FLRN_ANTEI
33	2	15.4	6	1	ACPH_RABIT

RESULT 1

## ALIGNMENTS

34	2	15.4	7	1	ALL3_CARMA	P81806	carcinus	ma
35	2	15.4	7	1	E105_LITRU	P82101	litoria	rub
36	2	15.4	7	1	FAR1_HELTI	P41871	helisoma	tr
37	2	15.4	7	1	FAR1_MACRS	P83274	macrobrachi	
38	2	15.4	7	1	FAR1_PROCL	P38499	procambarus	
39	2	15.4	7	1	FAR2_PROCL	P38498	procambarus	
40	2	15.4	7	1	GFRP_MOUSE	P99025	mus musculus	
41	2	15.4	7	1	NNPI_LEPDE	P42984	leptinotars	
42	2	15.4	7	1	PPH2_LYCES	P83379	lycopersico	
43	2	15.4	7	1	UN06_PINPS	P81675	pinus pinas	
44	2	15.4	8	1	AL15_CARMA	P81818	carcinus	ma
45	2	15.4	8	1	AL16_CARMA	P81819	carcinus	ma
46	2	15.4	8	1	ALL6_CALVO	P41841	calliphora	
47	2	15.4	8	1	ALL6_CYPDPO	P82157	cydia pomon	
48	2	15.4	8	1	ALL8_CARMA	P81811	carcinus	ma
49	2	15.4	8	1	ALL9_CARMA	P81812	carcinus	ma
50	2	15.4	8	1	B44K_PORGI	P81886	porphyromon	
51	2	15.4	8	1	CAD1_ENTFA	P13288	enterococcu	
52	2	15.4	8	1	CLP_THICU	P80488	thiobacillu	
53	2	15.4	8	1	COM2_CONPU	P58785	conus purpu	
54	2	15.4	8	1	CPD1_ENTFA	P13269	enterococcu	
55	2	15.4	8	1	FAR1_PANRE	P41872	panagrellus	
56	2	15.4	8	1	FAR1_PENMO	P83316	penaeus mon	
57	2	15.4	8	1	FAR2_MACRS	P83275	macrobrachi	
58	2	15.4	8	1	FAR3_HOMAM	P41486	homarus ame	
59	2	15.4	8	1	FAR4_HOMAM	P41487	homarus ame	
60	2	15.4	8	1	FAR7_ASCSU	P43171	ascaris suu	
61	2	15.4	8	1	NPB_BOVIN	P15507	bos taurus	
62	2	15.4	8	1	RS7_MYCIT	P33564	mycobacteri	
63	2	15.4	8	1	UC26_MAIZE	P80632	zea mays (m	
64	2	15.4	8	1	UF06_MOUSE	P38644	mus musculus	
65	2	15.4	8	1	UH09_RAT	P56575	rattus norv	
66	2	15.4	8	1	UPA1_HUMAN	P30087	homo sapien	
67	2	15.4	8	1	VGLG_HSV2B	P81700	herpes simp	
68	2	15.4	9	1	BS43_SERPL	P83375	serratia pl	
69	2	15.4	9	1	BUK_CLOPA	P81337	clostridium	
70	2	15.4	9	1	FAR2_PANRE	P41873	panagrellus	
71	2	15.4	9	1	FAR3_MACRS	P83276	macrobrachi	
72	2	15.4	9	1	FAR5_PANRE	P82661	panagrellus	
73	2	15.4	9	1	FAR6_MACRS	P83279	macrobrachi	
74	2	15.4	9	1	FAR8_MACRS	P83281	macrobrachi	
75	2	15.4	9	1	FAR9_CALSI	P38495	callinectes	
76	2	15.4	9	1	FIBB_ERYPA	P19346	erythrocebu	
77	2	15.4	9	1	FIBB_PAPAN	P19344	papio anubi	
78	2	15.4	9	1	FIBB_PAPHA	P19343	papio hamad	
79	2	15.4	9	1	FIBB_THERGE	P19342	theropithec	
80	2	15.4	9	1	MOSE_CLYJA	P19853	clypeaster	
81	2	15.4	9	1	NEUX_CAVPO	P34966	cavia porce	
82	2	15.4	9	1	NEUX_HUMAN	P04277	homo sapien	
83	2	15.4	9	1	OXYA_SCYCA	P42996	scyllorhinu	
84	2	15.4	9	1	OXYA_SQUAC	P42999	squalus aca	
85	2	15.4	9	1	OXVF_SCYCA	P42997	scyllorhinu	
86	2	15.4	9	1	OXVT_EISFO	P42998	eisenia foe	
87	2	15.4	9	1	OXVT_RABIT	P32878	oryctolagus	
88	2	15.4	9	1	OXVW_SQUAC	P43000	squalus aca	
89	2	15.4	9	1	PPH1_LYCES	P83380	lycopersico	
90	2	15.4	9	1	RE42_LITRU	P82075	litoria rub	
91	2	15.4	9	1	TAL1_PICJA	P17440	pichia jadi	
92	2	15.4	9	1	TAL3_PICJA	P17441	pichia jadi	
93	2	15.4	9	1	TKC1_CALVO	P41517	calliphora	
94	2	15.4	9	1	TKLC_LOCOMI	P16223	locusta mig	
95	2	15.4	9	1	ULAE_HUMAN	P31931	homo sapien	
96	2	15.4	9	1	UPA7_HUMAN	P30093	homo sapien	
97	2	15.4	10	1	BPP_VIPAS	P13151	vipera aspi	
98	2	15.4	10	1	COXO_RAT	P80432	rattus norv	
99	2	15.4	10	1	COXO_THUOB	P80982	thunmus obe	
100	2	15.4	10	1	CU30_LOCOMI	P11735	locusta mig	

```
TM2A_METWA          STANDARD;          PRT;          12 AA.
ID  TM2A_METWA
AC  P80652;
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE  (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE  methyltransferase 28 kDa subunit) (Fragment).
OS  Methanosarcina mazei (Methanosarcina frisia).
OC  Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC  Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX  NCBI_TaxID=2209;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX  MEDLINE=96370840; PubMed=8774736;
RA  Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT  "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT  coenzyme M methyltransferase from Methanosarcina mazei Go1
RT  reconstituted in ether lipid liposomes.";
RL  Eur. J. Biochem. 239:857-864 (1996).
CC  -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC  METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC  TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC  TETRAHYDROMETHANOPTERIN.
CC  -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC  mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC  (methylthio)ethanesulfonate.
CC  -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW  Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT  NON_TER 12
SQ  SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match          30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 EPVL 9
DB  ||||
    5 EPVL 8

RESULT 2
MAX6_BOMMX
ID  MAX6_BOMMX          STANDARD;          PRT;          20 AA.
AC  P83085;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Maximin 6.
OS  Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX  NCBI_TaxID=161274;
RN  [1]
RP  SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC  TISSUE=Skin secretion;
RA  Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT  "Isolation and structural characterisation of antimicrobial peptides
RT  from the venom of the Chinese large-webbed bell toad (Bombina
RT  maxima).";
RL  Submitted (JUL-2001) to the SWISS-PROT data bank.
CC  -!- FUNCTION: Has antimicrobial activity.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW  Amphibian defense peptide; Antibiotic.
SQ  SEQUENCE 20 AA; 1934 MW; F2C52CB5D69AFD18 CRC64;

Query Match          30.8%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 EPVL 9
DB  ||||
    5 EPVL 8

TM2A_METWA          STANDARD;          PRT;          12 AA.
ID  TM2A_METWA
AC  P80652;
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE  (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE  methyltransferase 28 kDa subunit) (Fragment).
OS  Methanosarcina mazei (Methanosarcina frisia).
OC  Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC  Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX  NCBI_TaxID=2209;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX  MEDLINE=96370840; PubMed=8774736;
RA  Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT  "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT  coenzyme M methyltransferase from Methanosarcina mazei Go1
RT  reconstituted in ether lipid liposomes.";
RL  Eur. J. Biochem. 239:857-864 (1996).
CC  -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC  METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC  TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC  TETRAHYDROMETHANOPTERIN.
CC  -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC  mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC  (methylthio)ethanesulfonate.
CC  -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW  Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT  NON_TER 12
SQ  SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match          30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 EPVL 9
DB  ||||
    5 EPVL 8

MAX6_BOMMX
ID  MAX6_BOMMX          STANDARD;          PRT;          20 AA.
AC  P83085;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Maximin 6.
OS  Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX  NCBI_TaxID=161274;
RN  [1]
RP  SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC  TISSUE=Skin secretion;
RA  Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT  "Isolation and structural characterisation of antimicrobial peptides
RT  from the venom of the Chinese large-webbed bell toad (Bombina
RT  maxima).";
RL  Submitted (JUL-2001) to the SWISS-PROT data bank.
CC  -!- FUNCTION: Has antimicrobial activity.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW  Amphibian defense peptide; Antibiotic.
SQ  SEQUENCE 20 AA; 1934 MW; F2C52CB5D69AFD18 CRC64;

Query Match          30.8%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 EPVL 9
DB  ||||
    5 EPVL 8

MAX8_BOMMX
ID  MAX8_BOMMX          STANDARD;          PRT;          20 AA.
AC  P83087;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Maximin 8.
OS  Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX  NCBI_TaxID=161274;
RN  [1]
RP  SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC  TISSUE=Skin secretion;
RA  Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT  "Isolation and structural characterisation of antimicrobial peptides
RT  from the venom of the Chinese large-webbed bell toad (Bombina
RT  maxima).";
RL  Submitted (JUN-2001) to the SWISS-PROT data bank.
CC  -!- FUNCTION: Has antimicrobial activity.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW  Amphibian defense peptide; Antibiotic.
SQ  SEQUENCE 20 AA; 1977 MW; EC7541AD6BE2F949 CRC64;

Query Match          30.8%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 LGPV 12
DB  ||||
    2 LGPV 5

MAX8_BOMMX
ID  MAX8_BOMMX          STANDARD;          PRT;          20 AA.
AC  P83087;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Maximin 8.
OS  Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX  NCBI_TaxID=161274;
RN  [1]
RP  SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC  TISSUE=Skin secretion;
RA  Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT  "Isolation and structural characterisation of antimicrobial peptides
RT  from the venom of the Chinese large-webbed bell toad (Bombina
RT  maxima).";
RL  Submitted (JUN-2001) to the SWISS-PROT data bank.
CC  -!- FUNCTION: Has antimicrobial activity.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW  Amphibian defense peptide; Antibiotic.
SQ  SEQUENCE 20 AA; 1977 MW; EC7541AD6BE2F949 CRC64;

Query Match          30.8%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 LGPV 12
DB  ||||
    2 LGPV 5
```

```

QY      9 LGPV 12
Db      2 LGPV 5

RESULT 5
PAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FWRFanide-like neuropeptide AP9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FWRFanide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 LGPV 11
Db      2 LGPV 4

RESULT 6
BPP3 BOTIN
ID BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
PR: C37196; C37196
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW Hypotensive agent; Pyrrolidone CARBOXYLIC ACID.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

QY      9 LGPV 11
Db      2 LGPV 5

RESULT 7
CRBL ICASP
ID CRBL ICASP STANDARD; PRT; 13 AA.
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotactic peptide (I-CP).
OS Icaria sp. (Ropalidian wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (in) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 LGPV 11
Db      5 LGPV 7

RESULT 8
VG16 BACSU
ID VG16 BACSU STANDARD; PRT; 13 AA.
AC P80867;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vegetative protein 16 (VEG16) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RX STRAIN=168 / IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463(1997).
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1372 MW; 20FB27BDC9ECA2D7 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 EPV 8
Db      5 EPV 7

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RESULT 9
AF33 MALPA STANDARD; PRT; 15 AA.
AC P81317;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
SEQUENCE, AND FUNCTION.
RP TISSUE=Seed;
RC MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT Cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not P.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0007275; P:development; NAS.
KW Fungicide; Antibiotic.
FT NON_TER 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQE 6
DB 8 YQE 10

RESULT 10
FGF1-CANFA STANDARD; PRT; 15 AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
GN FGF1 OR FGF-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
SEQUENCE.
RP MEDLINE=89231704; PubMed=2714282;
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC THAN DOES HBGF.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC PIR; S03955; S03955.

DR

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DR InterPro; IPR002348; IL1_HBGF.
DR PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDADA1 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4
DB 7 LLY 9

RESULT 11
LPL_THETH STANDARD; PRT; 15 AA.
AC P21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu leader peptide.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=88121725; PubMed=3323845;
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium
RT in Escherichia coli.";
RL Mol. Gen. Genet. 210:490-497(1987).
CC -!- FUNCTION: Involved in control of the biosynthesis of leucine.

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DR EMBL; X06604; CAA29823.1; -
KW Leucine biosynthesis; Leader peptide.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 23.1%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 13 GPV 15

RESULT 12
HBD_CLOPA STANDARD; PRT; 16 AA.
AC P81343;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (Beta-
DE hydroxybutyryl-CoA dehydrogenase) (BHBD) (CP 26) (fragment).
GN HBD.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]

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RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=96291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-CoA + NADP(+) = 3-
acetoacetyl-CoA + NADPH.
CC -|- PATHWAY: BUTYRATE/BUTANOL-PRODUCING PATHWAY.
CC -|- SIMILARITY: BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
DR InterPro; IPR006180; 3HGDH.
DR PROSITE; PS00067; 3HGDH; PARTIAL.
KW Oxidoreductase; NADP; Fatty acid metabolism.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1570 MW; E3AD430D5C575785 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 6 VLG 8

RESULT 13
PA2_NAJASP
ID PA2_NAJASP STANDARD; PRT; 16 AA.
AC Q10756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
DE (Muscarnic inhibitor) (Fragment).
OS Naja sputatrix (Malayan spitting cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Naja.
OC NCBI_TaxID=33626;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96195757; PubMed=8638927;
RA Miyoshi S.-I., Tu A.T.;
RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
acetylcholine receptor inhibitor.";
RL Arch. Biochem. Biophys. 328:17-25(1996).
CC -|- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
transmission at the postsynaptic site. Binds to the muscarinic
acetylcholine receptor.
CC -|- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -|- COFACTOR: Binds 1 calcium ion (By similarity).
CC -|- SUBUNIT: Monomer.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
SUBFAMILY.
CC PIR; S65520; S65520.
DR HSP; P00598; IPOA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PROSITE; PS00119; PA2 ASP; PARTIAL.
DR PROSITE; PS00118; PA2 HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834BBS585F0 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 LYQ 5
DB 2 LYQ 4

RESULT 14
PGTL_PELAC
ID PGTL_PELAC STANDARD; PRT; 16 AA.
AC P80563;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)
DE (transhydroxylase) (fragment).
OS Pelobacter acidigallici.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OC NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
RT "One molecule of molybdopterin guanine dinucleotide is associated
with each subunit of the heterodimeric Mo-Fe-S protein
transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
and mass spectrometry.";
RL Eur. J. Biochem. 237:406-413(1996).
CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-
trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
tetrahydroxybenzene.
CC -|- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR; S65430; S65430.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1620 MW; 56348D53A0AD6EE3 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 13 GPV 15

RESULT 15
BOL4_MEGPE
ID BOL4_MEGPE STANDARD; PRT; 17 AA.
AC P07495;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin IV.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;
OC Apidae; Bombus
OC NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -|- FUNCTION: Mast cell degranulating peptide.
DR PIR; D22595; D22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1873 MW; A34A43514BCFDFB6 CRC64;

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Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
   |||
Db 13 VLG 15

RESULT 16
BOL5 MEGPE
ID _BOL5_MEGPE STANDARD; PRT; 17 AA.
AC P07496;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin V.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Argiolas A., Pisano J.J.;
RX MEDLINE=85105003; PubMed=2578459;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
CC PIR: E22595; E22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1731 MW; B076C091571606A5 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
   |||
Db 3 VLG 5

RESULT 17
EFG_THEAQ
ID _EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUSA OR FUS.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

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CC EF-G/EF-2 SUBFAMILY.
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DR EMBL; X66322; CAA46997.1; -.
DR HAMAP; MF_00054; -.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2054 MW; EA46E1EF05F86E1D CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQE 6
   |||
Db 2 YQE 4

RESULT 18
MDH_ACIDE
ID _MDH_ACIDE STANDARD; PRT; 17 AA.
AC P80540;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.
OS Acidovorax delafieldii.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Acidovorax.
OX NCBI_TaxID=47920;
RN [1]
RP SEQUENCE
RC STRAIN=CCUG 12929;
RX MEDLINE=97334132; PubMed=9190829;
RA Charnock C.;
RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
RT Brevundimonas species are the first reported MDHs in Proteobacteria
RT which resemble lactate dehydrogenases in primary structure.";
RL J. Bacteriol. 179:4066-4070(1997).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1662 MW; 110E8111A516909E CRC64;

Query Match      23.1%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PVR 13
   |||
Db 4 PVR 6

RESULT 19
PCG6_PACGO
ID PCG6_PACGO STANDARD; PRT; 18 AA.
AC P82419;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Ponericin G6.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST GRAM-POSITIVE BACTERIA AND
CC S.CEREVISIAE. HAS NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1818.15; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide; Amidation.
FT MOD RES 18 18
FT SEQUENCE 18 AA; 1819 MW; 94876D83F60E8D3E CRC64;
SQ
Query Match 23.1%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
Db |||
5 VLG 7

RESULT 20
FLA3 SPIAU
ID FLA3 SPIAU STANDARD; PRT; 19 AA.
AC P21986;
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE Flagellar filament 32 kDa core protein (Minor) (Fragment).
OS Spirochaeta aurantia.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Spirochaeta.
OX NCBI_TaxID=147;
RN [1]
RP SEQUENCE.
RC STRAIN=M1;
RX MEDLINE=91123217; PubMed=1991729;
RA Parales J. Jr., Greenberg E.P.;
RT "N-terminal amino acid sequences and amino acid compositions of the
RT Spirochaeta aurantia flagellar filament polypeptides.";
RL J. Bacteriol. 173:1357-1359(1991).
CC -!- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF
CC REPEATING UNITS OF FLAA AROUND A CORE THAT CONTAINS ONE OR ALL OF
CC FIVE ANTIGENICALLY RELATED POLYPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
KW Flagella; Periplasmic.
FT NON TER 19 19
FT SEQUENCE 19 AA; 2084 MW; 3D06277582B1A979 CRC64;
SQ
Query Match 23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
Db |||
15 VLG 17

RESULT 21
OXLA_OPHHA
ID OXLA_OPHHA STANDARD; PRT; 19 AA.

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AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-1999 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-amino acid oxidase (EC 1.4.3.2) (LAO) (LAAO) (Fragment).
OS Ophiophagus hannah (King cobra) (Naja hannah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Ophiophagus.
OX NCBI_TaxID=8665;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94361525; PubMed=8080286;
RA Ponnudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malayan
RT pit viper (Calloselasma rhodostoma) venom.";
RL Arch. Biochem. Biophys. 313:373-378(1994).
RN [2]
RP SEQUENCE OF 1-15.
RC TISSUE=Venom;
RX MEDLINE=97449790; PubMed=9304806;
RA Ahn M.Y., Lee B.M., Kim Y.S.;
RT "Characterization and cytotoxicity of L-amino acid oxidase from the
RT venom of king cobra (Ophiophagus hannah)".
RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC -!- FUNCTION: Has cytotoxic activity (By similarity).
CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
CC + NH(3) + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- PTM: Glycosylated.
CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
CC -!- STRONG, TO MOUSE FIG-1.
KW Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Toxin.
FT CONFLICT 1 1
FT NON TER 19 19
FT SEQUENCE 19 AA; 2298 MW; DD911ASB414F1427 CRC64;
SQ
Query Match 23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QEP 7
Db |||
10 QEP 12

RESULT 22
PCG7_PACGO
ID PCG7_PACGO STANDARD; PRT; 19 AA.
AC P82420;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G7.
OS Pachycondyla goeldii (Ponerine ant.).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST GRAM-POSITIVE BACTERIA AND
CC S.CEREVISIAE. HAS NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- MASS SPECTROMETRY: MW=1876.14; METHOD=MALDI.  
 KW Antibiotic; Insect immunity; Fungicide  
 SQ SEQUENCE 19 AA; 1876 MW; 4DA4876D83F6088D CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
 ||||  
 Db 5 VLG 7

## RESULT 23

UK1 HUMAN STANDARD; PRT; 19 AA.  
 AC P31940;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of epidermal keratinocytes (Spot 1118) (Fragments).  
 DE Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Keratinocytes;  
 RX MEDLINE=93162043; PubMed=1286667;  
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
 RA Vandekerckhove J.;  
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
 RT protein database of normal human epidermal keratinocytes.";  
 RL Electrophoresis 13:960-969(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 7.24, ITS MW IS: 23.5 kDa.  
 DR Aarhus/Ghent-2DPAGE; 1118; IEF.  
 FT NON TER 1 1  
 FT UNSURE 6 6  
 FT NON\_CONS 6 7  
 FT NON\_CONS 12 13  
 FT UNSURE 17 17  
 FT NON TER 19 19  
 SQ SEQUENCE 19 AA; 2087 MW; EF7515F79D50DE12 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7  
 ||||  
 Db 13 QEP 15

## RESULT 24

UP25 UPEIN STANDARD; PRT; 19 AA.  
 ID UP25 UPEIN  
 AC P82031;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Uperin 2.5.  
 OS Uperoleia inundata (Floodplain toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104953;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Rattery M.J., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;

RT "Novel uperin peptides from the dorsal glands of the Australian  
 RT floodplain toadlet Uperoleia inundata.";  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M.LUTEUS,  
 CC L.MESENTERIODES AND S.UBERIS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1940; METHOD=FAB.  
 KW Amphibian defense peptide; Antibiotic.  
 SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
 ||||  
 Db 9 VLG 11

## RESULT 25

UP27 UPEMJ STANDARD; PRT; 19 AA.  
 ID UP27 UPEMJ  
 AC P82039;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Uperin 2.7.  
 OS Uperoleia mjobergii (Australian toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104954;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "New antibiotic uperin peptides from the dorsal glands of the  
 RT Australian toadlet Uperoleia mjobergii.";  
 RL Aust. J. Chem. 49:1325-1331(1996).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1946; METHOD=FAB.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 19 AA; 1949 MW; 24E4F83A6BA35F21 CRC64;

Query Match 23.1%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
 ||||  
 Db 16 VLG 18

## RESULT 26

UP28 UPEMJ STANDARD; PRT; 19 AA.  
 ID UP28 UPEMJ  
 AC P82040;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Uperin 2.8.  
 OS Uperoleia mjobergii (Australian toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104954;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "New antibiotic uperin peptides from the dorsal glands of the

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RT  Australian toadlet Uperoleia mjobergii.;
RL  Aust. J. Chem. 49:1325-1331(1996).
CC  -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC  S.EPIDERMIS AND S.UBERIS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC  -!- MASS SPECTROMETRY: MW=1978; METHOD=FAB.
KW  Amphibian defense peptide.
SQ  SEQUENCE 19 AA; 1979 MW; 48524822C8A340F9 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 VLG 10
DB  16 VLG 18

RESULT 27
AF2L_MALPA
ID  AF2L_MALPA STANDARD; PRT; 20 AA.
AC  P83143;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Antifungal protein 2 large subunit (CW-2) (Fragment).
OS  Malva parviflora (Little mallow) (Cheeseweed).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC  eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX  NCBI_TaxID=145753;
RN  [1]
RP  SEQUENCE, AND FUNCTION.
RC  TISSUE=Seed;
RX  MEDLINE=20568734; PubMed=11118343;
RA  Wang X., Bunkers G.J.;
RT  "Potent heterologous antifungal proteins from cheeseweed (Malva
RT  parviflora).";
RL  Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC  -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC  not F.graminearum.
CC  -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC  -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC  concentration.
DR  GO: GO:0003799; F:antifungal peptide activity; IDA.
KW  Fungicide; Antibiotic.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 YQE 6
DB  8 YQE 10

RESULT 28
BIP_PHAVU
ID  BIP_PHAVU STANDARD; PRT; 20 AA.
AC  P80089;
DT  01-DEC-1992 (Rel. 24, Created)
DT  01-DEC-1992 (Rel. 24, Last sequence update)
DE  Luminal binding protein (78 kDa glucose-regulated protein homolog)
DE  (GRP 78) (Fragment).
OS  Phaseolus vulgaris (Kidney bean) (French bean).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX  NCBI_TaxID=3885;

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RN  [1]
RP  SEQUENCE.
RC  STRAIN=cv. Greensleeves; TISSUE=Cotyledon;
RX  MEDLINE=94221064; PubMed=1344885;
RA  D'Amico L., Valsasina B., Daminati M.G., Fabbrini M.S., Nititi G.,
RA  Bollini R., Ceriotti A., Vitale A.;
RT  "Bean homologs of the mammalian glucose-regulated proteins: induction
RT  by tunicamycin and interaction with newly synthesized seed storage
RT  proteins in the endoplasmic reticulum.";
RL  Plant J. 2:443-455(1992).
CC  -!- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF
CC  MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC  -!- INDUCTION: By tunicamycin.
CC  -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR  InterPro; IPR001023; Hsp70.
DR  PROSITE; PS00297; HSP70_1; PARTIAL.
DR  PROSITE; PS00329; HSP70_2; PARTIAL.
DR  PROSITE; PS01036; HSP70_3; PARTIAL.
KW  ATP-binding; Endoplasmic reticulum.
FT  UNSURE 4 4
FT  UNSURE 18 18 OR T.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 2147 MW; 809D43AF21A21476 CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 VLG 10
DB  6 VLG 8

RESULT 29
CD4_SHEEP
ID  CD4_SHEEP STANDARD; PRT; 20 AA.
AC  P05542;
DT  01-NOV-1988 (Rel. 09, Created)
DT  01-NOV-1988 (Rel. 09, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE  (Fragment).
GN  CD4.
OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
RP  SEQUENCE.
RC  MEDLINE=86166694; PubMed=3082751;
RX  Classon B.J., Tsagaratos J., Kirszbaum L., Maddox J., McKay C.R.,
RA  Brandon M., McKenzie I.F.C., Walker I.D.;
RT  "The L3T4 antigen in mouse and the sheep equivalent are
RT  immunoglobulin-like.";
RL  Immunogenetics 23:129-132(1986).
CC  -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC  RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC  -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
DR  PIR; B47642; B47642.
DR  GO: GO:0042101; C:T-cell receptor complex; ISS.
DR  GO: GO:0015026; F:coreceptor activity; ISS.
DR  GO: GO:0042289; F:MHC class II protein binding activity; ISS.
DR  GO: GO:0006955; P:immune response; ISS.
DR  GO: GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR  GO: GO:0030217; P:T-cell differentiation; ISS.
DR  GO: GO:0045058; P:T-cell selection; ISS.
DR  GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
KW  Immunoglobulin domain; T-cell; Immune response.
FT  NON TER 20 20
SQ  SEQUENCE 20 AA; 1928 MW; 421F09570FEA97EE CRC64;

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Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      |||
Db      4 VLG 6

RESULT 30
PRE3_LITIN
ID_FLR3_LITIN      STANDARD;      PRT;      20 AA.
AC P56249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 3.
OS Litoria infrafrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
the giant tree frog Litoria infrafrenata.";
RL J. pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
glands.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1956 MW; 7E4ABE30EA17B20C CRC64;

Query Match      23.1%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 VLG 10
      |||
Db      5 VLG 7

RESULT 31
FLRF_HIRME
ID_FLRP_HIRME      STANDARD;      PRT;      4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H. medicinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H. trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FL 2
      ||
Db      1 FL 2

RESULT 32
FLRN_ANTEL
ID_FLRN_ANTEL      STANDARD;      PRT;      4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinilidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuizen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nockner H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 4
SQ SEQUENCE 4 AA; 549 MW; 64540729A00000000 CRC64;

Query Match      15.4%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FL 2
      ||
Db      1 FL 2

RESULT 33
ACPH_RABIT
ID_ACPH_RABIT      STANDARD;      PRT;      6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;

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RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RL Anal. Biochem. 199;45:50(1991)
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR EIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol endopep ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VL 9
Db 5 VL 6

RESULT 34
ALL3_CARMA STANDARD; PRT; 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]_
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 796 MW; 672879DCB476B70 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EP 7
Db 1 EP 2

RESULT 35
EI05_LITRU STANDARD; PRT; 7 AA.
ID EI05_LITRU
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7 7 AMIDATION.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EP 7
Db 3 EP 4

RESULT 36
FAR1_HELTI STANDARD; PRT; 7 AA.
ID FAR1_HELTI
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRP-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7 AMIDATION.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FL 2
Db 4 FL 5

RESULT 37
FAR1_MACRS STANDARD; PRT; 7 AA.
ID FAR1_MACRS
AC P83274;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE FMRPamide-like neuropeptide FLP1 (DENSELRF-amide)  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk; Sarathongkum W., Jaidechoey S., Longyant S.,  
 RA Sithigorngul P.,  
 RA Sathigorngul W.;  
 RT "Novel FMRPamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540420 CRC64;  
 Query Match 15.4%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FL 2  
 Db 4 FL 5  
 RESULT 38  
 FAR1 PROCL STANDARD; PRT; 7 AA.  
 AC P38459;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRPamide homolog NF1.  
 OS Procamburus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacodea; Gambaridae; Procamburus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRPamide-related peptides from crayfish  
 RT pericardial organs.";  
 RL Peptides 14:137-143(1993).  
 CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
 Query Match 15.4%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FL 2  
 Db 4 FL 5  
 RESULT 39  
 FAR1 PROCL STANDARD; PRT; 7 AA.  
 AC P38459;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRPamide homolog NF1.  
 OS Procamburus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacodea; Gambaridae; Procamburus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRPamide-related peptides from crayfish  
 RT pericardial organs.";  
 RL Peptides 14:137-143(1993).  
 CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
 Query Match 15.4%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FL 2  
 Db 4 FL 5

FAR2 PROCL STANDARD; PRT; 7 AA.  
 AC P38458;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRPamide homolog DF2.  
 OS Procamburus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacodea; Gambaridae; Procamburus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRPamide-related peptides from crayfish  
 RT pericardial organs.";  
 RL Peptides 14:137-143(1993).  
 CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540420 CRC64;  
 Query Match 15.4%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FL 2  
 Db 4 FL 5  
 RESULT 40  
 GFRP MOUSE STANDARD; PRT; 7 AA.  
 AC P99025;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).  
 GN GCHFR OR GFRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Van J.X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP  
 CC CYCLOHYDROLASE 1. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE  
 CC (BY SIMILARITY).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC SWISS-2DPAGE; P99025; MOUSE.  
 DR INIT MET 0  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;  
 Query Match 15.4%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LL 3

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Db      .      3 LL 4

RESULT 41
MNP1_LEPDE
ID MNP1_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Led-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC -!- OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GP 11
   ||
   4 GP 5
Db

RESULT 42
PPH2_LYCES
ID PPH2_LYCES STANDARD; PRT; 7 AA.
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PM: Glycosylated.
CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.

FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FL 2
   ||
   1 FL 2
Db

RESULT 43
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LY 4
   ||
   1 LY 2
Db

RESULT 44
AL15_CARMA
ID AL15_CARMA STANDARD; PRT; 8 AA.
AC P81818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

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KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 45
ALL6_CARMA
ID ALL6_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 46
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Salivary gland;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.

KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 47
ALL6_CVDPO
ID ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LY 4
DB 3 LY 4

RESULT 48
ALL8_CARMA
ID ALL8_CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 795 MW; 922879CDCB47687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11  
 ||  
 Db 2 GP 3

RESULT 49  
 ALL9\_CARMA  
 ID ALL9\_CARMA STANDARD; PRT; 8 AA.  
 AC P81812;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 9.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 781 MW; 7C2879CDCB476878 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11  
 ||  
 Db 2 GP 3

RESULT 50  
 B44K\_PORGI  
 ID B44K\_PORGI STANDARD; PRT; 8 AA.  
 AC P81886;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE 44 kDa immunogenic protein (Fragment).  
 OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Porphyromonadaceae; Porphyromonas.  
 OX NCBI\_TaxID=837;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=VPB 3492;  
 RX MEDLINE=20198497; PubMed=10731616;  
 RA Norris J.M., Love D.N.;  
 RT "Serum antibody responses of cats to soluble whole cell antigens of  
 RT feline Porphyromonas gingivalis.";  
 RL Vet. Microbiol. 73:37-49 (2000).  
 CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.  
 KW Antigen.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQ 5  
 ||  
 Db 3 YQ 4

RESULT 51  
 CAD1\_ENTFA  
 ID CAD1\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 RT induces plasmid transfer in Streptococcus faecalis.";  
 RL FEBS Lett. 178:97-100 (1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PAD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VL 9  
 ||  
 Db 5 VL 6

RESULT 52  
 CLP\_THICU  
 ID CLP\_THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;

RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS; FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 785 MW; 91497B06DDC2D76D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PV 8  
 Db 2 PV 3

RESULT 53  
 ID\_CW2\_CONPU STANDARD; PRT; 8 AA.  
 AC P58785;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OC NCBI\_TaxID=41690;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN=Clipperton Island, TISSUE=Venom;  
 RX MEDLINE=9938839; PubMed=10461743;  
 RA Jacobsen R.B., Jlmenez B.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 Olivera B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 RT dynamics in the contryphan family.";  
 RL J. Pept. Res. 54:93-99(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Hydroxylation; D-amino acid.  
 FT DISULFID 2 4  
 FT MOD\_RES 4 4 D-LEUCINE.  
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LL 3  
 Db 4 LL 5

RESULT 54  
 ID\_CPDI\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13269;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CPDI.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OC NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85040388; PubMed=6436978;  
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B.;  
 RT "Isolation and structure of bacterial sex pheromone, CPDI.";

RL Science 226:849-850(1984).  
 CC -!- FUNCTION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC BACTERIOCIN PLASMID PPDI.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 Db 1 FL 2

RESULT 55  
 ID\_FAR1\_PANRE STANDARD; PRT; 8 AA.  
 AC P41872;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRPamide-like neuropeptide PFI (SDPNFLRP-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OC NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRPamide-like peptides from the free-living nematode  
 RT Panagrellus redivivus.";  
 RL Peptides 13:209-214(1992).  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
 CC CAUDALLY TO THE BASE OF THE PHARYNX.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 Db 5 FL 6

RESULT 56  
 ID\_FAR1\_PENMO STANDARD; PRT; 8 AA.  
 AC P83316;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRPamide-like neuropeptide FUPI (GDRNFLRP-amide).  
 OS Penaeus monodon (Pencoid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OC NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,  
 RA Chaivithangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRPamide-like neuropeptide sequences from the eyestalk

RT of the giant tiger prawn Penaeus monodon";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.

CC Neuropeptide; Amidation.  
 KW MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 ||  
 5 FL 6

Db

## RESULT 57

FAR2\_HOMAM  
 ID FAR2\_MACRS STANDARD; PRT; 8 AA.

AC P83275;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonoidea; Palaemonidae; Macrobrachium.  
 ON NCBI\_TaxID=79674;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P.; Sarathongkum W., Jaidechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).

CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
 DR Neuropeptide; Amidation.  
 KW MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 ||  
 5 FL 6

Db

## RESULT 58

FAR3\_HOMAM  
 ID FAR3\_MACRS STANDARD; PRT; 8 AA.

AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 CC Nephropoidea; Nephropidae; Homarus.  
 ON NCBI\_TaxID=6706;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Pericardial organs;

RT

RT

RT

RT

RT

RT

RT

RT

RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamide-like immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM  
 CC POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.

CC Neuropeptide; Amidation.  
 KW MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 ||  
 5 FL 6

Db

## RESULT 59

FAR4\_HOMAM

ID FAR4\_HOMAM STANDARD; PRT; 8 AA.

AC P41487;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 CC Nephropoidea; Nephropidae; Homarus.  
 ON NCBI\_TaxID=6706;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Pericardial organs;

RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamide-like immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).

CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC  
 CC NEUROMUSCULAR JUNCTIONS.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2  
 ||  
 5 FL 6

Db

## RESULT 60

FAR7\_ASCSU

ID FAR7\_ASCSU STANDARD; PRT; 8 AA.

AC P43171;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF7.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 CC Ascarididae; Ascaris.

```

OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel PMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC NEUROPEPTIDE FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 2 GP 3

RESULT 61
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -|- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
DB 1 FL 2

RESULT 62
RST_MYCIT
ID RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nait J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -|- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC rRNA (by similarity).
CC -|- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (by similarity).
CC -|- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08171; AAR25376.1; -.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; rRNA-binding; trRNA-binding.
FT INIT MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11
DB 4 GP 5

RESULT 63
UC26_MAIZE
ID UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0 ITS MW IS: 57.2 kDa.
CC Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 15.4%; Score 2; DB 1; Length 8;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EP 7  
DB 2 EP 3

## RESULT 64

UP06 MOUSE STANDARD; PRT; 8 AA.  
AC P38644;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast; PubMed=7523108;  
RX MEDLINE=9500907; Wichter L.L., He C., Selkirk J.K.;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.  
CQ NON TER 8  
FT SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;  
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EP 7  
DB 3 EP 4

## RESULT 65

UH09 RAT STANDARD; PRT; 8 AA.  
AC P56575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Fleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
Jungblut P.R.;  
RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
CQ NON TER 8  
FT SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;  
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QE 6  
DB 1 QE 2

## RESULT 66

UP01 HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Putiger S., Paquet N., Ravier F., Pasquali C.,  
Sanchez J.-C., James R., Tiesot J.-D., Bjellqvist B.,  
Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
CQ SWISS-2DPAGE; P30087; HUMAN.  
DR FT NON TER 1  
FT UNSURE 8  
FT NON TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;  
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QE 6  
DB 2 QE 3

## RESULT 67

VGLG HSV2B STANDARD; PRT; 8 AA.  
AC P81780;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Glycoprotein G (Fragment).  
OS Herpes simplex virus (type 2 / strain B4327UR).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=103921;  
RN [1]  
RP SEQUENCE.  
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;  
RL Submitted (APR-1999) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND  
2: GH, GB, GC, GG, GD, GI, AND GE.  
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN  
HSV-1.  
CQ Glycoprotein.  
KW NON TER 8  
FT SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;  
SQ

Query Match 15.4%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GP 11  
DB 6 GP 7

## RESULT 68

```

BS43_SERPL
ID -B843 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RX STRAIN=J7;
RC MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeunen J., Thonart P.;
RT "Characterization of serracin P, a phase-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen."
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
DR InterPro: IPR006498; Tail tube.
DR Pfam: PF04985; Phage_tube_1.
DR Antibiotic; Bacteriocin.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VL 9
DB 8 VL 9

RESULT 69
ID -BUK CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Buryate kinase (EC 2.7.2.7) (BK) (CP 36) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RX STRAIN=W5;
RC MEDLINE=98291870; PubMed=96299818;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
CC phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetate kinase family.
DR HAMAP; MF_00542; -; 1.
DR InterPro: IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
FT Transferase; Kinase.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

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Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LL 3
DB 4 LL 5

RESULT 70
ID -FAR2 PANRE STANDARD; PRT; 9 AA.
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode
RT Panagrellus redivivus."
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 15.4%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FL 2
DB 6 FL 7

RESULT 71
ID -FAR3 MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Rumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii."
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.

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FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FL 2  
Db 6 FL 7  
RESULT 72  
FAR5 PANRE  
ID FAR5 PANRE STANDARD; PRT; 9 AA.  
AC P82661;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PFS (AMRNALVRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
[1]  
RN SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of FMRFamide-related  
peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 VR 13  
Db 7 VR 8  
RESULT 73  
FAR6 MACRS  
ID FAR6 MACRS STANDARD; PRT; 9 AA.  
AC P83279;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP6 (DGRNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
[1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA MEDLINE=21107394; PubMed=11179812;  
RA Sithigorngul P., Saraiithongkum W., Longyant S., Panchan N.,  
RT "Three more novel FMRFamide-like neuropeptide sequences from the  
eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";  
RL Peptides 22:191-197(2001).  
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=WALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FL 2  
Db 6 FL 7  
RESULT 75  
FARP CALSI  
ID FARP CALSI STANDARD; PRT; 9 AA.  
AC P38495;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide.  
OS Callinectes sapidus (Blue crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.  
OX NCBI\_TaxID=6763;  
[1]  
RN SEQUENCE.  
RA MEDLINE=92270479; PubMed=1815216;  
RA Krajniak K.G.;  
RT "The identification and structure-activity relations of a  
cardioactive FMRFamide-related peptide from the blue crab Callinectes  
sapidus.";  
RL Peptides 12:1295-1302(1991).

KW Neuropeptide; Amidation.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FL 2  
Db 6 FL 7  
RESULT 74  
FAR8 MACRS  
ID FAR8 MACRS STANDARD; PRT; 9 AA.  
AC P83281;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
[1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA MEDLINE=21107394; PubMed=11179812;  
RA Sithigorngul P., Saraiithongkum W., Longyant S., Panchan N.,  
RT "Three more novel FMRFamide-like neuropeptide sequences from the  
eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";  
RL Peptides 22:191-197(2001).  
CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=WALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FL 2  
Db 6 FL 7  
RESULT 75  
FARP CALSI  
ID FARP CALSI STANDARD; PRT; 9 AA.  
AC P38495;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide.  
OS Callinectes sapidus (Blue crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.  
OX NCBI\_TaxID=6763;  
[1]  
RN SEQUENCE.  
RA MEDLINE=92270479; PubMed=1815216;  
RA Krajniak K.G.;  
RT "The identification and structure-activity relations of a  
cardioactive FMRFamide-related peptide from the blue crab Callinectes  
sapidus.";  
RL Peptides 12:1295-1302(1991).

CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;  
  
Query Match 15.4%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 FL 2  
Db 6 FL 7

Search completed: November 25, 2003, 19:28:27  
Job time : 5.68189 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 24.4128 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLPVR 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

- 1: sp.arched.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organella.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.rodent.\*
- 12: sp.virus.\*
- 13: sp.vertibrate.\*
- 14: sp.unclassified.\*
- 15: sp.rvirus.\*
- 16: sp.bacteriap.\*
- 17: sp.archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	30.8	16	12 Q9WMC6	Q9WMC6 sigma virus
2	4	30.8	17	10 Q9S8K1	Q9S8K1 solanum tub
3	4	30.8	18	4 Q9UCL4	Q9UCL4 homo sapien
4	4	30.8	20	4 Q96A79	Q96A79 homo sapien
5	3	23.1	7	8 Q9S182	Q9S182 gnatholebia
6	3	23.1	8	2 Q93SP2	Q93SP2 pseudomonas
7	3	23.1	8	2 Q9R4M3	Q9R4M3 enterococcu
8	3	23.1	8	8 Q9R4VC1	Q9R4VC1 varanus rud
9	3	23.1	8	8 Q8HR64	Q8HR64 clivia caul
10	3	23.1	8	10 Q8L802	Q8L802 zea mays (m
11	3	23.1	8	11 P82598	P82598 rattus norv
12	3	23.1	9	2 Q9R7H9	Q9R7H9 haemophilus
13	3	23.1	9	2 P83157	P83157 anabaena sp
14	3	23.1	14	9 Q9UCN5	Q9UCN5 homo sapien
15	3	23.1	10	2 Q47091	Q47091 escherichia
16	3	23.1	10	5 Q95NT8	Q95NT8 musca domes

17	3	23.1	10	6 Q9TRU6	Q9tru6 bos taurus
18	3	23.1	10	11 Q63389	Q63389 rattus norv
19	3	23.1	10	11 Q9JLI5	Q9jli5 mus musculu
20	3	23.1	10	12 Q9JIG8	Q9jig8 tt virus. o
21	3	23.1	10	13 Q90ZV8	Q90zv8 psittacus e
22	3	23.1	10	15 Q75595	Q75595 human immun
23	3	23.1	11	7 Q9TQB3	Q9tqb3 homo sapien
24	3	23.1	11	10 Q9S829	Q9s829 psophocarpu
25	3	23.1	12	4 Q9UMQ9	Q9umq9 homo sapien
26	3	23.1	12	4 Q81VL5	Q81vl5 homo sapien
27	3	23.1	12	8 Q9XNR6	Q9xnr6 pyiaetella l
28	3	23.1	12	11 Q925V7	Q925v7 mus musculu
29	3	23.1	12	13 Q90ZL3	Q90zl3 xenopus lae
30	3	23.1	13	2 Q50117	Q50117 mycobacteri
31	3	23.1	13	2 Q53693	Q53693 streptomyce
32	3	23.1	13	2 Q49230	Q49230 mycoplasma
33	3	23.1	13	2 Q9RFJ7	Q9rfj7 actinobacill
34	3	23.1	13	4 Q75905	Q75905 homo sapien
35	3	23.1	13	4 Q14461	Q14461 homo sapien
36	3	23.1	13	8 Q99188	Q99188 rivulus cau
37	3	23.1	13	8 Q94RE2	Q94re2 leptomonas
38	3	23.1	13	11 Q88176	Q88176 mus musculu
39	3	23.1	13	12 Q9PXB5	Q9pxb5 duck hepati
40	3	23.1	13	13 P82064	P82064 limnodynast
41	3	23.1	14	2 Q9R5P6	Q9r5p6 legionella
42	3	23.1	14	4 Q9UHM5	Q9uhm5 homo sapien
43	3	23.1	14	8 Q9MRF6	Q9mrf6 hordeum mur
44	3	23.1	14	12 Q8V1H7	Q8v1h7 hepatitis b
45	3	23.1	15	2 Q9JP39	Q9jp39 pseudomonas
46	3	23.1	15	2 Q9R598	Q9r598 micrococcus
47	3	23.1	15	4 Q9UCC2	Q9ucc2 homo sapien
48	3	23.1	15	6 Q9TRN9	Q9trn9 sus scrofa
49	3	23.1	15	8 Q9TH04	Q9th04 grus ameri
50	3	23.1	15	8 P92818	P92818 paralichthy
51	3	23.1	15	8 Q9XLJ8	Q9xlj8 grus leucog
52	3	23.1	15	8 Q9TH03	Q9th03 grus paradi
53	3	23.1	15	10 Q8SAP4	Q8sap4 solanum tub
54	3	23.1	15	10 P82431	P82431 nicotiana t
55	3	23.1	15	11 Q9QV34	Q9qv34 rattus sp.
56	3	23.1	16	2 Q44610	Q44610 buchnera ap
57	3	23.1	16	2 Q9R4X4	Q9r4x4 pseudomonas
58	3	23.1	16	2 P82597	P82597 bacillus sp
59	3	23.1	16	4 Q9NPQ7	Q9npq7 homo sapien
60	3	23.1	16	5 Q9TWN2	Q9twn2 macrobodelia
61	3	23.1	16	6 Q62810	Q62810 equus cabal
62	3	23.1	16	6 Q9TR97	Q9tr97 oryctolagus
63	3	23.1	16	8 P92070	P92070 euhadra her
64	3	23.1	16	8 Q9T2Q6	Q9t2q6 solanum tub
65	3	23.1	16	11 Q8CIS2	Q8cis2 mus musculu
66	3	23.1	17	2 Q55091	Q55091 shigella so
67	3	23.1	17	2 Q9EUP4	Q9eup4 thermus the
68	3	23.1	17	2 Q9R560	Q9r560 bacillus su
69	3	23.1	17	3 Q00074	Q00074 aspergillus
70	3	23.1	17	4 Q9UJH1	Q9ujh1 homo sapien
71	3	23.1	17	4 Q9UPK4	Q9upk4 homo sapien
72	3	23.1	17	4 Q9UCL9	Q9ucl9 homo sapien
73	3	23.1	17	4 Q9UC43	Q9uc43 homo sapien
74	3	23.1	17	5 Q17205	Q17205 bombyx mori
75	3	23.1	17	5 Q26832	Q26832 trypanosoma
76	3	23.1	17	5 Q9TVY3	Q9tv33 bombyx mori
77	3	23.1	17	5 Q9TVX7	Q9tvx7 bombyx mori
78	3	23.1	17	5 Q17203	Q17203 bombyx mori
79	3	23.1	17	6 Q9TRY8	Q9try8 sus sp. ins
80	3	23.1	17	11 Q9QUU4	Q9quj4 mus sp. mep
81	3	23.1	17	11 Q9QUW6	Q9quw6 rattus sp.
82	3	23.1	17	11 Q9QZ24	Q9qz24 mus musculu
83	3	23.1	17	13 Q9PRU8	Q9pru8 gallus gall
84	3	23.1	18	4 Q9UC87	Q9uc87 homo sapien
85	3	23.1	18	4 Q9UC81	Q9uc81 homo sapien
86	3	23.1	18	4 Q9UM83	Q9um83 homo sapien
87	3	23.1	18	4 Q9UJ81	Q9uj81 homo sapien
88	3	23.1	18	4 Q9UCF4	Q9ucf4 homo sapien
89	3	23.1	18	4 Q9UCR5	Q9ucr5 homo sapien

90 O8ned1 homo sapien  
91 O43834 homo sapien  
92 Q9trf2 oryctolagus  
93 Q9trf57 sus scrofa  
94 Q8m0a0 tockus leuc  
95 Q8vbm8 mus musculu  
96 Q61840 mus musculu  
97 Q90912 gallus gall  
98 Q87587 chimpanzee  
99 Q87589 chimpanzee  
100 Q87593 chimpanzee

## ALIGNMENTS

## RESULT 1

Q9WMG6  
ID Q9WMG6 PRELIMINARY; PRT; 16 AA.  
AC Q9WMG6;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE 2 protein (Fragment).  
GN 2.  
OS Sigma virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; unclassified Rhabdoviridae.  
OX NCBI\_TaxID=11301;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212481; PubMed=8384742;  
RA Teninges D., Bras F., Dezelee S.;  
RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
RT overlap".  
RL Virology 193:1018-1023(1993).  
DR EMBL; S57847; RAD40699.1; -.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 30.8%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPVL 9

Db 10 EPVL 13

## RESULT 2

Q9S8K1  
ID Q9S8K1 PRELIMINARY; PRT; 17 AA.  
AC Q9S8K1;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE 20 kDa knittz-type proteinase inhibitor (Fragment).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95093035; PubMed=8000008;  
RA Mitsumori C., Yamagishi K., Fujino K., Kikuta Y.;  
RT "Detection of immunologically related Kunitz and Bowman-Birk  
RT proteinase inhibitors expressed during potato tuber development".  
RL Plant Mol. Biol. 26:961-969(1994).  
SQ SEQUENCE 17 AA; 1872 MW; 44F34F5775B0F832 CRC64;

Query Match 30.8%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLG 10

Db 7 PVLG 10

## RESULT 3

Q9UCL4  
ID Q9UCL4 PRELIMINARY; PRT; 18 AA.  
AC Q9UCL4;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE Insulin-like growth factor binding protein 30 kDa form (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93091816; PubMed=1726837;  
RA Roghani M., Segovia B., Whitechurch O., Binoux M.;  
RT "Purification from human cerebrospinal fluid of insulin-like growth  
RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form  
RT of IGFBP-3 and a new IGFBP species".  
RL Growth Regul. 1:125-130(1991).  
SQ SEQUENCE 18 AA; 1689 MW; 10F5516240C6298B CRC64;

Query Match 30.8%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12

Db 7 LGPV 10

## RESULT 4

Q96A79  
ID Q96A79 PRELIMINARY; PRT; 20 AA.  
AC Q96A79;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Connective tissue growth factor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Blom I.E., van Dijk A.J., de Weger R.A., Tilanus M.G.J.,  
RT "Identification of human CCN2 (connective tissue growth factor)  
RT promoter polymorphisms".  
RL J. Clin. Pathol. 54:192-196(2001).  
DR EMBL; AF316366; AAK60505.1; -.  
DR EMBL; AF316367; AAK60506.1; -.  
DR EMBL; AF316368; AAK60507.1; -.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2050 MW; 0110FF079D4516B6 CRC64;

Query Match 30.8%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPCR 13

Db 7 GPCR 10

## RESULT 5

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O99182
ID Q99182 PRELIMINARY; PRT; 7 AA.
AC Q99182;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI
OS Gnatholebias zonatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences."
RL Mol. Phylogenet. Evol. 13:289-301 (1999).
DR EMBL; AF002591; AAD01074.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQ 5
Db 2 LYQ 4

RESULT 6
Q93SP2
ID Q93SP2 PRELIMINARY; PRT; 8 AA.
AC Q93SP2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein QacEdelta1
DE (Fragment).
GN QACEDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=YM704; TRANSPOSON=class I integron;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AAK50441.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
Db 6 FLL 8

RESULT 7
Q9R4M3
ID Q9R4M3 PRELIMINARY; PRT; 8 AA.
AC Q9R4M3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COBI=ACTERIAL sex pheromone.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacilliales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=95290767; PubMed=7772836;
RA Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;
RT "Isolation and structure of the Enterococcus faecalis sex pheromone,
RT COBI, that induces conjugal transfer of the hemolysin/bacteriocin
RT plasmids, pOBI and pYII."
RL Biosci Biotechnol. Biochem. 59:703-705 (1995).
SQ SEQUENCE 8 AA; 741 MW; 83D87732C732CDC2 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10
Db 5 VLG 7

RESULT 8
Q94VCI
ID Q94VCI PRELIMINARY; PRT; 8 AA.
AC Q94VCI;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus rudicollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169851;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0 (2001).
DR EMBL; AF407521; AAL10116.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
Db 6 FLL 8

RESULT 9
Q8HR64
ID Q8HR64 PRELIMINARY; PRT; 8 AA.
AC Q8HR64;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Rps16 protein (Fragment).
GN RPS16.
OS Clivia caulescens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC   Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OX   Clivia
RN   NCBI_TaxID=152470;
RP   SEQUENCE FROM N.A.
RA   Conrad F., Reeves G., Rourke J.P.;
RT   "Phylogenetic relationships of the recently discovered species Clivia
RL   mirabilis.";
DR   Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AJ519544; CAD59437.1; -.
KW   Chloroplast.
FT   NON TER
SQ   SEQUENCE 8 AA; 909 MW; 9FA87729C732C9 CRC64;

Query Match      23.1%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 FLL 3
Db   4 FLL 6

RESULT 10
Q8L802      PRELIMINARY; PRT; 8 AA.
AC   Q8L802
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE   PACCAD clade; Panicoidae; Andropogoneae; Zea.
DE   Pat (Fragment).
GN   PAT.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoidae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ronning S.B., Berdal K.G., Vaithilingom M.M., Holst-Jensen A.;
RT   "Transformation event-specific quantitative real-time PCR for
RT   genetically modified Bt11 maize (Zea mays) and estimation of the
RT   impact of exogenous DNA on the limit of quantification.";
RL   Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AY123624; AAH89275.1; -.
FT   NON TER
FT   NON TER
SQ   SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match      23.1%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   11 PVR 13
Db   1 PVR 3

RESULT 11
P82598      PRELIMINARY; PRT; 8 AA.
AC   P82598
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   3kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=20198203; PubMed=10731662;

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RA   Kim K.-Y., Choi I., Kim S.-S.;
RT   "Purification and characterization of a novel inhibitor of the
RT   proliferation of hepatic stellate cells.";
RL   J. Biochem. 127:23-27(2000).
CC   -!- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC   HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC   ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC   -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC   PROTEIN.
FT   NON TER
FT   NON TER
SQ   SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match      23.1%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   6 EPV 8
Db   2 EPV 4

RESULT 12
Q9R7H9      PRELIMINARY; PRT; 9 AA.
AC   Q9R7H9
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Lipoprotein (Fragment).
GN   NLPD.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98083063; PubMed=9422600;
RA   Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., Golomb M.;
RT   "The tryptophanase gene cluster of Haemophilus influenzae type b:
RT   evidence for horizontal gene transfer.";
RL   J. Bacteriol. 180:107-118(1998).
DR   EMBL; AF003252; AAB96582.1; -.
FT   NON TER
FT   NON TER
SQ   SEQUENCE 9 AA; 1152 MW; 35A017673B4412D7 CRC64;

Query Match      23.1%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   11 PVR 13
Db   2 PVR 4

RESULT 13
P83157      PRELIMINARY; PRT; 9 AA.
AC   P83157
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
OS   Anabaena sp. (strain L31).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX   NCBI_TaxID=29412;
RN   [1]
RP   SEQUENCE.
RA   Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL   Submitted (OCT-2001) to the SWISS-PROT data bank.
CC   -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC   CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC   -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

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CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE  
 CC FAMILY.  
 DR InterPro; IPR001189; SODismutase.  
 DR PROSITE; PS0088; SOD MN; PARTIAL.  
 KW Oxidoreductase; Iron; Metal-binding.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7  
 Db 4 QEP 6

## RESULT 14

ID Q9UCN5 PRELIMINARY; PRT; 9 AA.  
 AC Q9UCN5;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92291065; PubMed=1601862;  
 RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;  
 RT "Identification of cell-surface heparin/heparan sulfate-binding  
 RT proteins of a human uterine epithelial cell line (RL95).";  
 RL J. Biol. Chem. 267:11930-11939(1992).  
 SQ SEQUENCE 9 AA; 1008 MW; CBS6D0544732C732 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9  
 Db 1 PVL 3

## RESULT 15

ID Q47091 PRELIMINARY; PRT; 10 AA.  
 AC Q47091;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Colicin E1 (Fragment).  
 OS Escherichia coli.  
 OG Plasmid ColE1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86094231; PubMed=3936034;  
 RA Waleh N.S.; Johnson P.H.;  
 RT "Structural and functional organization of the colicin E1 operon."; Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).  
 RL EMBL; M12543; AAA23065.1; -;  
 KW Plasmid.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
 Db 7 VLG 9

## RESULT 16

ID Q95NT8 PRELIMINARY; PRT; 10 AA.  
 AC Q95NT8;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Cytochrome P450 (Fragment).  
 GN CYP6D3.  
 OS Musca domestica (House fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;  
 OC Muscidae; Musca.  
 OX NCBI\_TaxID=7370;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LPR;  
 RA Kasai S., Scott J.G.;  
 RT "5' flanking sequence of CYP6D3."; Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS;  
 RA Kasai S., Scott J.G.;  
 RT "Cytochrome P450 CYP6D3 5' flanking sequence."; Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF283258; AAK59543.1; -;  
 DR EMBL; AF283259; AAK69544.1; -;  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1190 MW; 550408A0572729C7 CRC64;

Query Match 23.1%; Score 3; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3  
 Db 4 FLL 6

## RESULT 17

ID Q9TRU6 PRELIMINARY; PRT; 10 AA.  
 AC Q9TRU6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE GAP-3, GTPase-activating protein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92112868; PubMed=1309786;  
 RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,  
 RA Burgess A.W.;  
 RT "The purification of a Rap1 GTPase-activating protein from bovine  
 RT brain cytosol."; J. Biol. Chem. 267:1546-1553(1992).  
 RL J. Biol. Chem. 267:1546-1553(1992).  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 23.1%; Score 3; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3  
 Db 1 FLL 3

RESULT 18  
 Q63389 PRELIMINARY; PRT; 10 AA.  
 AC Q63389;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Ornithine decarboxylase (ODC).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1] NCBI\_TaxID=10116;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
 RX MEDLINE=89255378; PubMed=2722815;  
 RA Wen L., Huang J.K., Blackshear P.J.;  
 RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential  
 RT regulatory elements, and comparison to the mouse gene.";  
 RL J. Biol. Chem. 264:9016-9021(1989).  
 DR EMBL; J04791; AAF66163.1; -;  
 SQ SEQUENCE 10 AA; 1074 MW; 30F6EE69D415BDC7 CRC64;

Query Match 23.1%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9  
 Db 8 PVL 10

RESULT 19  
 Q9JLI5 PRELIMINARY; PRT; 10 AA.  
 AC Q9JLI5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Melanocortin type 1 receptor MCL1R (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1] NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=20090876; PubMed=10623832;  
 RA Adachi S., Morii E., Kim D.-k., Ogihara H., Jippo T., Ito A., Lee Y.M.,  
 RA Kitamura Y.;  
 RT "Involvement of mi-transcription factor in expression of alpha-  
 RT melanocyte-stimulating hormone receptor in cultured mast cells of  
 RT mice.";  
 RL J. Immunol. 164:855-860(2000).  
 DR EMBL; AF176016; AAF37323.1; -;  
 KW Receptor.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 23.1%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QEP 7  
 Db 4 QEP 6

RESULT 20  
 Q9JIG8 PRELIMINARY; PRT; 10 AA.  
 AC Q9JIG8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ORF2.  
 OS TT virus.  
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.  
 RN [1] NCBI\_TaxID=68887;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TTV-SC232;  
 RX MEDLINE=20251008; PubMed=10790123;  
 RA Niel C., Saback F.L., Lampe E.;  
 RT "Coinfection with Multiple TT Virus Strains Belonging to Different  
 RT Genotypes Is a Common Event in Brazilian Healthy Adults.";  
 RL J. Clin. Microbiol. 38:1926-1930(2000).  
 DR EMBL; AF216453; AAF66889.1; -;  
 SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;

Query Match 23.1%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13  
 Db 7 PVR 9

RESULT 21  
 Q90ZV8 PRELIMINARY; PRT; 10 AA.  
 AC Q90ZV8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Adenylate kinase (Fragment).  
 OS Psittacus erithacus (grey parrot).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.  
 RN [1] NCBI\_TaxID=57247;  
 RP SEQUENCE FROM N.A.  
 RA Shapiro L.H., Dumbacher J.P.;  
 RT "Adenylate kinase intron 5: a new nuclear locus for avian  
 RT systematics";  
 RL Auk 118:248-255(2001).  
 DR EMBL; AF307895; AAK43534.1; -;  
 KW Kinase.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1099 MW; 23847A272731B777 CRC64;

Query Match 23.1%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4  
 Db 7 LLY 9

RESULT 22  
 Q75595 PRELIMINARY; PRT; 10 AA.  
 ID Q75595  
 AC Q75595;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=T12B;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RT "The Tat and C2-V3 Envelope Genes in the Molecular Epidemiology of
RL Human Immunodeficiency Virus-1.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57303; AAB17863.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;

Query Match      23.1%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 EPV 8
Db      |||
        2 EPV 4

RESULT 23
Q9TOB3
ID Q9TOB3 PRELIMINARY; PRT; 11 AA.
AC Q9TOB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class I related protein 1 (Fragment).
GN MR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98451457; PubMed=9780177;
RA Riegert P., Wanner V., Bahram S.;
RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-
related MR1 gene.";
RT J. Immunol. 161:4066-4077(1998).
DR EMBL; AF039526; AAD02172.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;

Query Match      23.1%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLL 3
Db      |||
        7 FLL 9

RESULT 24
Q9S8Z9
ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

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OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytocchemistry 31:731-735(1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABC77772D1 CRC64;

Query Match      23.1%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PVL 9
Db      |||
        7 PVL 9

RESULT 25
Q9UMQ9
ID Q9UMQ9 PRELIMINARY; PRT; 12 AA.
AC Q9UMQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
DR EMBL; AJ238490; CAB53366.1; -.
KW Hydroxylase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1432 MW; 28E901A093072338 CRC64;

Query Match      23.1%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLY 4
Db      |||
        9 LLY 11

RESULT 26
Q8IVIS
ID Q8IVIS PRELIMINARY; PRT; 12 AA.
AC Q8IVIS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pro-alpha-1 collagen type 1 (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064528; PubMed=6183642;
RA Chu M.L., Myers J.C., Bernard M.P., Ding J.F., Ramirez F.;
RT "Cloning and characterization of five overlapping cDNAs specific for

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RT the human pro alpha 1(I) collagen chain.";  
RL Nucleic Acids Res. 10:5925-5934 (1982).  
DR EMBL: J00113; AAN86574.1; -.  
KW Collagen.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1330 MW; 85A00329C66862CA CRC64;

Query Match 23.1%; Score 3; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
Db |||  
7 GPV 9

## RESULT 27

Q9XNR6 PRELIMINARY; PRT; 12 AA.  
ID Q9XNR6;  
AC Q9XNR6;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).  
GN NAD3.  
OS Pyllaiaella littoralis.  
OG Mitochondrion.  
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;  
OC Acinetosporaceae; Pyllaiaella.  
OX NCBI\_TaxID=2885;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=toscov.  
RX MEDLINE=99346148; PubMed=10415341;  
RA Oudot M.P., Kloareg B., Loiseaux-de Goer S.;  
RT "The Mitochondrial Pyllaiaella littoralis nad11 gene contains only the  
RT N-terminal FeS-binding domain.";  
RL Gene 235:131-137 (1999).  
DR EMBL: AF110139; AAD44051.1; -.  
KW Mitochondrion; Ubiquinone.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3  
Db |||  
2 FLL 4

## RESULT 28

Q925V7 PRELIMINARY; PRT; 12 AA.  
ID Q925V7;  
AC Q925V7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Alpha 1 type I collagen (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rippe R.A., Umezawa A., Kimball J.P., Breindl M., Brenner D.A.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U50767; AAA96053.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1296 MW; 98E20329C668705A CRC64;

Query Match 23.1%; Score 3; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
Db |||  
7 GPV 9

## RESULT 29

Q90ZL3 PRELIMINARY; PRT; 12 AA.  
ID Q90ZL3;  
AC Q90ZL3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Casein kinase 2 alpha subunit (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilhelm V., Neckelmann G., Allende C.C., Allende J.B.;  
RT "The Genomic Structure of Two Protein Kinase CK2 alpha Genes of  
RT Xenopus laevis and Features of the Putative Promoter Region.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY032954; AAK50341.1; -.  
KW Kinase.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1320 MW; D005098DFD15A772 CRC64;

Query Match 23.1%; Score 3; DB 13; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
Db |||  
3 GPV 5

## RESULT 30

Q50117 PRELIMINARY; PRT; 13 AA.  
ID Q50117;  
AC Q50117;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE U650w.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith D.R.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Robison K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U15184; AAA63055.1; -.  
SQ SEQUENCE 13 AA; 1503 MW; CAABF1429DED5412 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 BPV 8  
Db |||  
4 BPV 6



## RESULT 31

Q53693 PRELIMINARY; PRT; 13 AA.  
 AC Q53693;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Leader peptide.  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=33903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CU-18;  
 RX MEDLINE=96105213; PubMed=8529876;  
 RA De Rossi E., Leva R., Gusbetti L., Manachini P.L., Riccardi G.;  
 RT "Cloning, sequencing and expression of the ilvNC gene cluster from  
 Streptomyces avermitilis.";  
 RL Gene 166:127-132(1995).  
 DR EMBL; L39268; AAA93097.1; -;  
 SQ SEQUENCE 13 AA; 1499 MW; 5E080E40FD4E32C7 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 |||  
 Db 7 VLG 9

## RESULT 32

Q49230 PRELIMINARY; PRT; 13 AA.  
 AC Q49230;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical 1.6 kDa protein (Fragment).  
 OS Mycoplasma genitalium.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G-37;  
 RA Peterson S.N.;  
 RT "Characterization and analysis of the Mycoplasma genitalium genome.";  
 RL Thesis (1992), University of North Carolina Medical School, USA.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G-37;  
 RX MEDLINE=94075230; PubMed=8253680;  
 RA Peterson S.N., Hu P.C., Bott K.F., Hutchison C.A. III.;  
 RT "A survey of the Mycoplasma genitalium genome by using random  
 RT sequencing.";  
 RL J. Bacteriol. 175:7918-7930(1993).  
 DR EMBL; U01781; AAD10602.1; -;  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1642 MW; EC726B2670F6D2C1 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3  
 |||  
 Db 8 FLL 10

## RESULT 33

Q9RFJ7 PRELIMINARY; PRT; 13 AA.

AC Q9RFJ7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ApXI (Fragment)  
 OS Actinobacillus lignieresii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=720;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC49236;  
 RX MEDLINE=20293481; PubMed=10931859;  
 RA Schaller A., Kuhnert P., de la Puente-Redondo V.A., Nicolet J.,  
 RA Frey J.;  
 RT "ApX toxins in Pasteurellaceae species from animals.";  
 RL Vet. Microbiol. 74:365-376(2000).  
 DR EMBL; AF188870; AAF23115.1; -;  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1466 MW; 076D88D59020C874 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 |||  
 Db 10 VLG 12

## RESULT 34

O75905 PRELIMINARY; PRT; 13 AA.  
 AC O75905; Q9HAQ9;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Prosaposin (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98426155; PubMed=9751800;  
 RA Sun Y., Jin P., Witte D.P., Grabowski G.A.;  
 RT "Isolation and characterization of the human prosaposin promoter.";  
 RL Gene 218:37-47(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sun Y., Jin P., Grabowski G.A.;  
 RT "Isolation and characterization of the human prosaposin promoter.";  
 RL Gene 0:0-0(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21205763; PubMed=11309366;  
 RA Hukova H., Cervenkova M., Ledvinov J., Tochackova M., Hrebicek M.,  
 RA Poupetova H., Befekadu A., Berna L., Paton B.C., Harzer K., Boeser A.,  
 RA Smid F., Elleder M.;  
 RT "A novel mutation in the coding region of the prosaposin gene leads to  
 RT a complete deficiency of prosaposin and saposins, and is associated  
 RT with a complex sphingolipidosis dominated by lactosylceramide  
 RT accumulation.";  
 RL Hum. Mol. Genet. 10:927-940(2001).  
 DR EMBL; AF057307; AAC64921.2; -;  
 DR EMBL; AF307850; AAG31635.1; -;  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1383 MW; 57585B6C1784D727 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3  
Db 5 FLL 7

RESULT 35

Q14461 PRELIMINARY; PRT; 13 AA.

AC Q14461; Q14842;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE Glycophorin B (Fragment).

GN GYFB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

FN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90264417; PubMed=1971625;

RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;

RT "Identification of the crossing-over point of a hybrid gene encoding human glycophorin variant Sta. Similarity to the crossing-over point in haptoglobin-related genes.";

RL J. Biol. Chem. 265:9259-9263(1990).

RN [2]

RP SEQUENCE OF 1-9 FROM N.A.

RA Carttron J.P.;

RL Submitted (JUL-1989) to the EMBL/GenBank/DBDJ databases.

RN [3]

RP SEQUENCE OF 1-9 FROM N.A.

RX MEDLINE=90005483; PubMed=2792104;

RA Vignal A., Rahuel C., El-Malliki B., London J., Le Vankim C., Blanchard C.D.;

RT "Molecular analysis of glycophorin A and B gene structure and expression in homozygous Miltenberger class V (M1. V) human erythrocytes.";

RL Eur. J. Biochem. 184:337-344(1989).

DR EMBL; M33505; AAA53152.1; -

DR EMBL; X15824; CAA33822.1; -

FT NON TER 1

SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5  
Db 11 LYQ 13

RESULT 36

O99188 PRELIMINARY; PRT; 13 AA.

AC O99188;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Cytochrome oxidase I (Fragment).

GN COI.

OS Rivulus caudomarginatus.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Cyprinodontiformes; Aplocheilidae; Rivulidae; Rivulus.

OX NCBI\_TaxID=60318;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20072928; PubMed=10603257;

RA Murphy W.J., Thomson J.E., Collier G.E.;

RT "Phylogeny of the Neotropical killifish family Rivulidae (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA sequences.";

RL Mol. Phylogenet. Evol. 13:289-301(1999).

DR EMBL; AF002597; AAD01080.1; -

KW Mitochondrion.

FT NON TER 1

SQ SEQUENCE 13 AA; 1705 MW; 404DF35AEFFE79C7 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5  
Db 2 LYQ 4

RESULT 37

Q94RE2 PRELIMINARY; PRT; 13 AA.

AC Q94RE2;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE ATPase (Fragment).

GN A6.

OS Leptomonas seymouri.

OG Mitochondrion.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leptomonas.

OX NCBI\_TaxID=5684;

RN [1]

RP SEQUENCE FROM N.A.

RA Merzlyak E.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Kolesnikov A.A.;

RT "Cyb and A6 gene transcribed and edited in polycistron.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AJ313532; CAC67493.1; -

KW Mitochondrion.

FT NON TER 1

FT NON TER 13

SQ SEQUENCE 13 AA; 1626 MW; 471B78F48BDCCEB7 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLY 4  
Db 10 LLY 12

RESULT 38

O88176 PRELIMINARY; PRT; 13 AA.

AC O88176;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Neural cell adhesion molecule (Fragment).

GN NCAM1 OR NCAM.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RN STRAIN=Balb-c; TISSUE=Liver;

```
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

  Query Match      23.1%; Score 3; DB 11; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 5 PVL 7

RESULT 39
Q9PXB5 PRELIMINARY; PRT; 13 AA.
AC Q9PXB5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE 170 kDa DHBV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE.
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;

  Query Match      23.1%; Score 3; DB 12; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 7 PVL 9

RESULT 40
P82064 PRELIMINARY; PRT; 13 AA.
AC P82064;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE FLETCHERIN.
OS Limnodynastes fletcheri (Barking marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=39403;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW -!- MASS SPECTROMETRY: MW=1197; METHOD=FAB.
Amphibian skin.
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SQ SEQUENCE 13 AA; 1197 MW; 56B5BB1FAEA7C723 CRC64;

  Query Match      23.1%; Score 3; DB 13; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
Db 2 GPV 4

RESULT 41
Q9R5P6 PRELIMINARY; PRT; 14 AA.
AC Q9R5P6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Major outer membrane protein 31 kDa subunit, MOMP 31 kDa subunit
DE (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RX MEDLINE=92121130; PubMed=1310095;
RA Hofman P.S., Seyer J.H., Butler C.A.;
RT "Molecular characterization of the 28- and 31-kilodalton subunits of
RT the Legionella pneumophila major outer membrane protein.";
RL J. Bacteriol. 174:908-913(1992).
FT NON TER 1
FT NON TER 14
SQ SEQUENCE 14 AA; 1490 MW; 3541B0FB1AF55F48 CRC64;

  Query Match      23.1%; Score 3; DB 2; Length 14;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
Db 1 GPV 3

RESULT 42
Q9UHM5 PRELIMINARY; PRT; 14 AA.
AC Q9UHM5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Islet cell autoantigen ICA69 (Fragment).
GN ICA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Friday R.P., Trucco M., Pietropaolo M.;
RT "Refined genomic organization of the diabetes autoantigen ICA69 gene
RT locus.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF147807; AAF20021.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1656 MW; 1AEB6ACD19E2F9CB CRC64;

  Query Match      23.1%; Score 3; DB 4; Length 14;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 5
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Db          6 LYQ 8

RESULT 43
Q9MRP6
ID Q9MRP6 PRELIMINARY; PRT; 14 AA.
AC Q9MRP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE PSI 9 kDa protein (Fragment).
GN PSAC.
OS
OC Chloroplast.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=97361;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Conservation of the start codon by editing in ndhD-encoded
RT transcribed is not restricted to dicotyledonous plants.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278355; CAB96127.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1589 MW; 8F14E36A13B7D911 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 2 LGP 4

RESULT 44
Q8V1H7
ID Q8V1H7 PRELIMINARY; PRT; 14 AA.
AC Q8V1H7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Truncated HBsAg.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FH10;
RA Wen Y.M., Liu F., Ma Z.M.;
RT "Structural and functional analysis of hepatitis B virus genomes in
RT fulminant hepatitis B patients.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461362; AAL66336.1; -.
SQ SEQUENCE 14 AA; 1427 MW; 2F487846CB391E28 CRC64;

Query Match 23.1%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 9 LGP 11

RESULT 45
Q9JP39
ID Q9JP39 PRELIMINARY; PRT; 15 AA.
AC Q9JP39;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE HRPK (Fragment).
GN HRPK.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RX MEDLINE=97348579; PubMed=9204563;
RA Alfano J.R., Kim H.S., Delaney T.P., Collmer A.;
RT "Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrpA
RT gene encodes an Avr-like protein that acts in an hrp-dependent manner
RT within tobacco cells.";
RL Mol. Plant Microbe Interact. 10:580-588(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=61;
RX MEDLINE=20243785; PubMed=10781092;
RA Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L.,
RA Petnicki-Ocwieja T., van Dijk K., Collmer A.;
RT "The Pseudomonas syringae Hrp Pathogenicity Island has a tripartite
RT mosaic structure composed of a cluster of type III secretion genes
RT bounded by exchangeable effector and conserved effector loci that
RT contribute to parasitic fitness and pathogenicity in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4856-4861(2000).
DR EMBL; AF232003; AAF71482.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1696 MW; C0E7FAC1E44EAB20 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 4 PVL 6

RESULT 46
Q9RS98
ID Q9RS98 PRELIMINARY; PRT; 15 AA.
AC Q9RS98;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DNA topoisomerase I (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Micrococcus.
OX NCBI_TaxID=1270;
RN [1]
RP SEQUENCE.
RX MEDLINE=93249439; PubMed=8387285;
RA Anderlucci D., Pedrini A.M.;
RT "Structural similarities between M. luteus and E. coli DNA
RT topoisomerase I.";
RL Biochem. Biophys. Res. Commun. 192:657-664(1993).
SQ SEQUENCE 15 AA; 1508 MW; D36D28F43AA6E2F9 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 5 LGP 7

RESULT 47

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Q9UCC2
ID Q9UCC2 PRELIMINARY; PRT; 15 AA.
AC Q9UCC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993)
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
DB 4 GPV 6

RESULT 48
Q9TRN9 PRELIMINARY; PRT; 15 AA.
ID Q9TRN9;
AC Q9TRN9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE LOW MR zona pellucida binding protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92378826; PubMed=1510840;
RA Parry R.V., Barker P.J., Jones R.;
RT "Characterization of low Mr zona pellucida binding proteins from boar
RT spermatozoa and seminal plasma.";
RL Mol. Reprod. Dev. 33:108-115(1992)
SQ SEQUENCE 15 AA; 1574 MW; C8C0FAB43F233D6C CRC64;

Query Match 23.1%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
DB 1 EPV 3

RESULT 49
Q9TH04 PRELIMINARY; PRT; 15 AA.
ID Q9TH04;
AC Q9TH04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus americana (whooping crane).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=9117;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=LMS B3394;
RA Glenn T.C., Stephan W., Braun M.J.;
RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
RT DNA Variation.";
RL Conserv. Biol. 0:0-0(1999).
DR EMBL; AF112373; AAD23994.1; -.
KW Mitochondrion.
FT NON TER 15
SQ SEQUENCE 15 AA; 1759 MW; A7F711A65B9F934F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 13 VLG 15

RESULT 50
P92818 PRELIMINARY; PRT; 15 AA.
ID P92818;
AC P92818;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit-4L (Fragment).
OS Paralichthys olivaceus (Flounder).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Satoh K.;
RT "Characterization of cloned mitochondrial fragments from the Japanese
RT flounder.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000674; BAA20924.1; -.
KW Mitochondrion.
FT NON TER 15
SQ SEQUENCE 15 AA; 1613 MW; D1BAA2018C95FE80 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 12 FLL 14

RESULT 51
Q9XLJ8 PRELIMINARY; PRT; 15 AA.
ID Q9XLJ8;
AC Q9XLJ8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus leucogeranus (Siberian crane).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=40819;
RN [1]
RP SEQUENCE FROM N.A.
```

RA Glenn T.C., Stephan W., Braun M.J.;  
 RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial  
 DNA Variation."  
 RL Conserv. Biol. 0:0-0(1999).  
 DR EMBL; AF112371; AAD23992.1; -.  
 KW Mitochondrion.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1807 MW; A7FFB3A65B8A734F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 Db 13 VLG 15

## RESULT 52

Q9TH03  
 ID Q9TH03 PRELIMINARY; PRT; 15 AA.  
 AC Q9TH03;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE NADH dehydrogenase subunit 6 (Fragment).  
 GN N06.  
 OS Grus paradisea (Blue crane).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.  
 OX NCBI\_TaxID=40825;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Glenn T.C., Stephan W., Braun M.J.;  
 RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial  
 DNA Variation."  
 RL Conserv. Biol. 0:0-0(1999).  
 DR EMBL; AF112372; AAD23993.1; -.  
 KW Mitochondrion.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1807 MW; A7FFB3A65B8A734F CRC64;

Query Match 23.1%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLG 10  
 Db 13 VLG 15

## RESULT 53

Q9SAP4  
 ID Q9SAP4 PRELIMINARY; PRT; 15 AA.  
 AC Q9SAP4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Serine proteinase inhibitor (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CV. Irish Cobbler;  
 RA Yamagishi K., Kikuta Y.;  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X70376; CAA49837.1; -.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1667 MW; 8093D41B4CA0D1EC CRC64;

Query Match 23.1%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3  
 Db 9 FLL 11

## RESULT 54

P82431  
 ID P82431 PRELIMINARY; PRT; 15 AA.  
 AC P82431;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 100 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CV. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -|- SUBCELLULAR LOCATION: CELL WALL.  
 CC -|- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1694 MW; 5F3B8D2E48187626 CRC64;

Query Match 23.1%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPV 8  
 Db 1 EPV 3

## RESULT 55

Q9QV34  
 ID Q9QV34 PRELIMINARY; PRT; 15 AA.  
 AC Q9QV34;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE CHOLIC acid transport protein P50 (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94183413; PubMed=8136027;  
 RA Hoffmann A., Mullner S., Ziegler K., Fasold H.;  
 RT "Purification and partial sequence of proteins involved in the cholic  
 acid transport into rat liver hepatocytes."  
 RL J. Protein Chem. 12:765-769(1993).  
 SQ SEQUENCE 15 AA; 1597 MW; D719DFB7C75AC0B CRC64;

Query Match 23.1%; Score 3; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVL 9  
 Db 11

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Db          3 PVL 5

RESULT 56
Q44610
ID Q44610 PRELIMINARY; PRT; 16 AA.
AC Q44610
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Shikimate dehydrogenase (Fragment).
GN AROB.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
CC NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95212914; PubMed=7535281;
RA Roubaksh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
RT gene.";
RL Gene 155:107-112(1995).
DR EMBL; U10499; AAA79128.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPV 8
Db 13 EPV 15

RESULT 57
Q9R4X4
ID Q9R4X4 PRELIMINARY; PRT; 16 AA.
AC Q9R4X4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-JUN-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Exotoxin A (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CC NCBI_TaxID=287;
RN [1]
RP SEQUENCE.
RX MEDLINE=94356232; PubMed=8075811;
RA Wolz C., Lehmann R., Vasil M.L., Bischoff R., Doring G.;
RT "A new extracellular protein of Pseudomonas aeruginosa Pa103 regulated
RT by regA.";
RL Microbiology 140:1755-1761(1994).
SQ SEQUENCE 16 AA; 1628 MW; D6C94C87E6823274 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11
Db 13 LGP 15

RESULT 58
P82597
ID P82597 PRELIMINARY; PRT; 16 AA.
AC P82597
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

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DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Thermostable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23)
DE (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RX STRAIN=H-257;
RX MEDLINE=20198254; PubMed=10731713;
RA Imamura S., Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from
RT the moderately thermophilic Bacillus sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -!- FUNCTION: HYDROLYSES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
CC OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
CC TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
CC OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 23.1%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
Db 5 PVL 7

RESULT 59
Q9NPQ7
ID Q9NPQ7 PRELIMINARY; PRT; 16 AA.
AC Q9NPQ7
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE AK001912 hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
RA Leirach H., Poustka A., Lundeberg J.;
RT "The European IMAGE consortium for integrated Molecular analysis of
RT human gene transcripts.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389982; CAB97537.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1484 MW; 97C92837C881A371 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12
Db 14 GPV 16

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RESULT 60
Q9TWN2
ID Q9TWN2 PRELIMINARY; PRT; 16 AA.
AC Q9TWN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Sialidase L (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP MEDLINE=95071287; PubMed=7980443;
RX Poole R.C., Halesrap A.P.;
RT "N-terminal protein sequence analysis of the rabbit erythrocyte
RT lactate transporter suggests identity with the cloned monocarboxylate
RT transport protein MCT1."
RL Biochem. J. 303:755-759(1994).
SQ SEQUENCE 16 AA; 1438 MW; 2AB33D7BAEAFB0D CRC64;
[1]
RN [1]
RP MEDLINE=94308136; PubMed=8034634;
RX Chou M.Y., Li S.C., Kiso M., Hasegawa A., Li Y.T.;
RT "Purification and characterization of sialidase L, a NeuAc alpha 2--
RT >3Gal-specific sialidase."
RL J. Biol. Chem. 269:18821-18826(1994).
SQ SEQUENCE 16 AA; 1910 MW; 0822879C79EC6EE0 CRC64;

Query Match 23.1%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQ 5
Db 7 LYQ 9

RESULT 61
O62810
ID O62810 PRELIMINARY; PRT; 16 AA.
AC O62810;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pregnancy-associated glycoprotein (Fragment).
GN PAG.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99225331; PubMed=10208966;
RA Green J.A., Xie S., Szafranska B., Gan X., Newman A.G., McDowell K.,
RA Roberts R.M.;
RT "Identification of a new aspartic proteinase expressed by the outer
RT chorionic cell layer of the equine placenta."
RL Biol. Reprod. 60:1069-1077(1999).
DR EMBL; AF061188; AAC15768.1; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1830 MW; 733B85DC7AAC213F CRC64;

Query Match 23.1%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLQ 10
Db 6 VLQ 8

RESULT 62
Q9TR97
ID Q9TR97 PRELIMINARY; PRT; 16 AA.
AC Q9TR97;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Lactate transporter (Fragment).
OS Oryctolagus cuniculus (Rabbit).
[1]
RN [1]
RP MEDLINE=95071287; PubMed=7980443;
RX Poole R.C., Halesrap A.P.;
RT "N-terminal protein sequence analysis of the rabbit erythrocyte
RT lactate transporter suggests identity with the cloned monocarboxylate
RT transport protein MCT1."
RL Biochem. J. 303:755-759(1994).
SQ SEQUENCE 16 AA; 1438 MW; 2AB33D7BAEAFB0D CRC64;

Query Match 23.1%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GPV 12
Db 6 GPV 8

RESULT 63
P92070
ID P92070 PRELIMINARY; PRT; 16 AA.
AC P92070;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
OS Euhadra herklotsi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
NCBI_TaxID=58912;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons
RT of complete gene organization of Euhadra, Cepaea and Albinaria and
RT implications of unusual tRNA secondary structures."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71694; CAA96364.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 16 AA; 1836 MW; 258908495BFBFCAE CRC64;

Query Match 23.1%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLL 3
Db 10 FLL 12

RESULT 64
Q9TQ06
ID Q9TQ06 PRELIMINARY; PRT; 16 AA.
AC Q9TQ06;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Cytochrome-C reductase 11 kDa subunit (EC 1.10.2.2) (Fragment).
OS Solanum tuberosum (Potato).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
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RN SEQUENCE.
RP MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 16 AA; 1904 MW; AFC237AE7549E2B5 CRC64;

Query Match 23.1%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 8 VLG 10

RESULT 65
Q8CIS2 PRELIMINARY; PRT; 16 AA.
AC Q8CIS2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Plasminogen (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX PubMed=12149246;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Parner R.J., Miles L.A.;
RT "Localization of Regulatory Elements Mediating Constitutive and
RT Cytokine-stimulated Plasminogen Gene Expression.";
RL J. Biol. Chem. 277:38579-38588(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
RA Parner R.J., Miles L.A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY134430; AAN15805.1; -.
FT NON TER 16
SQ SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;

Query Match 23.1%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 10 FLL 12

RESULT 66
Q5091 PRELIMINARY; PRT; 17 AA.
AC Q5091;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Beta-lactamase (Fragment).
GN AMPC.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=624;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=OS10;
RX MEDLINE=84170267; PubMed=6369321;

RA Olsson O., Bergstrom S., Lindberg F.P., Normark S.;
RT "ampC beta-lactamase hyperproduction in Escherichia coli: Natural
RT ampicillin resistance generated by horizontal chromosomal DNA transfer
RT from Shigella.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7556-7560(1983).
DR EMBL; K01234; AAA26514.1; -.
DR InterPro; IPR001586; Beta_lactamase_C.
DR PROSITE; PS00336; BETA_LACTAMASE_C; 1.
FT NON TER 17
SQ SEQUENCE 17 AA; 1756 MW; 7FAC3A40A4809623 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10
DB 15 VLG 17

RESULT 67
Q9EUP4 PRELIMINARY; PRT; 17 AA.
AC Q9EUP4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cell division associated protein (Fragment).
GN DIVIVA.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN-KT8;
RA Spada S., Gibert Y., Pembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the ylmB homologue of Thermus
RT thermophilus.";
RL DNA Seq. 11:5007-5014(2001).
DR EMBL; AJ297409; CAC21427.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2084 MW; 0C642E1D509D87E3 CRC64;

Query Match 23.1%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQE 6
DB 10 YQE 12

RESULT 68
Q9R560 PRELIMINARY; PRT; 17 AA.
AC Q9R560;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Menaghiol oxidase (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_
RP SEQUENCE.
RX MEDLINE=93356600; PubMed=8394685;
RA Lemma E., Schagger H., Kroger A.;
RT "The menaghiol oxidase of Bacillus subtilis W23.";
RL Arch. Microbiol. 159:574-578(1993).
SQ SEQUENCE 17 AA; 1750 MW; 87A251230A5831C3 CRC64;

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Query Match 23.1%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPV 12  
Db 11 GPV 13

RESULT 69  
Q00074 PRELIMINARY; PRT; 17 AA.  
AC Q00074;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Extracellular acid protease (Fragment).  
GN PEPA.  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=N400;  
RC MEDLINE=95163121; PubMed=7532112;  
RA Jarai G., Buxton F.;  
RT "Nitrogen, carbon, and pH regulation of extracellular acidic proteases  
of Aspergillus niger.";  
RL Curr. Genet. 26:238-244(1994).  
DR EMBL: U03507; AAC48920.1; --  
DR MEROPS; A01.016; --  
KW Protease.  
FT NON TER 17  
SQ SEQUENCE 17 AA; 1694 MW; FF01D0BEC9FEAE0B CRC64;

Query Match 23.1%; Score 3; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLG 10  
Db 11 VLG 13

RESULT 70  
Q9UJH1 PRELIMINARY; PRT; 17 AA.  
AC Q9UJH1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE D9436M11.2 (Retinosis (X-linked, juvenile) 1 (XLRSL1))  
DE (Fragment).  
GN RSL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Grafham D.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z94056; CAB40073.1; --  
FT NON TER 17  
SQ SEQUENCE 17 AA; 2029 MW; 8100E1B78C52C7FB CRC64;

Query Match 23.1%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1-FLL 3  
Db 11

Db 8 FLL 10

RESULT 71  
Q9UPK4 PRELIMINARY; PRT; 17 AA.  
AC Q9UPK4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE UCRY HUMAN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.B., McCready P.M., Skowronski E., Adamson A.W.,  
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,  
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,  
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
RA Kobayashi A., Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a  
serine protease gene cluster.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC005321; AAC27374.1; --  
FT NON TER 17  
SQ SEQUENCE 17 AA; 2166 MW; B73A34E7EDB2DE5D CRC64;

Query Match 23.1%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGP 11  
Db 6 LGP 8

RESULT 72  
Q9UCL9 PRELIMINARY; PRT; 17 AA.  
AC Q9UCL9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Proteoglycan 80 kDa polypeptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=93054750; PubMed=1429726;  
RA Perides G., Rahemulla F., Lane W.S., Asher R.A., Bignami A.;  
RT "Isolation of a large aggregating proteoglycan from human brain.";  
RL J. Biol. Chem. 267:23883-23887(1992).  
SQ SEQUENCE 17 AA; 1771 MW; 1BDA8561B2F71614 CRC64;

Query Match 23.1%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PVR 13  
Db 11 PVR 13

RESULT 73  
Q9UC43 PRELIMINARY; PRT; 17 AA.  
ID Q9UC43

```

AC Q9UC43;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DE 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interferon-alpha-induced protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96132854; PubMed=8557639;
RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;
RT "Purification, microsequencing, and immunolocalization of p36, a new
RT interferon-alpha-induced protein that is associated with human lupus
RT inclusions."
RL J. Biol. Chem. 271:1118-1126(1996).
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 23.1%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVL 9
DB 8 PVL 10

RESULT 74
Q17205
ID Q17205 PRELIMINARY; PRT; 17 AA.
AC Q17205;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE A.L6 protein (Fragment).
DE A.L6.
GN A.L6.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=703;
RX MEDLINE=90040707; PubMed=2810362;
RA Spoerel N.A., Nguyen H.T., Rickbush T.H., Kafatos F.C.;
RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:
RT Hybridization and Sequence Analysis of Multiple Developmentally Middle
RT A/B Chorion Gene Pairs."
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15562; CAA33575.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1877 MW; 577145043395539D CRC64;

Query Match 23.1%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 6 FLL 8

RESULT 75
Q26832
ID Q26832 PRELIMINARY; PRT; 17 AA.
AC Q26832;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Iatad 1.2) variant surface glycoprotein ELC gene (Fragment).
OS Trypanosoma brucei.

```

```

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278091; PubMed=2942540;
RA Brown K.H., Brentano S.T., Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA."
RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14020; AAA30305.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1973 MW; 9E00FBD261B8FFBF CRC64;

Query Match 23.1%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLL 3
DB 14 FLL 16

Search completed: November 25, 2003, 19:34:14
Job time : 25.4128 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 33.1802 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	13	100.0	13	22	Colostrinin derive
2	13	100.0	13	22	Colostrinin peptid
3	13	100.0	13	22	Colostrinin peptid
4	13	100.0	13	22	Colostrinin peptid
5	13	100.0	13	22	Ewe colostrinin pe
6	13	100.0	13	23	Colostrinin consti
7	13	100.0	13	23	Colostrinin consti
8	9	69.2	15	23	Neural cell regula
9	9	69.2	16	23	Antiviral composi

10	8	61.5	12	23	AAU83299	Antiviral composi
11	8	61.5	13	23	AAU83302	Antiviral composi
12	8	61.5	13	23	AAU83305	Antiviral composi
13	8	61.5	14	23	AAU83316	Antiviral composi
14	7	53.8	7	22	AAE07190	Colostrinin peptid
15	7	53.8	8	22	AAE07200	Modified colostrin
16	7	53.8	8	23	AAU83286	Antiviral composi
17	7	53.8	13	23	AAU83309	Antiviral composi
18	7	53.8	16	23	AAU83336	Antiviral composi
19	7	53.8	17	15	AAE58340	Hypotensive polyde
20	7	53.8	19	15	AAE58341	Hypotensive polyde
21	7	53.8	19	20	AAE17233	Casein antimicrobi
22	6	46.2	7	22	AAE72273	Colostrinin derive
23	6	46.2	7	22	AAE72526	Colostrinin peptid
24	6	46.2	7	22	AAE72558	Colostrinin peptid
25	6	46.2	7	22	AAE59337	Ewe colostrinin pe
26	6	46.2	7	23	AAE20255	Colostrinin consti
27	6	46.2	7	23	AAE51062	Colostrinin consti
28	6	46.2	7	23	AAO14604	Neural cell regula
29	6	46.2	9	22	AAE59356	Ewe colostrinin pe
30	6	46.2	11	23	AAU83297	Antiviral composi
31	6	46.2	12	23	AAU83300	Antiviral composi
32	6	46.2	14	23	AAU83325	Antiviral composi
33	6	46.2	19	23	AAU83341	Antiviral composi
34	5	38.5	9	23	AAU83290	Antiviral composi
35	5	38.5	13	18	AAW43973	Human myelin oligo
36	5	38.5	13	23	AAU83314	Antiviral composi
37	5	38.5	14	23	AAU83320	Antiviral composi
38	5	38.5	15	18	AAW37539	Human myelin oligo
39	5	38.5	15	23	AAU99584	Human zinc finger
40	5	38.5	15	23	AAU83332	Antiviral composi
41	5	38.5	16	23	AAU83339	Antiviral composi
42	5	38.5	18	20	AAU33019	Human serine prote
43	5	38.5	20	16	AAE80294	Trehalose releasin
44	5	38.5	20	16	AAE80296	Trehalose releasin
45	5	38.5	20	18	AAW37541	Human myelin oligo
46	4	30.8	5	14	AAE65510	Endothelin antagon
47	4	30.8	6	19	AAW75347	Hexapeptide #2 bin
48	4	30.8	6	19	AAW75279	Hexapeptide #2 bin
49	4	30.8	6	22	AAU08616	Human olfactory re
50	4	30.8	6	22	AAE63026	Amino acid sequenc
51	4	30.8	6	22	AAE63034	Amino acid sequenc
52	4	30.8	6	22	AAE63043	Amino acid sequenc
53	4	30.8	6	22	AAE63065	Amino acid sequenc
54	4	30.8	6	22	AAE63106	Amino acid sequenc
55	4	30.8	6	22	AAE63108	Amino acid sequenc
56	4	30.8	6	22	AAE87132	Human TANGO 393 cy
57	4	30.8	6	22	AAE87133	Mouse TANGO 393 cy
58	4	30.8	6	23	AAO18910	Human butyrylcholi
59	4	30.8	6	24	ABU67261	Olfactory receptor
60	4	30.8	6	24	ABU58261	Peptide binding to
61	4	30.8	6	24	ABU58271	Peptide binding to
62	4	30.8	6	24	ABU58273	Peptide binding to
63	4	30.8	6	24	ABU58291	Poliovirus-binding
64	4	30.8	6	24	ABU58293	Poliovirus-binding
65	4	30.8	6	24	ABU58312	Peptide binding to
66	4	30.8	7	17	AAW04280	Milk derived non-a
67	4	30.8	7	18	AAW30407	HRE-I affinity pep
68	4	30.8	7	23	ABG60365	Selective targetin
69	4	30.8	7	23	ABG34932	Human bone marrow
70	4	30.8	7	24	ABG34933	Human bone marrow
71	4	30.8	7	24	ABJ19880	MHC binding peptid
72	4	30.8	8	15	AAE58333	Hypotensive polyde
73	4	30.8	8	17	AAE84066	Retinal pigment ep
74	4	30.8	8	22	ABP13191	HIV A02 super moti
75	4	30.8	8	22	ABP14660	HIV A03 super moti
76	4	30.8	8	22	ABP19350	HIV B62 super moti
77	4	30.8	8	22	ABP21575	HIV A03 motif pol
78	4	30.8	8	22	ABP23480	HIV A11 motif pol
79	4	30.8	8	23	AAW49592	Human beta-defensi
80	4	30.8	8	24	ABJ20035	MHC binding peptid
81	4	30.8	8	24	ABJ20044	MHC binding peptid
82	4	30.8	9	15	AAU38067	Hepatitis B virus-

83 4 30.8 9 15 AAY38223 HIV-derived HLA-bi  
 84 4 30.8 9 15 AAY38224 HIV-derived HLA-bi  
 85 4 30.8 9 15 AAR73798 Antigen fragment 1  
 86 4 30.8 9 15 AAR62873 Metal binding CDR3  
 87 4 30.8 9 17 AAR98049 Pseudosteralin E,  
 88 4 30.8 9 19 AAW67187 aPL immunoreactive  
 89 4 30.8 9 19 AAW67194 aPL immunoreactive  
 90 4 30.8 9 19 AAW67198 aPL immunoreactive  
 91 4 30.8 9 19 AAW54412 MHC Class I peptid  
 92 4 30.8 9 20 AAY53442 HIV-1 RT protein (  
 93 4 30.8 9 20 AAY45635 Immunogenic peptid  
 94 4 30.8 9 20 AAY45792 Immunogenic peptid  
 95 4 30.8 9 20 AAY45793 Immunogenic peptid  
 96 4 30.8 9 20 AAY45794 Immunogenic peptid  
 97 4 30.8 9 20 AAY45795 Immunogenic peptid  
 98 4 30.8 9 20 AAY46637 Immunogenic peptid  
 99 4 30.8 9 20 AAY46638 Immunogenic peptid  
 100 4 30.8 9 20 AAY40291 Amino acid sequenc

## ALIGNMENTS

## RESULT 1

AAB72277 standard; peptide; 13 AA.

AC AAB72277;  
 DT 14-MAY-2001 (first entry)  
 XX Colostrinin derived cytokine inducing peptide SEQ ID 32.  
 DE Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis and  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 13 AA;  
 Query Match 100.0%; Score 13; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQEPVLGPVR 13  
 Db 1 FLLYQEPVLGPVR 13  
 RESULT 2  
 AAB72530 standard; Peptide; 13 AA.  
 ID AAB72530 standard; Peptide; 13 AA.  
 XX AAB72530;  
 AC AAB72530;  
 DT 09-MAY-2001 (first entry)  
 XX Colostrinin peptide #31.  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX Unidentified.  
 OS Unidentified.  
 XX WO200112650-A2.  
 PN WO200112650-A2.  
 XX 22-FEB-2001.  
 PD 17-AUG-2000; 2000WO-US22665.  
 PF 17-AUG-1999; 99US-0149310.  
 PR (TEXA ) UNIV TEXAS SYSTEM.  
 PA Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 DR Modulating oxidative stress level in a cell, involves contacting the  
 XX cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 PT Claim 6; Page 26; 48pp; English.  
 XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX SQ Sequence 13 AA;  
 Query Match 100.0%; Score 13; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQEPVLGPVR 13  
 Db 1 FLLYQEPVLGPVR 13  
 RESULT 3  
 AAB72562 standard; Peptide; 13 AA.  
 ID AAB72562 standard; Peptide; 13 AA.  
 XX AAB72562;  
 AC AAB72562;  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #31.  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX  
OS Unidentified.  
XX  
XX WO200112651-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 17-AUG-2000; 2000WO-US22774.  
XX  
XX 17-AUG-1999; 99US-0149633.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Boldogh I;  
XX  
XX WPI; 2001-226545/23.  
XX  
XX Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX Claim 6; Page 22; 35pp; English.  
XX  
XX The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 100.0%; Score 13; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQEPVLGPVR 13  
Db 1 FLLYQEPVLGPVR 13  
RESULT 4  
AAB59338  
ID AAB59338 standard; Peptide; 13 AA.  
XX  
XX AAB59338;  
XX  
XX 21-MAR-2001 (first entry)  
XX  
XX Ewe colostrinin peptide fragment C-13.  
DE  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX  
XX Ovis sp.  
OS  
XX WO200075173-A2.  
PN  
XX 14-DEC-2000.  
PD  
XX 02-JUN-2000; 2000WO-GB02128.  
PF  
XX 02-JUN-1999; 99GB-0012852.  
PR  
XX (REGE-) REGEN THERAPEUTICS PLC.  
PA  
XX Georgiades JA;  
XX  
XX WPI; 2001-071058/08.  
DR  
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
XX and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
XX Claim 7; Page 27; 63pp; English.  
XX  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 100.0%; Score 13; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQEPVLGPVR 13  
Db 1 FLLYQEPVLGPVR 13  
RESULT 5  
AAB20259  
ID AAB20259 standard; peptide; 13 AA.  
XX  
XX AAE20259;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX Colostrinin constituent peptide #31.  
DE  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 13  
FT /note= "Optionally C-terminal amide"  
XX  
XX WO200213850-A1.  
PN  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2000; 2000WO-US22776.  
PF  
XX 17-AUG-2000; 2000WO-US22776.  
PR  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX  
XX WPI; 2002-269151/31.  
DR  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX Claim 6; Page 26; 51pp; English.  
PS  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 13 AA;

Query Match 100.0%; Score 13; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13  
 |||||

Db 1 FLLYQEPVLGPVR 13

# RESULT 6

AA014605  
 ID AA014605 standard; Peptide; 13 AA.

XX AC AA014605;

DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 203-214).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Modified-site 13

XX FT /note= "optional C-terminal amidation"

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 203-214. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

SQ Sequence 13 AA;

Query Match 100.0%; Score 13; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13  
 |||||

Db 1 FLLYQEPVLGPVR 13

# RESULT 7

AA014608  
 ID AA014608 standard; peptide; 13 AA.

XX AC AA014608;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 31.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
 FT Modified-site 13

XX FT /note= "Optional C-terminal amide"

XX PN WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

PS Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

```
CC the method of the invention.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
Db 1 FLLYQEPVLGPVR 13
RESULT 8
AAU83327
ID AAU83327 standard; Peptide; 15 AA.
XX
AC AAU83327;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #45.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
PS Disclosure; Page 8; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 16 AA;
Query Match 69.2%; Score 9; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVL 9
Db 8 FLLYQEPVL 16
RESULT 10
AAU83299
ID AAU83299 standard; Peptide; 12 AA.
XX
AC AAU83299;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #17.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
```

```
CC the method of the invention.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 13; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVLGPVR 13
Db 1 FLLYQEPVLGPVR 13
RESULT 8
AAU83327
ID AAU83327 standard; Peptide; 15 AA.
XX
AC AAU83327;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #45.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
PS Disclosure; Page 8; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
SQ Sequence 15 AA;
Query Match 69.2%; Score 9; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLYQEPVL 9
Db 7 FLLYQEPVL 15
RESULT 9
AAU83335
ID AAU83335 standard; Peptide; 16 AA.
XX
```



PF 17-JAN-2001; 2001US-0764017.  
 XX 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 61.5%; Score 8; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.097;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FLLYQEPV 8  
 Db 5 FLLYQEPV 12  
 |||||  
 RESULT 11  
 AAU83302  
 ID AAU83302 standard; Peptide; 13 AA.  
 XX  
 AC AAU83302;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #20.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 XX monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX

CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 61.5%; Score 8; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FLLYQEPV 8  
 Db 6 FLLYQEPV 13  
 |||||  
 RESULT 12  
 AAU83305  
 ID AAU83305 standard; Peptide; 13 AA.  
 XX  
 AC AAU83305;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #23.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 XX monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 61.5%; Score 8; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FLLYQEPV 8  
 Db 6 FLLYQEPV 13  
 |||||  
 RESULT 12  
 AAU83305  
 ID AAU83305 standard; Peptide; 13 AA.  
 XX  
 AC AAU83305;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #23.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 XX monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 61.5%; Score 8; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYQEPV 8  
 Db 6 FLYQEPV 13

RESULT 13  
 AAU83316  
 ID AAU83316 standard; Peptide; 14 AA.  
 XX  
 AC AAU83316;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #34.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 14 AA;

Query Match 61.5%; Score 8; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYQEPV 8  
 Db 7 FLYQEPV 14

RESULT 14  
 AAU83316  
 ID AAU83316 standard; Peptide; 14 AA.  
 XX  
 AC AAU83316;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Colostrinin peptide 6.  
 XX

Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 central nervous system disorder; neurodegenerative disorder; weight loss;  
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 acquired immunological deficiency; neurological disorder; dementia;  
 antiviral.  
 Unidentified.  
 WO200155199-A1.  
 02-AUG-2001.  
 26-JAN-2001; 2001WO-GB00329.  
 26-JAN-2000; 2000GB-0001825.  
 (REGE-) REGEN THERAPEUTICS PLC.  
 Georgiades JA;  
 WPI; 2001-488775/53.  
 Peptide useful as an inter alia in the treatment of e.g. disorders of  
 the immune system and the central nervous system comprises ten  
 amino-terminal amino acid sequence derived from peptides present in  
 colostrinin -  
 Claim 1; Page 15; 40pp; English.  
 The invention relates to colostrinin peptide fragments which are useful,  
 inter alia, in the treatment of chronic disorders of the immune system  
 and the central nervous system. Colostrinin peptides are used as a  
 medicament in the treatment of neurological disorders e.g., dementia,  
 neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 neurosis, in acquired immunological deficiencies, chronic bacterial and  
 viral infections and diseases characterised by the presence of beta-  
 amyloid plaques and as a dietary supplement for babies, small children,  
 adults and senile persons, who have been subjected to chemotherapy or  
 have suffered from cachexia or weight loss due to the chronic disease.  
 Colostrinin peptides are also used as food additives and as an auxiliary  
 withdrawal treatment for drug addicts, after a period of detoxification  
 and in persons dependent on stimulants. Colostrinin peptides are used to  
 prepare antibodies and to treat emotional disturbances, e.g. emotional  
 disturbances of psychiatric patients in a state of depression. These  
 colostrinin peptides improves the development of immune system in a new  
 born child and to correct the immunological deficiencies in a child.  
 The present sequence is colostrinin peptide 6 related to the invention.  
 Colostrinin peptide 6 corresponds to position 204-210 of beta-caesin.

Query Match 53.8%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQEPV 8  
 Db 1 LLYQEPV 7

RESULT 15  
 AAU83316  
 ID AAU83316 standard; Peptide; 8 AA.  
 XX  
 AC AAU83316;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Modified colostrinin cyclic peptide #6.  
 XX  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.  
 XX  
 XX Synthetic.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Val found at the C-terminal end"  
 XX  
 XX WO200155199-A1.  
 XX  
 XX PD 02-AUG-2001.  
 XX  
 XX PF 26-JAN-2001; 2001WO-GB00329.  
 XX PR 26-JAN-2000; 2000GB-0001825.  
 XX (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Georgiades JA;  
 XX WPI; 2001-488775/53.  
 XX  
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -  
 XX  
 XX Example 2; Page 9; 40pp; English.  
 XX  
 CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is modified colostrinin cyclic peptide #6 related to  
 CC the invention.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 53.8%; Score 7; DB 22; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LLYQEPV 8  
 DB 2 LLYQEPV 8  
 |||||  
 |||||  
 RESULT 16  
 AAU83286  
 ID AAU83286 standard; Peptide; 8 AA.  
 XX  
 XX AAU83286;  
 XX  
 XX 23-APR-2002 (first entry)  
 XX  
 XX Query Match 53.8%; Score 7; DB 23; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQEP 7  
 DB 2 FLLYQEP 8  
 |||||  
 |||||  
 RESULT 17  
 AAU83309  
 ID AAU83309 standard; Peptide; 13 AA.  
 XX  
 XX AAU83309;  
 XX  
 XX 23-APR-2002 (first entry)  
 XX  
 XX Antiviral composition peptide-A, fragment #27.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 XX Synthetic.  
 XX  
 XX US2002004579-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 17-JAN-2001; 2001US-0764017.  
 XX  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 XX Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 53.8%; Score 7; DB 23; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQEP 7  
 DB 2 FLLYQEP 8  
 |||||  
 |||||  
 RESULT 17  
 AAU83309  
 ID AAU83309 standard; Peptide; 13 AA.  
 XX  
 XX AAU83309;  
 XX  
 XX 23-APR-2002 (first entry)  
 XX  
 XX Antiviral composition peptide-A, fragment #27.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 XX Synthetic.  
 XX  
 XX US2002004579-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 17-JAN-2001; 2001US-0764017.  
 XX  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX

XX Antiviral composition peptide-A, fragment #4.  
 DE Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 XX Synthetic.  
 XX  
 XX US2002004579-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 17-JAN-2001; 2001US-0764017.  
 XX  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 XX Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 53.8%; Score 7; DB 23; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQEP 7  
 DB 2 FLLYQEP 8  
 |||||  
 |||||  
 RESULT 17  
 AAU83309  
 ID AAU83309 standard; Peptide; 13 AA.  
 XX  
 XX AAU83309;  
 XX  
 XX 23-APR-2002 (first entry)  
 XX  
 XX Antiviral composition peptide-A, fragment #27.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 XX Synthetic.  
 XX  
 XX US2002004579-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 17-JAN-2001; 2001US-0764017.  
 XX  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX



XX 22-SEP-1994 (first entry)  
 DT Hypotensive polypeptide.  
 DE  
 XX Hypotensive; antioxiative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 KW  
 XX Lactobacillus helveticus.  
 OS  
 XX JP06041191-A.  
 FN  
 XX 15-FEB-1994.  
 PD  
 XX 03-MAR-1993; 93JP-0043047.  
 PF  
 XX 04-MAR-1992; 92JP-0047340.  
 PR  
 XX (CALV ) CALPIS SHOKUHN KOGYO KK.  
 PA  
 XX WPI; 1994-089332/11.  
 DR  
 XX New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxiative and calcium absorption promoting  
 PT activity  
 PT  
 XX Claim 1-2; Page 10; 10pp; Japanese.  
 PS  
 XX Sequences (AAB5819-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxiative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 CC  
 XX Sequence 19 AA;  
 SQ  
 Query Match 53.8%; Score 7; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PVLGPVR 13  
 DB |||||  
 6 PVLGPVR 12  
 RESULT 21  
 AAY17233  
 ID AAY17233 standard; peptide; 19 AA.  
 AC  
 XX AAY17233;  
 AC  
 XX 09-AUG-1999 (first entry)  
 DT  
 DE Casein antimicrobial peptide.  
 DE  
 XX Antimicrobial peptide; casein; dental caries; periodontal disease;  
 KW antiplaque agent.  
 KW  
 XX Bos sp.  
 OS  
 XX WO9926971-Al.  
 FN  
 XX 03-JUN-1999.  
 PD  
 XX 24-NOV-1998; 98WO-AU00972.  
 PF  
 XX 24-NOV-1997; 97AU-0000514.  
 PR  
 XX (UYME ) UNIV MELBOURNE.  
 PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.  
 PA  
 XX Dashper SG, Malkoski M, O'Brien-Simpson NM, Reynolds EC;  
 PI Talbo GH;

XX WPI; 1999-357812/30.  
 DR  
 XX Antimicrobial peptides, useful for prevention and treatment of  
 PT periodontal disease  
 PT  
 XX Claim 1; Page 43; 57pp; English.  
 PS  
 XX Sequences AAY17229-245 represent non-glycosylated antimicrobial peptides  
 CC that are derived from casein. The peptides are useful in antimicrobial  
 CC compositions for treating or preventing dental caries or periodontal  
 CC disease. The new peptides are clinically efficacious, safe and natural  
 CC antiplaque agents, unlike prior art agents which have undesirable side-  
 CC effects, negligible intra-oral activity, or an incompatibility with  
 CC toothpaste formulations.  
 CC  
 XX Sequence 19 AA;  
 SQ  
 Query Match 53.8%; Score 7; DB 20; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PVLGPVR 13  
 DB |||||  
 13 PVLGPVR 19  
 RESULT 22  
 AAB72273  
 ID AAB72273 standard; peptide; 7 AA.  
 AC  
 XX AAB72273;  
 AC  
 XX 14-MAY-2001 (first entry)  
 DT  
 XX Colostrin derived cytokine inducing peptide SEQ ID 28.  
 DE  
 XX Colostrin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 KW  
 XX Synthetic.  
 OS  
 XX WO200111937-A2.  
 FN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22818.  
 PF  
 XX 17-AUG-1999; 99US-0149311.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 PI  
 XX WPI; 2001-202804/20.  
 DR  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrin as an immunological  
 PT regulator -  
 PT  
 XX Claim 1; Page 34; 50pp; English.  
 PS  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.  
XX  
SQ Sequence 7 AA;  
Query Match 46.2%; Score 6; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQE 6  
Db 2 FLLYQE 7  
RESULT 23  
AAB72526  
ID AAB72526 standard; Peptide; 7 AA.  
XX  
XX AAB72526;  
AC AAB72526;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #27.  
XX  
KW Dermatological; oxidative stress regulator; colostrinin.  
XX Unidentified.  
OS  
XX WO200112650-A2.  
XX  
PN 22-FEB-2001.  
XX  
PD 2 FLLYQE 7  
PF 17-AUG-2000; 2000WO-US22665.  
XX  
PR 17-AUG-1999; 99US-0149310.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
XX Claim 6; Page 26; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidizing species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 7 AA;  
Query Match 46.2%; Score 6; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQE 6  
Db 2 FLLYQE 7  
RESULT 24  
AAB72558  
ID AAB72558 standard; Peptide; 7 AA.  
XX

AC AAB72558;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #27.  
XX  
KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX Unidentified.  
OS  
XX WO200112651-A2.  
XX  
PN 22-FEB-2001.  
XX  
PD 17-AUG-2000; 2000WO-US22774.  
XX  
PF 17-AUG-1999; 99US-0149633.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Boldogh I;  
XX WPI; 2001-226545/23.  
XX  
PT Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX Claim 6; Page 22; 35pp; English.  
XX  
CC The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
SQ Sequence 7 AA;  
Query Match 46.2%; Score 6; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQE 6  
Db 2 FLLYQE 7  
RESULT 25  
AAB59337  
ID AAB59337 standard; Peptide; 7 AA.  
XX  
XX AAB59337;  
AC AAB59337;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostrinin peptide fragment C-12.  
XX  
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX  
OS Ovis sp.  
XX  
PN WO200075173-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-GB02128.  
XX  
PR 02-JUN-1999; 99GB-0012852.  
XX  
XX (REGE-) REGEN THERAPEUTICS PLC.  
PA  
PI Georgiades JA;

XX DR WPI; 2001-071058/08.  
 XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX Claim 7; Page 27; 63pp; English.  
 XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX SQ Sequence 7 AA;  
 Query Match 46.2%; Score 6; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FLLYQE 6  
 Db 2 FLLYQE 7  
 RESULT 26  
 AA20255  
 ID AAE20255 standard; peptide; 7 AA.  
 XX AC AAE20255;  
 XX DT 18-JUN-2002 (first entry)  
 XX DE Colostrinin constituent peptide #27.  
 XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 XX OS Unidentified.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optionally C-terminal amide"  
 FT WO200213850-A1.  
 XX PN 21-FEB-2002.  
 XX PD 17-AUG-2000; 2000WO-US22776.  
 XX PF 17-AUG-2000; 2000WO-US22776.  
 XX PR (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA Stanton GJ, Hughes TK, Boldogh I;  
 XX PI WPI; 2002-269151/31.  
 XX DR Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX Claim 6; Page 26; 51pp; English.  
 XX CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or

CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.  
 XX SQ Sequence 7 AA;  
 Query Match 46.2%; Score 6; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 FLLYQE 6  
 Db 2 FLLYQE 7  
 RESULT 27  
 AA51062  
 ID AAM51062 standard; Peptide; 7 AA.  
 XX AC AAM51062;  
 XX DT 30-MAY-2002 (first entry)  
 XX DE Colostrinin constituent peptide (casein amino acids 202-208).  
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 7 /note= "optional C-terminal amidation"  
 FT WO200213849-A1.  
 XX PN 21-FEB-2002.  
 XX PD 17-AUG-2000; 2000WO-US22775.  
 XX PF 17-AUG-2000; 2000WO-US22775.  
 XX PR 17-AUG-2000; 2000WO-US22775.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX REGE-} REGEN THERAPEUTICS PLC.  
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2002-269150/31.  
 XX DR Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -  
 XX Claim 1; Page 34; 54pp; English.  
 XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 202-208. Methods are claimed for: inducing a

CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the  
 CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 46.2%; Score 6; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQE 6  
 |||||  
 Db 2 FLLYQE 7  
 |||||  
 RESULT 28  
 AAO14604  
 ID AAO14604 standard; peptide; 7 AA.  
 XX  
 AC AAO14604;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX  
 DE Neural cell regulatory colostrinin peptide 27.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optional C-terminal amide"  
 FT  
 XX WO200213851-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22777.  
 XX  
 PR 17-AUG-2000; 2000WO-US22777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -  
 XX  
 XX Claim 7; Page 22; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 46.2%; Score 6; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQE 6  
 |||||  
 Db 2 FLLYQE 7  
 |||||  
 RESULT 29  
 AAB59356  
 ID AAB59356 standard; Peptide; 9 AA.  
 XX  
 AC AAB59356;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment derived sequence #16.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 XX  
 PR 02-JUN-1999; 99GB-0012852.  
 XX  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 XX Claim 8; Page 27; 63pp; English.  
 PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 46.2%; Score 6; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQE 6  
 |||||  
 Db 4 FLLYQE 9  
 |||||





XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 14 AA;

SQ

Query Match 46.2%; Score 6; DB 23; Length 14;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQE 6

Db 9 FLLYQE 14

RESULT 33

AAU83341

ID AAU83341 standard; Peptide; 19 AA.

AC AAU83341;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #59.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

OS

XX US2002004579-A1.

PN 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA

XX Friedland B, Hirschman SZ, Taraporewala IB;

PI WPI; 2002-163727/21.

DR

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 19 AA;

SQ

Query Match 46.2%; Score 6; DB 23; Length 19;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQE 6

Db 14 FLLYQE 19

RESULT 34

AAU83290

ID AAU83290 standard; Peptide; 9 AA.

XX AAU83290;

AC

XX 23-APR-2002 (first entry)

DT

XX Antiviral composition peptide-A, fragment #8.

DE

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

OS

XX US2002004579-A1.

PN 10-JAN-2002.

PD

XX 17-JAN-2001; 2001US-0764017.

PF

XX 22-OCT-1996; 96US-0735236.

PR

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA

XX Friedland B, Hirschman SZ, Taraporewala IB;

PI WPI; 2002-163727/21.

DR

XX New peptides compositions, useful for treating viral infections and

PT stimulating the immune system -

XX Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising

CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides

CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful

CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the

CC invention.

XX Sequence 9 AA;

SQ

Query Match 38.5%; Score 5; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQ 5

Db 5 FLLYQ 9

RESULT 35

AAW43973

ID AAW43973 standard; peptide; 13 AA.

XX AAW43973;

AC

XX 22-APR-1998 (first entry)

DT

XX DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-193.  
XX KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;  
KW autoimmune response; MBP; myelin basic protein; demyelinating.  
XX OS Homo sapiens.  
XX PN WO9735879-A1.  
XX PD 02-OCT-1997.  
XX PF 01-MAY-1996; 96WO-US06072.  
XX PR 28-MAR-1996; 96US-0623406.  
XX PA (IMMU-) IMMULOGIC PHARM CORP.  
XX PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;  
XX WPI; 1997-489564/45.  
XX DR Human myelin oligodendrocyte glyco-protein peptide - useful to treat  
PT multiple sclerosis in mammal by down-regulating auto-immune response  
XX PS Disclosure; Fig 2; 108pp; English.  
XX CC The present sequence represents a novel peptide of human myelin  
CC oligodendrocyte glycoprotein (MOG). The peptides of human MOG and  
CC MBP (myelin basic protein) can be used to treat multiple sclerosis  
CC in a mammal by down-regulating an autoimmune response in the mammal.  
CC They can also be used to diagnose and treat other demyelinating  
CC autoimmune diseases in humans, or to prepare antibodies for the  
CC detection or diagnosis of autoimmune diseases.  
XX SQ Sequence 13 AA;  
Query Match 38.5%; Score 5; DB 18; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PVLGP 11  
Db |||||  
8 PVLGP 12  
RESULT 36  
AAU83314  
ID AAU83314 standard; Peptide; 13 AA.  
AC AAU83314;  
XX DT 23-APR-2002 (first entry)  
XX DE Antiviral composition peptide-A, fragment #32.  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX OS Synthetic.  
XX PN US2002004579-A1.  
XX PD 10-JAN-2002.  
XX PF 17-JAN-2001; 2001US-0764017.  
XX PR 22-OCT-1996; 96US-0735236.  
XX PR 25-JUN-1999; 99US-0344095.  
XX PA (ADVI-) ADVANCED VIRAL RES CORP.  
XX PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX PS Disclosure; Page 8; 37pp; English.  
XX CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
XX AAU83282-AAU83401 represent peptides used in the composition of the  
XX invention.  
XX SQ Sequence 13 AA;  
Query Match 38.5%; Score 5; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQ 5  
Db |||||  
9 FLLYQ 13  
RESULT 37  
AAU83320  
ID AAU83320 standard; Peptide; 14 AA.  
XX AC AAU83320;  
XX DT 23-APR-2002 (first entry)  
XX DE Antiviral composition peptide-A, fragment #38.  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX OS Synthetic.  
XX PN US2002004579-A1.  
XX PD 10-JAN-2002.  
XX PF 17-JAN-2001; 2001US-0764017.  
XX PR 22-OCT-1996; 96US-0735236.  
XX PR 25-JUN-1999; 99US-0344095.  
XX PA (ADVI-) ADVANCED VIRAL RES CORP.  
XX PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX PS Disclosure; Page 8; 37pp; English.  
XX CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.

XX WPI; 2002-163727/21.  
XX PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX PS Disclosure; Page 8; 37pp; English.  
XX CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
XX AAU83282-AAU83401 represent peptides used in the composition of the  
XX invention.  
XX SQ Sequence 13 AA;  
Query Match 38.5%; Score 5; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FLLYQ 5  
Db |||||  
9 FLLYQ 13  
RESULT 37  
AAU83320  
ID AAU83320 standard; Peptide; 14 AA.  
XX AC AAU83320;  
XX DT 23-APR-2002 (first entry)  
XX DE Antiviral composition peptide-A, fragment #38.  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX OS Synthetic.  
XX PN US2002004579-A1.  
XX PD 10-JAN-2002.  
XX PF 17-JAN-2001; 2001US-0764017.  
XX PR 22-OCT-1996; 96US-0735236.  
XX PR 25-JUN-1999; 99US-0344095.  
XX PA (ADVI-) ADVANCED VIRAL RES CORP.  
XX PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX PS Disclosure; Page 8; 37pp; English.  
XX CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.

CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 38.5%; Score 5; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLYQ 5  
 |||||  
 Db 10 FLLYQ 14  
 RESULT 38  
 AAW37539  
 ID AAW37539 standard; peptide; 15 AA.  
 XX  
 AC AAW37539;  
 XX  
 DT 22-APR-1998 (first entry)  
 XX  
 DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-195.  
 XX  
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;  
 KW autoimmune response; MBP; myelin basic protein; demyelinating.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9735879-A1.  
 XX  
 PD 02-OCT-1997.  
 XX  
 PF 01-MAY-1996; 96WO-US06072.  
 XX  
 PR 28-MAR-1996; 96US-0623406.  
 XX  
 PA (IMMU-) IMMULOGIC PHARM CORP.  
 XX  
 PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;  
 XX  
 XX WPI; 1997-489564/45.  
 XX  
 DT Human myelin oligodendrocyte glyco-protein peptide - useful to treat  
 PT multiple sclerosis in mammal by down-regulating auto-immune response  
 PT  
 PS Claim 1; Page 12; 108pp; English.  
 XX  
 CC The present sequence represents a novel peptide of human myelin  
 CC oligodendrocyte glycoprotein (MOG). The peptide of human MOG and  
 CC MBP (myelin basic protein) can be used to treat multiple sclerosis  
 CC in a mammal by down-regulating an autoimmune response in the mammal.  
 CC They can also be used to diagnose and treat other demyelinating  
 CC autoimmune diseases in humans, or to prepare antibodies for the  
 CC detection or diagnosis of autoimmune diseases.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 38.5%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PVLGP 11  
 |||||  
 Db 7 PVLGP 11  
 RESULT 39  
 AAU99584  
 ID AAU99584 standard; peptide; 15 AA.  
 XX  
 AC AAU99584;  
 XX

DT 21-OCT-2002 (first entry)  
 XX  
 DE Human zinc finger protein NY-REN-21 antigen 52.03, N-terminus.  
 XX  
 KW Human; zinc finger protein NY-REN-21 antigen 52.03; tumour;  
 KW embryonic development deformity; diabetes; menstrual disorder;  
 KW peptic ulcer; arrhythmia; anaemia; epilepsy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1341657-A.  
 XX  
 PD 27-MAR-2002.  
 XX  
 PF 07-SEP-2000; 2000CN-0125079.  
 XX  
 PR 07-SEP-2000; 2000CN-0125079.  
 XX  
 PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-520725/56.  
 XX  
 PT Novel zinc finger protein NY-REN-21 antigen 52.03 -  
 XX  
 PS Example 6; Page 21 (disclosure); 35pp; Chinese.  
 XX  
 CC The present invention relates to the isolation of human zinc finger  
 CC protein NY-REN-21 antigen 52.03, and the polynucleotide encoding it.  
 CC Also described is the process for preparing the protein by DNA  
 CC recombination and the application of the polypeptide and  
 CC polynucleotide in treating various diseases such as embryonic  
 CC development deformities, tumours, diabetes, menstrual disorders,  
 CC peptic ulcers, arrhythmia, anaemia and epilepsy. The present sequence  
 CC representing the N-terminal peptide of human zinc finger protein  
 CC NY-REN-21 antigen 52.03 is used in an enzyme-linked immunosorbent  
 CC assay (ELISA) in the examples of the present invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 38.5%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PVLGP 11  
 |||||  
 Db 10 PVLGP 14  
 RESULT 40  
 AAU83332  
 ID AAU83332 standard; Peptide; 15 AA.  
 XX  
 AC AAU83332;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #50.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.



Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
DB 6 PVLGP 10

RESULT 43  
AAR80294  
ID AAR80294 standard; Protein; 20 AA.  
XX AC AAR80294;  
XX DT 19-JAN-1996 (first entry)  
XX DE Trehalose releasing enzyme N-terminal fragment.  
XX KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;  
KW alpha-maltotriosyltrehalose; alpha-maltotetrasyltrehalose;  
KW maltopentaosyltrehalose; sweetener; taste-improving agent;  
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;  
KW pharmaceuticals.  
XX OS Arthrobacter sp. Q36.  
XX PN EP671470-A2.  
XX XX  
XX PD 13-SEP-1995.  
XX PF 07-MAR-1995; 95EP-0301474.  
XX PR 07-MAR-1994; 94JP-0059840.  
XX PR 07-MAR-1994; 94JP-0059834.  
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;  
XX OS WPI; 1995-312772/41.  
XX PN DNA encoding a trehalose releasing enzyme - which releases trehalose  
XX PT from a non-reducing saccharide having a trehalose structure as an  
XX PT end unit.  
XX PS Example 4; Page 25; 45pp; English.  
XX CC The trehalose releasing enzyme can be used for the preparation of  
CC trehalose with high yields and efficiency from non-reducing  
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,  
CC alpha-maltotriosyltrehalose, alpha-maltotetrasyltrehalose and  
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,  
CC taste-improving agent, quality-improving agent, stabiliser, filler,  
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.  
CC This is the N-terminal sequence of the enzyme.  
XX SQ Sequence 20 AA;

Query Match 38.5%; Score 5; DB 16; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
DB 11 PVLGP 15

RESULT 44  
AAR80296  
ID AAR80296 standard; Protein; 20 AA.  
XX AC AAR80296;  
XX XX

DT 19-JAN-1996 (first entry)  
XX Trehalose releasing enzyme internal fragment.  
DE  
XX  
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;  
KW alpha-maltotriosyltrehalose; alpha-maltotetrasyltrehalose;  
KW maltopentaosyltrehalose; sweetener; taste-improving agent;  
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;  
KW pharmaceuticals.  
XX OS Arthrobacter sp. Q36.  
XX PN EP671470-A2.  
XX XX  
XX PD 13-SEP-1995.  
XX PF 07-MAR-1995; 95EP-0301474.  
XX PR 07-MAR-1994; 94JP-0059840.  
XX PR 07-MAR-1994; 94JP-0059834.  
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;  
XX OS WPI; 1995-312772/41.  
XX PN DNA encoding a trehalose releasing enzyme - which releases trehalose  
XX PT from a non-reducing saccharide having a trehalose structure as an  
XX PT end unit.  
XX PS Example 4; Page 26; 45pp; English.  
XX CC The trehalose releasing enzyme can be used for the preparation of  
CC trehalose with high yields and efficiency from non-reducing  
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,  
CC alpha-maltotriosyltrehalose, alpha-maltotetrasyltrehalose and  
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,  
CC taste-improving agent, quality-improving agent, stabiliser, filler,  
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.  
CC This is an internal sequence of the enzyme.  
XX SQ Sequence 20 AA;

Query Match 38.5%; Score 5; DB 16; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
DB 1 PVLGP 5

RESULT 45  
AAW37541  
ID AAW37541 standard; peptide; 20 AA.  
XX AC AAW37541;  
XX DT 22-APR-1998 (first entry)  
XX DE Human myelin oligodendrocyte glycoprotein peptide MOG 181-200.  
XX KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;  
KW autoimmune response; MBP; myelin basic protein; demyelinating.  
XX OS Homo sapiens.  
XX PN WO9735879-A1.  
XX PD 02-OCT-1997.  
XX PF 01-MAY-1996; 96WO-US06072.

XX 28-MAR-1996; 96US-0623406.  
 XX (IMMU-) IMMULOGIC PHARM CORP.  
 XX Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;  
 XX WPI; 1997-489564/45.  
 XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat  
 XX multiple sclerosis in mammal by down-regulating auto-immune response  
 XX  
 XX Claim 1; Page 12; 108pp; English.  
 XX The present sequence represents a novel peptide of human myelin  
 XX oligodendrocyte glycoprotein (MOG). The peptide of human MOG and  
 XX MBP (myelin basic protein) can be used to treat multiple sclerosis  
 XX in a mammal by down-regulating an autoimmune response in the mammal.  
 XX They can also be used to diagnose and treat other demyelinating  
 XX autoimmune diseases in humans, or to prepare antibodies for the  
 XX detection or diagnosis of autoimmune diseases.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 38.5%; Score 5; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 PVLGP 11  
 Db 7 PVLGP 11  
 RESULT 46  
 AAR65510  
 ID AAR65510 standard; peptide; 5 AA.  
 XX AAR65510;  
 AC  
 XX 15-DEC-1994 (first entry)  
 DT  
 XX Endothelin antagonist cyclic pentapeptide.  
 DE  
 XX Endothelin; antagonist; hyperlipidaemia; hyperlipaemia; hypolipaeamic.  
 XX cyclic.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-Trp"  
 FT Misc-difference 2 /note= "D-Glu"  
 FT Misc-difference 4 /note= "D-Val"  
 FT Modified-site 1.5  
 FT /note= "Leu(5) is condensed onto D-Trp(1) to form  
 FT a cyclic pentapeptide"  
 XX  
 XX JP05194254-A.  
 PN  
 XX 03-AUG-1993.  
 PD  
 XX 22-JAN-1992; 92JP-0031540.  
 PF  
 XX 22-JAN-1992; 92JP-0031540.  
 PR  
 XX (BANY ) BANYU PHARM CO LTD.  
 PA  
 XX WPI; 1993-278210/35.  
 DR  
 XX Anti-hyperlipidaemic agent contg. endothelin antagonist - pref.  
 XX cyclic penta:peptide

XX Disclosure; Page 8; 31pp; Japanese.  
 PS  
 XX A therapeutic drug for treating hyperlipidaemia is claimed, which  
 CC contains an endothelin antagonist as active component. The endothelin  
 CC antagonist is a peptide of the type disclosed in EP-460679 or is a  
 CC specified cyclic pentapeptide described by a highly generic formula.  
 CC The present sequence is a specific example of the generic  
 CC cyclic pentapeptide.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 30.8%; Score 4; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 EPVL 9  
 Db 2 EPVL 5  
 RESULT 47  
 AAW75347  
 ID AAW75347 standard; peptide; 6 AA.  
 XX AAW75347;  
 AC  
 XX 02-FEB-1999 (first entry)  
 DT  
 XX Hexapeptide #2 binds anti-Ad5 fibre head MAb 7A2.7.  
 DE  
 XX Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;  
 KW viral surface protein; hexapeptide expression library; adenovirus;  
 KW major histocompatibility complex; MHC; fibronectin; gene therapy;  
 KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.  
 XX  
 XX Synthetic.  
 OS  
 XX FR2758821-A1.  
 FN  
 XX 31-JUL-1998.  
 PD  
 XX 30-JAN-1997; 97FR-0001005.  
 PF  
 XX 30-JAN-1997; 97FR-0001005.  
 PR  
 XX 09-SEP-1997; 97FR-0011166.  
 PR  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 XX Boulanger P, Hong SS, Karayan L;  
 XX WPI; 1998-416458/36.  
 XX  
 XX Use of peptide(s) for facilitating or modulating attachment of  
 FT adenovirus to cells - useful for, e.g. treating or preventing  
 FT infection and improving uptake of gene therapy vectors  
 XX  
 XX Example 2; Fig 1; 48pp; French.  
 PS  
 XX The invention relates to methods for selecting and identifying a  
 CC cellular receptor for a virus, by immobilising, on a support, a  
 CC monoclonal antibody targeted to a viral surface protein that determines  
 CC attachment of the virus to the receptor. The immobilised antibody is  
 CC incubated with a hexapeptide expression library and peptides bound to the  
 CC immobilised antibody are eluted by competitive binding with recombinant  
 CC fragments of the viral surface protein. In a reverse method, the viral  
 CC surface protein is immobilised and incubated with the peptide library. In  
 CC this case, the bound peptides are eluted by competitive binding with the  
 CC monoclonal antibody. The hexapeptides AAW75346-W75360 represent  
 CC peptides isolated by biopanning the library with the immobilised  
 CC monoclonal antibody (MAb) 7A2.7 and eluted using an adenovirus type 5  
 CC fibre head protein (AAW75335).  
 CC The methods are used to identify peptides from MHC Class I and/or

CC type III fibronectin proteins that allow or facilitate attachment by  
CC adenovirus (Ad) to host cells and/or entry into the cells, and to  
CC identify ligands that modulate Ad infection mediated by these peptides,  
CC e.g. to treat or prevent Ad infections or to facilitate infection by Ad  
CC gene therapy vectors used to treat genetic diseases, acquired immune  
CC deficiency syndrome or cancer.  
XX Sequence 6 AA;  
SQ Query Match 30.8%; Score 4; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 LGPV 12  
Db 1 LGPV 4  
RESULT 48  
AAW75279  
ID AAW75279 standard; peptide; 6 AA.  
XX AC AAW75279;  
XX DT 25-MAR-2003 (updated)  
DT 02-FEB-1999 (first entry)  
XX DE Hexapeptide #2 binds anti-Ad5 fibre head MAb 7A2.7.  
XX KW Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;  
KW viral surface protein; hexapeptide expression library; adenovirus;  
KW major histocompatibility complex; MHC; fibronectin; gene therapy;  
KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.  
XX OS Synthetic.  
XX FR2758885-A1.  
XX 31-JUL-1998.  
XX PF 10-JUL-1997; 97FR-0008796.  
XX PR 30-JAN-1997; 97FR-0001005.  
PR 10-JUL-1997; 97FR-0008796.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX PI Boulanger P, Hong SS, Karayan L;  
XX WPI; 1998-416493/36.  
XX PT Selection and identification of cellular receptors for viruses -  
PT used to control attachment and entry of adenovirus into cells, e.g.  
PT for treating infection or in gene therapy  
XX Example 2; Fig 1; 43pp; French.  
XX The invention relates to methods for selecting and identifying a  
CC cellular receptor for a virus, by immobilising, on a support, a  
CC monoclonal antibody targeted to a viral surface protein that determines  
CC attachment of the virus to the receptor. The immobilised antibody is  
CC incubated with a hexapeptide expression library and peptides bound to the  
CC immobilised antibody are eluted by competitive binding with recombinant  
CC fragments of the viral surface protein. In a reverse method, the viral  
CC surface protein is immobilised and incubated with the peptide library. In  
CC this case, the bound peptides are eluted by competitive binding with the  
CC monoclonal antibody. The hexapeptides AAW75278-W75292 represent  
CC peptides isolated by biopanning the library with the immobilised  
CC monoclonal antibody (MAb) 7A2.7 and eluted using an adenovirus type 5  
CC fibre head protein (AAW75267).  
CC The methods are used to identify peptides from MHC Class I and/or  
CC type III fibronectin proteins that allow or facilitate attachment by  
CC adenovirus (Ad) to host cells and/or entry into the cells, and to

CC identify ligands that modulate Ad infection mediated by these peptides,  
CC e.g. to treat or prevent Ad infections or to facilitate infection by Ad  
CC gene therapy vectors used to treat genetic diseases, acquired immune  
CC deficiency syndrome or cancer.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 6 AA;  
SQ Query Match 30.8%; Score 4; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 LGPV 12  
Db 1 LGPV 4  
RESULT 49  
AAU08616  
ID AAU08616 standard; Peptide; 6 AA.  
XX AC AAU08616;  
XX DT 18-DEC-2001 (first entry)  
DT Human olfactory receptor PCR primer design motif #1.  
XX DE Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;  
KW food additive; cosmetic; fragrance; pharmaceutical additive.  
XX OS Homo sapiens.  
XX PN WO200168805-A2.  
XX 20-SEP-2001.  
XX PF 13-MAR-2001; 2001WO-US07771.  
XX PR 13-MAR-2000; 2000US-0188914.  
PR 24-MAR-2000; 2000US-0192033.  
PR 12-APR-2000; 2000US-0198474.  
PR 24-APR-2000; 2000US-0199335.  
PR 26-MAY-2000; 2000US-0207702.  
PR 23-JUN-2000; 2000US-0213849.  
PR 16-AUG-2000; 2000US-0226534.  
PR 07-SEP-2000; 2000US-0230732.  
PR 07-FEB-2001; 2001US-0268862.  
XX PA (SENO-) SENOMYX INC.  
XX Zozulya S;  
XX WPI; 2001-570867/64.  
XX PT Nucleic acids encoding human olfactory G protein-coupled receptors,  
PT useful for screening for compounds involved in olfactory sensation,  
PT where the compounds can be used in the food, pharmaceutical and  
PT cosmetic industries to customise odours -  
PT Disclosure; Page 42; 319pp; English.  
XX The invention relates to nucleic acids encoding human olfactory  
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's  
CC specifically recognise molecules, odourants, that elicit specific  
CC olfactory sensation. The human olfactory receptors and polynucleotides  
CC encoding them are useful for screening a library of chemical compounds  
CC for compounds that are involved in olfactory sensation. Modulators of  
CC their activity are useful for pharmacological and genetic modulation of  
CC olfactory signalling pathways. Therefore, they can be used in the food,  
CC pharmaceutical and cosmetic industries to customise odours and  
CC fragrances. The present sequence is a human olfactory receptor  
CC protein motif end used to design PCR primers against the first  
CC transmembrane domain.



```

XX SQ Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLLY 4
XX ||||
XX 2 FLLY 5
XX
XX RESULT 50
XX AAG63026
XX ID AAG63026 standard; peptide; 6 AA.
XX AC AAG63026;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX PA (VITE-) VI TECHNOLOGIES INC.
XX PI Hammond DJ;
XX DR WPI; 2001-475677/51.
XX XX
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 4; Page 27; 39pp; English.
XX
XX CC The present sequence represents a Hepatitis A virus (HAV)-binding
XX CC domain. It was identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding
XX CC of ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX
XX SQ Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLLY 4
XX ||||
XX 1 FLLY 4
XX
XX Db
XX
XX RESULT 52
XX AAG63043
XX ID AAG63043 standard; peptide; 6 AA.
XX AC AAG63043;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.

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XX WO200140265-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US42515.
XX
XX 02-DEC-1999; 99US-0453115.
XX
XX (VITE-) VI TECHNOLOGIES INC.
XX
XX Hammond DJ;
XX
XX WPI; 2001-475677/51.
XX
XX Identifying ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins, involves differentiating specific or
XX non-specific false positive interactions from target-specific
XX interactions -
XX
XX Claim 4; Page 27; 39pp; English.
XX
XX The present sequence represents a Hepatitis A virus (HAV)-binding
XX domain. It was identified using the method of the invention. The method
XX identifies ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins. The method comprise differentiating false
XX positive interactions (either specific or non-specific) from
XX target-specific interaction, by distinguishing non-specific binding of
XX ligands to agents in the screening solution from specific binding
XX between a ligand and target. The method is useful for identifying
XX ligands that interact with the target, and for multiple screenings of
XX the same surface-immobilized library for a number of different ligands.
XX
XX Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLLY 4
XX ||||
XX Db 1 FLLY 4
XX
XX RESULT 53
XX AAG63065
XX ID AAG63065 standard; peptide; 6 AA.
XX
XX AC AAG63065;
XX
XX 01-OCT-2001 (first entry)
XX
XX Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX
XX Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX virus binding domain.
XX
XX Unidentified.
XX
XX WO200140265-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US42515.
XX
XX 02-DEC-1999; 99US-0453115.
XX
XX (VITE-) VI TECHNOLOGIES INC.
XX
XX Hammond DJ;
XX
XX WPI; 2001-475677/51.
XX
XX

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PT Identifying ligands that interact with a target by Quick Assay for
PT Selecting Affinity Resins, involves differentiating specific or
PT non-specific false positive interactions from target-specific
PT interactions -
XX
XX Claim 10; Page 28; 39pp; English.
XX
XX The present sequence represents a Hepatitis A virus (HAV)-binding
XX domain. It was identified using the method of the invention. The method
XX identifies ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins. The method comprise differentiating false
XX positive interactions (either specific or non-specific) from
XX target-specific interaction, by distinguishing non-specific binding of
XX ligands to agents in the screening solution from specific binding
XX between a ligand and target. The method is useful for identifying
XX ligands that interact with the target, and for multiple screenings of
XX the same surface-immobilized library for a number of different ligands.
XX
XX Sequence 6 AA;
XX
XX Query Match 30.8%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FLLY 4
XX ||||
XX Db 1 FLLY 4
XX
XX RESULT 54
XX AAG63106
XX ID AAG63106 standard; peptide; 6 AA.
XX
XX AC AAG63106;
XX
XX 01-OCT-2001 (first entry)
XX
XX Amino acid sequence of a Poliovirus-binding domain.
XX
XX Poliovirus; Quick Assay for Selecting Affinity Resins;
XX virus binding domain.
XX
XX Unidentified.
XX
XX WO200140265-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US42515.
XX
XX 02-DEC-1999; 99US-0453115.
XX
XX (VITE-) VI TECHNOLOGIES INC.
XX
XX Hammond DJ;
XX
XX WPI; 2001-475677/51.
XX
XX Identifying ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins, involves differentiating specific or
XX non-specific false positive interactions from target-specific
XX interactions -
XX
XX Claim 30; Page 30; 39pp; English.
XX
XX The present sequence represents a Poliovirus-binding domain. It was
XX identified using the method of the invention. The method identifies
XX ligands that interact with a target by Quick Assay for Selecting Affinity
XX Resins. The method comprise differentiating false positive interactions
XX (either specific or non-specific) from target-specific interaction, by
XX distinguishing non-specific binding of ligands to agents in the
XX screening solution from specific binding between a ligand and target.
XX The method is useful for identifying ligands that interact with the
XX

```

CC target, and for multiple screenings of the same surface-immobilized  
CC library for a number of different ligands.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLY 4  
|  
|  
|  
|  
Db 1 FLLY 4

## RESULT 55

AAG63108  
ID AAG63108 standard; peptide; 6 AA.

XX AC AAG63108;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a Poliovirus-binding domain.

XX KW Poliovirus; Quick Assay for Selecting Affinity Resins;  
XX virus binding domain.

XX OS Unidentified.

XX PN WO200140265-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US42515.

XX PR 02-DEC-1999; 99US-0453115.

XX PA (VITE-) VI TECHNOLOGIES INC.

XX PI Hammond DU;

XX DR WPI; 2001-475677/51.

XX PT Identifying ligands that interact with a target by Quick Assay for  
PT Selecting Affinity Resins, involves differentiating specific or  
PT non-specific false positive interactions from target-specific  
PT interactions -

XX PS Claim 30; Page 30; 39pp; English.

XX CC The present sequence represents a Poliovirus-binding domain. It was  
CC identified using the method of the invention. The method identifies  
CC ligands that interact with a target by Quick Assay for Selecting Affinity  
CC Resins. The method comprise differentiating false positive interactions  
CC (either specific or non-specific) from target-specific interaction, by  
CC distinguishing non-specific binding of ligands to agents in the  
CC screening solution from specific binding between a ligand and target.  
CC The method is useful for identifying ligands that interact with the  
CC target, and for multiple screenings of the same surface-immobilized  
CC library for a number of different ligands.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLY 4  
|  
|  
|  
|  
Db 1 FLLY 4

## RESULT 56

AAG63108  
ID AAG63108 standard; peptide; 6 AA.

## AAB87132

ID AAB87132 standard; peptide; 6 AA.

XX AC AAB87132;

XX DT 04-MAY-2001 (first entry)

XX DE Human TANGO 393 cytoplasmic domain, SEQ ID NO:134.

XX KW Secreted protein; transmembrane protein; TANGO; human; drug screening;  
XX activity modulator; expression modulator; cancer; immunological disorder;  
XX cytostatic; immunomodulatory; gene therapy.

XX OS Homo sapiens.

XX PN WO200109162-A2.

XX PD 08-FEB-2001.

XX PF 31-JUL-2000; 2000WO-US20935.

XX PR 30-JUL-1999; 99US-0365164.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Fraser CC, Sharp JD, Kirst SJ, Barnes TM, Wrighton N, Myers PS;  
XX Pan Y;

XX DR WPI; 2001-138647/14.

XX CC Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful  
XX for the prevention, diagnosis and treatment of, e.g. cancers and immune  
XX disorders -

XX PS Disclosure; Page 279; 332pp; English.

XX CC The invention relates to novel secreted/transmembrane proteins, and  
CC nucleic acids encoding them. The novel proteins are designated TANGO 339,  
CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO  
CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a  
CC murine TANGO 393 is also included within the scope of the invention. The  
CC invention also encompasses fragments and variants of the proteins of the  
CC invention, and nucleic acids encoding them. The invention additionally  
CC relates to host cells comprising a nucleic acid of the invention; methods  
CC for the production of a protein of the invention; an antibody specific  
CC for a protein of the invention; methods for detecting a protein or  
CC nucleic acid of the invention; and methods of identifying agents which  
CC bind to or modulate the activity of a protein of the invention. The novel  
CC secreted proteins, nucleic acids encoding them, and antibodies against  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression or activity of the secreted  
CC proteins. The secreted proteins of the invention may also be used to  
CC identify modulators of expression or activity, which may be useful in  
CC the treatment of disorders associated with the proteins of the  
CC invention e.g., cancers and immunological disorders. The present  
CC sequence represents a fragment of a human TANGO protein of the  
CC invention.

XX SQ Sequence 6 AA;

Query Match 30.8%; Score 4; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLGP 11  
|  
|  
|  
|  
Db 2 VLGP 5

## RESULT 57

AAB87133  
ID AAB87133 standard; peptide; 6 AA.

XX



DR WPI; 2003-327314/31.  
 XX Novel amplification primer sequence pair for amplifying nucleic acid  
 PT encoding an olfactory receptor ligand-binding region -  
 XX  
 XX Disclosure; Column 14; 46pp; English.  
 XX  
 CC The invention relates to an amplification primer sequence pair for  
 CC amplifying a nucleic acid encoding an olfactory receptor ligand-binding  
 CC region, comprising a primers appearing as ACA04888 and ACA04889.  
 CC Also included is a kit for amplifying olfactory receptor sequences  
 CC comprising the primers. The primers are useful for generating a nucleic  
 CC acid sequence that encodes a ligand-binding region of an olfactory  
 CC receptor. The amplified nucleic acid is genomic DNA, mRNA or cDNA derived  
 CC from olfactory neurons or the olfactory epithelium. The olfactory  
 CC receptors are 7 transmembrane receptors, manipulation of which can  
 CC modulate an animals olfactory response, and can be used to generate novel  
 CC odourants. The present sequence is a olfactory receptor peptide consensus  
 CC sequence used design degenerate PCR primer used to amplify an olfactory  
 CC receptor ligand-binding region.  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 30.8%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLY 4  
 DB 2 FLLY 5  
 ||||  
 ||||

RESULT 60  
 ABUS8261  
 ID ABUS8261 standard; Peptide; 6 AA.  
 XX  
 AC ABUS8261;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #7.  
 XX  
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002155106-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 01-DEC-2000; 2000US-0727963.  
 XX  
 PR 01-DEC-2000; 2000US-0727963.  
 XX  
 PA (HAMM/) HAMMOND D J.  
 XX  
 PI Hammond DJ;  
 XX  
 DR WPI; 2003-198483/19.  
 XX  
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -  
 XX  
 XX Claim 4; Page 31; 35pp; English.  
 PS  
 XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological

CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 30.8%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FLLY 4  
 DB 1 FLLY 4  
 ||||  
 ||||

RESULT 61  
 ABUS8271  
 ID ABUS8271 standard; Peptide; 6 AA.  
 XX  
 AC ABUS8271;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #12.  
 XX  
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002155106-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 01-DEC-2000; 2000US-0727963.  
 XX  
 PR 01-DEC-2000; 2000US-0727963.  
 XX  
 PA (HAMM/) HAMMOND D J.  
 XX  
 PI Hammond DJ;  
 XX  
 DR WPI; 2003-198483/19.  
 XX  
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -  
 XX  
 XX Claim 4; Page 31; 35pp; English.  
 PS  
 XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands. one  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
 ||||  
 Db 1 FLLY 4

RESULT 62

ABUS8273  
 ID ABUS8273 standard; Peptide; 6 AA.

XX AC ABUS8273;

XX DT 14-APR-2003 (first entry)

XX Peptide binding to hepatitis A virus in the presence of fibrinogen #14.

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.

XX OS Synthetic.

XX PN US2002155106-A1.

XX PD 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX PS WPI; 2003-198483/19.

XX New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -

XX Claim 10; Page 31; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
 ||||  
 Db 1 FLLY 4

RESULT 63

ABUS8291  
 ID ABUS8291 standard; Peptide; 6 AA.

XX AC ABUS8291;

XX DT 14-APR-2003 (first entry)

XX Poliovirus-binding peptide #6.

XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.

XX OS Synthetic.

XX PN US2002155106-A1.

XX PD 24-OCT-2002.

XX PF 01-DEC-2000; 2000US-0727963.

XX PR 01-DEC-2000; 2000US-0727963.

XX PA (HAMM/) HAMMOND D J.

XX PI Hammond DJ;

XX PS WPI; 2003-198483/19.

XX New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -

XX Claim 30; Page 32; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX Sequence 6 AA;

Query Match 30.8%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
 ||||  
 Db 1 FLLY 4

RESULT 64  
ABU58293  
ID ABU58293 standard; Peptide; 6 AA.  
AC ABU58293;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Poliovirus-binding peptide #8.  
XX  
KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
KW surface-immobilised library; blood composition.  
XX  
OS Synthetic.  
XX  
PN US2002155106-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 01-DEC-2000; 2000US-0727963.  
XX  
PR 01-DEC-2000; 2000US-0727963.  
XX  
PR (HAMM/) HAMMOND D J.  
XX  
PI Hammond DJ;  
XX  
PI WPI; 2003-198483/19.  
XX  
DR New peptide comprising a porcine parvovirus-binding, hepatitis A  
XX virus-binding or prion-binding domain, useful for screening a library  
XX of surface-immobilized ligands that bind to target molecules -  
XX  
PS Claim 30; Page 32; 35pp; English.  
XX  
CC The invention relates to a peptide, having a sequence of less than 20  
CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
CC A virus (HAV)-binding, or prion-binding domain. Also included are  
CC a composition comprising the peptide, removing a target from a biological  
CC fluid, identifying a ligand for a target or targets and identifying a  
CC peptide that binds to a virus present in a blood composition. The peptide  
CC is useful for identifying a ligand for a target or targets (Hepatitis A  
CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
CC peptide that binds to a virus present in a blood composition. It is used  
CC to screen a library of surface-immobilised ligands that bind to target  
CC molecules. The peptide allows for multiple screenings of the same  
CC surface-immobilised library for a number of different ligands.  
CC The present sequence is a peptide of the invention, targeting one  
CC of the above listed targets.  
XX  
SQ Sequence 6 AA;  
Query Match 30.8%; Score 4; DB 24; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLLY 4  
Db 1 FLLY 4  
RESULT 65  
ABU58312  
ID ABU58312 standard; Peptide; 6 AA.  
XX  
AC ABU58312;  
XX  
DT 14-APR-2003 (first entry)  
XX

DE Peptide binding to hepatitis A virus in the presence of fibrinogen #23.  
XX  
KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
KW surface-immobilised library; blood composition.  
XX  
OS Synthetic.  
XX  
PN US2002155106-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 01-DEC-2000; 2000US-0727963.  
XX  
PR 01-DEC-2000; 2000US-0727963.  
XX  
PR (HAMM/) HAMMOND D J.  
XX  
PI Hammond DJ;  
XX  
PI WPI; 2003-198483/19.  
XX  
DR New peptide comprising a porcine parvovirus-binding, hepatitis A  
XX virus-binding or prion-binding domain, useful for screening a library  
XX of surface-immobilized ligands that bind to target molecules -  
XX  
PS Claim 4; Page 31; 35pp; English.  
XX  
CC The invention relates to a peptide, having a sequence of less than 20  
CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
CC A virus (HAV)-binding, or prion-binding domain. Also included are  
CC a composition comprising the peptide, removing a target from a biological  
CC fluid, identifying a ligand for a target or targets and identifying a  
CC peptide that binds to a virus present in a blood composition. The peptide  
CC is useful for identifying a ligand for a target or targets (Hepatitis A  
CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
CC peptide that binds to a virus present in a blood composition. It is used  
CC to screen a library of surface-immobilised ligands that bind to target  
CC molecules. The peptide allows for multiple screenings of the same  
CC surface-immobilised library for a number of different ligands.  
CC The present sequence is a peptide of the invention, targeting one  
CC of the above listed targets.  
XX  
SQ Sequence 6 AA;  
Query Match 30.8%; Score 4; DB 24; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FLLY 4  
Db 1 FLLY 4  
RESULT 66  
AAW04280  
ID AAW04280 standard; peptide; 7 AA.  
XX  
AC AAW04280;  
XX  
DT 06-JUN-1997 (first entry)  
XX  
DE Milk derived non-anti-hypertensive peptide.  
XX  
KW Non-anti-hypertensive; fermentation; animal milk; Lactobacillus;  
KW microorganism; digestion; protease; reduction; blood pressure.  
XX  
OS Mammalian spp.  
XX  
PN EP737690-A2.

XX PD 16-OCT-1996.

XX XX

PF 10-APR-1996; 96EP-0302522.

XX XX

PR 10-APR-1995; 95JP-0084247.

XX XX

PA (CALV ) CALPIS FOOD IND CO LTD.

XX XX

PI Maeno M;

XX XX

DR WPI; 1996-457284/46.

XX XX

PT Antihypertensive compsns. derived from milk - by fermentation or

PT protease digestion

XX XX

PS Example 1; Page 6; 10pp; English.

XX XX

CC The present non-anti-hypertensive (NAH) peptide was prepared by

CC fermenting an animal milk starting material with a Lactobacillus

CC microorganism, especially L. helveticus, L. delbrueckii subspecies

CC bulgaricus or L. acidophilus, or digesting it with a protease at

CC 20-50 degrees C for 3-30 hours, obtaining an eluent by

CC ultrafiltration and then fractionating the eluent by reverse phase

CC HPLC. The change in the systolic blood pressure of spontaneously

CC hypertensive rats treated intragastrically with 1 mg/kg of body

CC weight of the present NAH peptide was plus 1.2 +/- 9.8 mmHg.

XX XX

SQ Sequence 7 AA;

Query Match 30.8%; Score 4; DB 17; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5

DB 1 LLYQ 4

RESULT 67

AAW30407

ID AAW30407 standard; peptide; 7 AA.

XX XX

AC AAW30407;

XX XX

DT 22-APR-1998 (first entry)

XX XX

DE HRE-I affinity peptide SEQ ID NO:25.

XX XX

KW Binding site; HRE-I; screening; H-Ras; target gene; plasmid;

KW inhibition; affinity peptide.

XX XX

OS Synthetic.

XX XX

PN WO9737030-A1.

XX XX

PD 09-OCT-1997.

XX XX

PF 31-MAR-1997; 97WO-JP01105.

XX XX

PR 03-OCT-1996; 96JP-0263345.

PR 01-APR-1996; 96JP-0101990.

XX XX

PA (YAWH ) NIPPON STEEL CHEM CO.

PA (YAWA ) NIPPON STEEL CORP.

XX XX

PI Kato T;

XX XX

DR WPI; 1997-503115/46.

XX XX

PT Plasmid for screening peptide(s) which bind target genes - for

PT treatment of conditions associated with H-Ras

XX XX

PS Claim 41; Page 65; 127pp; Japanese.

XX XX

CC A novel plasmid has been developed for screening peptides which bind

CC target genes. The plasmid comprises a sequence encoding the test

CC peptide, a promoter comprising the target gene, and a reporter gene

CC bound to the promoter. The present sequence represents a specifically

CC claimed peptide with affinity to HRE-I. The plasmids are used for

CC screening for peptides which bind to target genes. The identified

CC peptides can be used for the treatment of conditions associated with

CC the inhibition of the expression the genes, and treatment of conditions

CC associated with H-Ras.

XX XX

SQ Sequence 7 AA;

Query Match 30.8%; Score 4; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGPV 12

DB 1 LGPV 4

RESULT 68

ABG60365

ID ABG60365 standard; Peptide; 7 AA.

XX XX

AC ABG60365;

XX XX

DT 30-JUL-2002 (first entry)

XX XX

DE Selective targeting peptide #40.

XX XX

KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;

KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;

KW viral infection; cardiovascular disease; degenerative disease; ischaemia;

KW inflammation; macular degeneration; antiinflammatory; antidiabetic;

KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;

KW gene therapy.

XX XX

OS Synthetic.

XX XX

PN WO200220769-A1.

XX XX

PD 14-MAR-2002.

XX XX

PF 07-SEP-2001; 2001WO-US27692.

XX XX

PR 08-SEP-2000; 2000US-231266P.

PR 17-JAN-2001; 2001US-0765101.

XX XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX XX

PI Arap W, Pasqualini R;

XX XX

DR WPI; 2002-415731/44.

XX XX

PT Targeting peptides identified by phage display, useful for targeting

PT delivery to an organ or tissue, particularly for treating a disease,

PT e.g. cancer, inflammatory or autoimmune diseases, infections or

PT cardiovascular disease -

XX XX

PS Claim 22; Page 62; 317pp; English.

XX XX

CC The invention relates to an isolated peptide of 100 amino acids or less

CC in size useful for targeting delivery to an organ or tissue, particularly

CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory

CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral

CC infection, cardiovascular disease or degenerative disease. The peptide is

CC also useful for inducing apoptosis, particularly to a subject with

CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,

CC inflammation or macular degeneration. Furthermore, the peptide is useful

CC for diagnosing the diseases cited above. Targeting peptides of the



CC invention can also be used to deliver an agent to a foetus, by attaching  
CC a peptide to the agent and administering the peptide to a pregnant  
CC subject. Sequences ABG60326-ABG60574 represent selective targeting  
CC peptides of the invention.

SQ Sequence 7 AA;  
Query Match 30.8%; Score 4; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13  
Db 4 GPVR 7

RESULT 69  
ABG34932  
ID ABG34932 standard; Peptide; 7 AA.  
XX  
AC ABG34932;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human bone marrow targeting peptide #4.  
XX  
KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;  
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;  
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;  
KW inflammatory disease; arthritis; atherosclerosis; cancer;  
KW autoimmune disease; bacterial infection; viral infection.

OS Homo sapiens.  
XX  
FN WO200220722-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 07-SEP-2001; 2001WO-US27702.  
XX  
PR 08-SEP-2000; 2000US-231266P.  
PR 17-JAN-2001; 2001US-0765101.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Arap W, Pasqualini R;  
XX  
DR WPI; 2002-383050/41.

PT Identifying targeting peptides useful for treating e.g. diabetes  
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,  
PT comprises exposing a sample to a phage display library and recovering  
PT phage bound to the sample -

PS Claim 56; Page 202; 298pp; English.

XX This invention relates to a novel method for identifying disease  
XX targeting peptides. The method comprises exposing a sample from an  
XX organ, tissue or cell type of interest, to a phage display library and  
XX recovering phage bound to the sample (the phage expresses targeting  
XX peptides). The peptides identified by the method of the invention may  
XX have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,  
XX antiatherosclerotic, antidiabetic, antibacterial and antiviral  
XX activities. The methods and composition are useful for identifying  
XX targeting peptides and one or more receptors for a targeting peptide.  
XX The targeting peptides are used for selective delivery of therapeutic  
XX agents, including gene therapy vectors and fusion proteins, to specific  
XX organs, tissues, or cell types in subject. The targeting peptide may  
XX also be used for treating diseases such as diabetes mellitus,  
XX inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune  
XX diseases, bacterial and viral infections and Hodgkin's disease. The  
XX present sequence represents a targeting peptide of the invention.

SQ Sequence 7 AA;  
Query Match 30.8%; Score 4; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
Db 4 PVLG 7

RESULT 70  
ABG34933  
ID ABG34933 standard; Peptide; 7 AA.  
XX  
AC ABG34933;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human bone marrow targeting peptide #5.  
XX  
KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;  
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;  
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;  
KW inflammatory disease; arthritis; atherosclerosis; cancer;  
KW autoimmune disease; bacterial infection; viral infection.

OS Homo sapiens.  
XX  
FN WO200220722-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 07-SEP-2001; 2001WO-US27702.  
XX  
PR 08-SEP-2000; 2000US-231266P.  
PR 17-JAN-2001; 2001US-0765101.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Arap W, Pasqualini R;  
XX  
DR WPI; 2002-383050/41.

PT Identifying targeting peptides useful for treating e.g. diabetes  
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,  
PT comprises exposing a sample to a phage display library and recovering  
PT phage bound to the sample -

PS Claim 56; Page 202; 298pp; English.

XX This invention relates to a novel method for identifying disease  
XX targeting peptides. The method comprises exposing a sample from an  
XX organ, tissue or cell type of interest, to a phage display library and  
XX recovering phage bound to the sample (the phage expresses targeting  
XX peptides). The peptides identified by the method of the invention may  
XX have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,  
XX antiatherosclerotic, antidiabetic, antibacterial and antiviral  
XX activities. The methods and composition are useful for identifying  
XX targeting peptides and one or more receptors for a targeting peptide.  
XX The targeting peptides are used for selective delivery of therapeutic  
XX agents, including gene therapy vectors and fusion proteins, to specific  
XX organs, tissues, or cell types in subject. The targeting peptide may  
XX also be used for treating diseases such as diabetes mellitus,  
XX inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune  
XX diseases, bacterial and viral infections and Hodgkin's disease. The  
XX present sequence represents a targeting peptide of the invention.

SQ Sequence 7 AA;

Query Match 30.8%; Score 4; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
 Db 1 VLGP 4  
 RESULT 71  
 ABJ19880  
 ID ABJ19880 standard; Peptide; 7 AA.  
 XX  
 AC ABJ19880;  
 XX  
 DT 10-APR-2003 (first entry)  
 XX  
 DE MHC binding peptide SEQ ID No 45.  
 XX  
 KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200294981-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 16-MAY-2002; 2002WO-IL00383.  
 XX  
 PR 16-MAY-2001; 2001US-290958P.  
 PR 29-MAY-2001; 2001US-0865548.  
 XX  
 PA (TECR ) TECHNION RES & DEV FOUND LTD.  
 XX  
 PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;  
 DR WPI; 2003-210043/20.  
 XX  
 XX Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -  
 XX  
 PS Claim 37; Page 61; 238pp; English.  
 XX  
 CC The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
 CC sequences of the invention may be used in a gene therapy application.  
 CC This sequence represents a peptide relating to the method for identifying  
 CC MHC binding peptides of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 30.8%; Score 4; DB 24; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 EPVL 9  
 Db 4 EPVL 7  
 RESULT 72  
 AAR58333  
 ID AAR58333 standard; peptide; 8 AA.

XX AAR58333;  
 AC  
 DT 22-SEP-1994 (first entry)  
 XX  
 DE Hypotensive polypeptide.  
 XX  
 KW Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 XX  
 OS Lactobacillus helveticus.  
 XX  
 PN JP06041191-A.  
 XX  
 PD 15-FEB-1994.  
 XX  
 PF 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 PA (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 XX  
 DR WPI; 1994-089332/11.  
 XX  
 XX New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxidative and calcium absorption promoting  
 PT activity  
 XX  
 PS Claim 1-2; Page 9; 10pp; Japanese.  
 XX  
 CC Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 30.8%; Score 4; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 GPVR 13  
 Db 1 GPVR 4  
 RESULT 73  
 AAR84066  
 ID AAR84066 standard; peptide; 8 AA.  
 XX  
 AC AAR84066;  
 XX  
 DT 21-AUG-1996 (first entry)  
 XX  
 DE Retinal pigment epithelial cell growth factor N-terminal peptide.  
 XX  
 KW Growth factor; proliferation; retina; pigment; ophthalmic disease;  
 KW retinitis pigmentosa; erythema; retinal detachment.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "X= undefined amino acid"  
 FT Misc-difference 6 /note= "X= undefined amino acid"  
 FT  
 XX JP08053362-A.  
 XX  
 PD 27-FEB-1996.  
 XX  
 PF 11-AUG-1994; 94JP-0189147.

compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX  
XX  
SQ Sequence 8 AA;

Query Match 30.8%; Score 4; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7  
|||  
1 YQEP 4

Db

RESULT 75

ABP14660

ID ABP14660 standard; Peptide; 8 AA.

XX  
XX AC ABP14660;

DT 15-JUL-2002 (first entry)

XX  
XX DE HIV A03 super motif pol peptide #34.

XX  
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX  
XX Human immunodeficiency virus type 1.

XX  
XX WO200124810-A1.

XX  
XX PD 12-APR-2001.

XX  
XX PF 05-OCT-2000; 2000WO-US27766.

XX  
XX PF 05-OCT-1999; 99US-0412863.

XX  
XX (EPIM-) EPIMUNE INC.

XX  
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
XX Baker DW, Celis E, Kubo RT, Grey HM;  
XX WPI; 2001-354887/37.

XX  
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -

XX  
XX Claim 32; Page 168; 448pp; English.

XX  
XX The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABU25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP1501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX  
SQ Sequence 8 AA;  
Query Match 30.8%; Score 4; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 YQEP 7  
| | | |  
Db 3 YQEP 6

Search completed: November 25, 2003, 19:27:22  
Job time : 34.1802 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; search time 20.8605 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLYQEPVLGPVR 13

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	US-10-281-652-32	Sequence 32, Appl
2	7	53.8	7	US-10-305-346-12	Sequence 12, Appl
3	7	53.8	19	US-10-280-833-7	Sequence 7, Appl
4	6	46.2	7	US-10-281-652-28	Sequence 28, Appl
5	4	30.8	6	US-09-727-963A-15	Sequence 15, Appl
6	4	30.8	6	US-09-727-963A-25	Sequence 25, Appl
7	4	30.8	6	US-09-727-963A-27	Sequence 27, Appl
8	4	30.8	6	US-09-727-963A-45	Sequence 45, Appl
9	4	30.8	6	US-09-727-963A-47	Sequence 47, Appl
10	4	30.8	6	US-09-804-291-519	Sequence 519, Appl
11	4	30.8	6	US-10-229-423-49	Sequence 49, Appl
12	4	30.8	6	US-10-156-820-48	Sequence 48, Appl
13	4	30.8	6	US-10-259-430-49	Sequence 49, Appl
14	4	30.8	7	US-09-865-548A-45	Sequence 45, Appl
15	4	30.8	8	US-09-865-548A-200	Sequence 200, Appl

16	4	30.8	8	12	US-10-137-867-382	Sequence 382, Appl
17	4	30.8	9	10	US-09-894-018-79	Sequence 79, Appl
18	4	30.8	9	10	US-09-894-018-181	Sequence 181, Appl
19	4	30.8	9	10	US-09-894-018-183	Sequence 183, Appl
20	4	30.8	9	10	US-09-835-853-11	Sequence 11, Appl
21	4	30.8	9	11	US-09-865-548A-145	Sequence 145, Appl
22	4	30.8	9	12	US-09-793-451-130	Sequence 130, Appl
23	4	30.8	9	12	US-09-793-451-156	Sequence 156, Appl
24	4	30.8	9	12	US-09-793-451-251	Sequence 251, Appl
25	4	30.8	9	12	US-09-793-451-357	Sequence 357, Appl
26	4	30.8	9	12	US-09-793-451-456	Sequence 456, Appl
27	4	30.8	9	12	US-09-793-451-460	Sequence 460, Appl
28	4	30.8	9	12	US-09-793-451-529	Sequence 529, Appl
29	4	30.8	9	12	US-09-793-451-540	Sequence 540, Appl
30	4	30.8	9	12	US-09-793-451-641	Sequence 641, Appl
31	4	30.8	9	12	US-10-283-722-130	Sequence 130, Appl
32	4	30.8	9	12	US-10-283-722-156	Sequence 156, Appl
33	4	30.8	9	12	US-10-283-722-251	Sequence 251, Appl
34	4	30.8	9	12	US-10-283-722-357	Sequence 357, Appl
35	4	30.8	9	12	US-10-283-722-456	Sequence 456, Appl
36	4	30.8	9	12	US-10-283-722-460	Sequence 460, Appl
37	4	30.8	9	12	US-10-283-722-529	Sequence 529, Appl
38	4	30.8	9	12	US-10-283-722-540	Sequence 540, Appl
39	4	30.8	9	12	US-10-283-722-641	Sequence 641, Appl
40	4	30.8	9	12	US-10-371-069-376	Sequence 376, Appl
41	4	30.8	9	12	US-10-371-069-382	Sequence 382, Appl
42	4	30.8	9	12	US-10-371-645-376	Sequence 376, Appl
43	4	30.8	9	12	US-10-371-645-382	Sequence 382, Appl
44	4	30.8	9	15	US-10-133-210-112	Sequence 112, Appl
45	4	30.8	9	15	US-10-133-210-113	Sequence 113, Appl
46	4	30.8	9	15	US-10-254-446A-122	Sequence 122, Appl
47	4	30.8	10	11	US-09-572-404B-1421	Sequence 1421, Appl
48	4	30.8	10	11	US-09-572-404B-1423	Sequence 1423, Appl
49	4	30.8	10	11	US-09-572-404B-2039	Sequence 2039, Appl
50	4	30.8	10	11	US-09-572-404B-2945	Sequence 2945, Appl
51	4	30.8	10	11	US-09-572-404B-3866	Sequence 3866, Appl
52	4	30.8	10	11	US-09-572-404B-3867	Sequence 3867, Appl
53	4	30.8	10	11	US-09-572-404B-3868	Sequence 3868, Appl
54	4	30.8	10	11	US-09-572-404B-3869	Sequence 3869, Appl
55	4	30.8	10	11	US-09-572-404B-3870	Sequence 3870, Appl
56	4	30.8	10	12	US-09-793-451-183	Sequence 183, Appl
57	4	30.8	10	12	US-09-793-451-206	Sequence 206, Appl
58	4	30.8	10	12	US-09-793-451-272	Sequence 272, Appl
59	4	30.8	10	12	US-09-793-451-303	Sequence 303, Appl
60	4	30.8	10	12	US-09-793-451-474	Sequence 474, Appl
61	4	30.8	10	12	US-09-793-451-502	Sequence 502, Appl
62	4	30.8	10	12	US-09-793-451-594	Sequence 594, Appl
63	4	30.8	10	12	US-09-793-451-596	Sequence 596, Appl
64	4	30.8	10	12	US-09-793-451-691	Sequence 691, Appl
65	4	30.8	10	12	US-10-239-313A-433	Sequence 433, Appl
66	4	30.8	10	12	US-10-200-708-132	Sequence 132, Appl
67	4	30.8	10	12	US-10-200-708-564	Sequence 564, Appl
68	4	30.8	10	12	US-10-200-708-662	Sequence 662, Appl
69	4	30.8	10	12	US-10-283-722-183	Sequence 183, Appl
70	4	30.8	10	12	US-10-283-722-206	Sequence 206, Appl
71	4	30.8	10	12	US-10-283-722-272	Sequence 272, Appl
72	4	30.8	10	12	US-10-283-722-303	Sequence 303, Appl
73	4	30.8	10	12	US-10-283-722-474	Sequence 474, Appl
74	4	30.8	10	12	US-10-283-722-502	Sequence 502, Appl
75	4	30.8	10	12	US-10-283-722-594	Sequence 594, Appl
76	4	30.8	10	12	US-10-283-722-596	Sequence 596, Appl
77	4	30.8	10	12	US-10-283-722-691	Sequence 691, Appl
78	4	30.8	10	15	US-10-001-546-18	Sequence 18, Appl
79	4	30.8	10	15	US-10-043-487-345	Sequence 345, Appl
80	4	30.8	11	12	US-10-239-313A-435	Sequence 435, Appl
81	4	30.8	12	9	US-09-739-852-11	Sequence 11, Appl
82	4	30.8	12	11	US-09-354-385-312	Sequence 312, Appl
83	4	30.8	12	12	US-10-237-852-34	Sequence 34, Appl
84	4	30.8	12	12	US-10-237-852-46	Sequence 46, Appl
85	4	30.8	12	12	US-10-405-231-11	Sequence 11, Appl
86	4	30.8	12	15	US-10-238-607-11	Sequence 11, Appl
87	4	30.8	13	11	US-09-983-802-439	Sequence 439, Appl
88	4	30.8	13	12	US-10-239-313A-436	Sequence 436, Appl

Sequence 22, Appl  
 Sequence 22, Appl  
 Sequence 6, Appl  
 Sequence 499, App  
 Sequence 197, App  
 Sequence 5, Appl  
 Sequence 77, Appl  
 Sequence 71, Appl  
 Sequence 550, App  
 Sequence 564, App  
 Sequence 238, App  
 Sequence 238, App

89 4 30.8 14 11 US-09-992-331-22  
 90 4 30.8 14 16 US-10-262-313-22  
 91 4 30.8 15 12 US-10-336-491-6  
 92 4 30.8 15 12 US-10-239-313A-499  
 93 4 30.8 15 12 US-10-350-405-197  
 94 4 30.8 15 12 US-10-376-121A-5  
 95 4 30.8 15 15 US-10-033-741-77  
 96 4 30.8 15 15 US-10-033-662-71  
 97 4 30.8 16 10 US-09-791-378-550  
 98 4 30.8 16 10 US-09-791-378-564  
 99 4 30.8 16 11 US-09-791-393-238  
 100 4 30.8 16 11 US-09-791-389-238

## ALIGNMENTS

RESULT 1  
 US-10-281-652-32  
 ; Sequence 32, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: 265,00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 32  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-32

Query Match 100.0%; Score 13; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLYQEPVLGPVR 13  
 Db 1 FLLYQEPVLGPVR 13

RESULT 2  
 US-10-305-346-12  
 ; Sequence 12, Application US/10305346  
 ; Publication No. US20030130195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMIOT, Jean  
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS  
 ; FILE REFERENCE: 6013-57"US"-1  
 ; CURRENT APPLICATION NUMBER: US/10/305,346  
 ; CURRENT FILING DATE: 2002-11-27  
 ; PRIOR APPLICATION NUMBER:  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide

; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins  
 US-10-305-346-12

Query Match 53.8%; Score 7; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQEPVL 9  
 Db 1 LYQEPVL 7

RESULT 3  
 US-10-280-833-7  
 ; Sequence 7, Application US/10280833  
 ; Publication No. US20030195150A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reynolds, Charles Eric  
 ; APPLICANT: Dashper, Stuart Geoffrey  
 ; APPLICANT: O'Brien-Simpson, Neil Martin  
 ; APPLICANT: Talbot, Gert Hoy  
 ; APPLICANT: Malkoski, Marina  
 ; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES  
 ; FILE REFERENCE: EDWP-001CON  
 ; CURRENT APPLICATION NUMBER: US/10/280,833  
 ; CURRENT FILING DATE: 2002-10-24  
 ; PRIOR APPLICATION NUMBER: 09/554,997  
 ; PRIOR FILING DATE: 2000-08-09  
 ; PRIOR APPLICATION NUMBER: PP 0514  
 ; PRIOR FILING DATE: 1997-11-24  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: bovine  
 US-10-280-833-7

Query Match 53.8%; Score 7; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLGPVR 13  
 Db 13 PVLGPVR 19

RESULT 4  
 US-10-281-652-28  
 ; Sequence 28, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: 265,00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide

US-10-281-652-28

Query Match 46.2%; Score 6; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQ 6  
Db 2 FLLYQ 7  
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|||||

RESULT 5

US-09-727-963A-15  
; Sequence 15, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-15

Query Match 30.8%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
Db 1 FLLY 4  
|||||  
|||||

RESULT 6

US-09-727-963A-25  
; Sequence 25, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-25

Query Match 30.8%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4

Db 1 FLLY 4  
|||||

RESULT 7

US-09-727-963A-27  
; Sequence 27, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-27

Query Match 30.8%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
Db 1 FLLY 4  
|||||  
|||||

RESULT 8

US-09-727-963A-45  
; Sequence 45, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand  
US-09-727-963A-45

Query Match 30.8%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLY 4  
Db 1 FLLY 4  
|||||  
|||||

RESULT 9

US-09-727-963A-47  
; Sequence 47, Application US/09727963A  
; Patent No. US20020155106A1

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; GENERAL INFORMATION:
; APPLICANT: V. I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-47

Query Match          30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

RESULT 10
US-09-804-291-519
; Sequence 519, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 519
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-804-291-519

Query Match          30.8%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

US-09-641-801-32.oligo.rapb

; GENERAL INFORMATION:
; APPLICANT: V. I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand
US-09-727-963A-47

Query Match          30.8%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 1 FLYY 4

RESULT 11
US-10-259-423-49
; Sequence 49, Application US/10259423
; Publication No. US20030175744A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-wai
; APPLICANT: Krutwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/10/259,423
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/465,901
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-259-423-49

Query Match          30.8%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYY 4
Db 2 FLYY 5

RESULT 12
US-10-156-820-48
; Sequence 48, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-10-156-820-48

Query Match          30.8%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 1 FLYY 12
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Db 1 LGPV 4

RESULT 13  
US-10-259-430-49  
; Sequence 49, Application US/10259430  
; Publication No. US20030082615A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Randall  
; APPLICANT: Yau, King-Mai  
; APPLICANT: Krautwurst, Dietmar  
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries  
; TITLE OF INVENTION: ad Methods of Making and Using Them  
; FILE REFERENCE: 001107.00105  
; CURRENT APPLICATION NUMBER: US/10/259,430  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/465,901  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/112,605  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-259-430-49

Query Match 30.8%; Score 4; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYY 4  
Db 2 FLYY 5

RESULT 14  
US-09-865-548A-45  
; Sequence 45, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE  
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/290,958  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-45

Query Match 30.8%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9  
Db 4 EPVL 7

RESULT 15  
US-09-865-548A-200  
; Sequence 200, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE  
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/290,958  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 200  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-200

Query Match 30.8%; Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9  
Db 4 EPVL 7

RESULT 16  
US-10-137-867-382  
; Sequence 382, Application US/10137867  
; Publication No. US20030207349A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C146  
; CURRENT APPLICATION NUMBER: US/10/137,867  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 382  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-867-382

Query Match 30.8%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

```
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      8 VLGP 11
      ||||
Db      4 VLGP 7

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-181

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      2 YOEP 5
      ||||

RESULT 19
US-09-894-018-183
; Sequence 183, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-79

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      2 YOEP 5
      ||||

RESULT 18
US-09-894-018-181
; Sequence 181, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-183

Query Match      30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      4 YOEP 7
      ||||
Db      5 YOEP 8
      ||||

RESULT 20
US-09-835-853-11
; Sequence 11, Application US/09835853
; Patent No. US20020165136A1
; GENERAL INFORMATION:
; APPLICANT: BASERGA, Renato L.
; APPLICANT: RESNICOFF, Mariana
; APPLICANT: HUANG, Ziwei
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/835,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/704,344
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-09-835-853-11

Query Match 30.8%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13
DB 5 GPVR 8

RESULT 21
US-09-865-548A-145
; Sequence 145, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
;
US-09-865-548A-145

Query Match 30.8%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9
DB 4 EPVL 7
```

```
RESULT 22
US-09-793-451-130
; Sequence 130, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-09-793-451-130

Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
DB 1 LLYQ 4

RESULT 23
US-09-793-451-156
; Sequence 156, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
;
US-09-793-451-156

Query Match 30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LLYQ 5
Db      2 LLYQ 5

RESULT 24
US-09-793-451-251
; Sequence 251, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-251

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
Db      1 LLYQ 4

RESULT 25
US-09-793-451-357
; Sequence 357, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens

US-09-793-451-357

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
Db      1 LLYQ 4

RESULT 26
US-09-793-451-456
; Sequence 456, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-456

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
Db      1 LLYQ 4

RESULT 27
US-09-793-451-460
; Sequence 460, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-460
```

; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 460  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-460

Query Match 30.8%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
 ||||  
 Db 5 LLYQ 8

## RESULT 28

US-09-793-451-529  
 ; Sequence 529, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2

; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 529

; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens

US-09-793-451-529

Query Match 30.8%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
 ||||  
 Db 5 LLYQ 8

## RESULT 29

US-09-793-451-540  
 ; Sequence 540, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2

; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 540  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-540

Query Match 30.8%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
 ||||  
 Db 1 LLYQ 4

## RESULT 30

US-09-793-451-641  
 ; Sequence 641, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2

; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 641

; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens

US-09-793-451-641

Query Match 30.8%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
 ||||  
 Db 5 LLYQ 8

## RESULT 31

US-10-283-722-130  
 ; Sequence 130, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits

```
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-130

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
        ||||
Db      1 LLYQ 4

RESULT 32
US-10-283-722-156
; Sequence 156, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-156

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
        ||||
Db      2 LLYQ 5

RESULT 33
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-251

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLYQ 5
        ||||
Db      1 LLYQ 4

RESULT 34
US-10-283-722-357
; Sequence 357, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-357

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2 LLYQ 5
      ||||
Db      3 LLYQ 6

RESULT 35
US-10-283-722-456
; Sequence 456, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 456
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-456

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 LLYQ 5
      ||||
Db      1 LLYQ 4

RESULT 36
US-10-283-722-460
; Sequence 460, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460

Oy      2 LLYQ 5
      ||||
Db      1 LLYQ 4

RESULT 37
US-10-283-722-529
; Sequence 529, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-529

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 LLYQ 5
      ||||
Db      5 LLYQ 8

RESULT 38
US-10-283-722-540
; Sequence 540, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
```

```

; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-540

```

```

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 LLYQ 5
Db      1 LLYQ 4

```

## RESULT 39

```

US-10-283-722-641
; Sequence 641, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits

```

```

; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS

```

```

; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641

```

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-641

```

```

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 LLYQ 5
Db      5 LLYQ 8

```

## RESULT 40

```

US-10-371-069-376

```

```

; Sequence 376, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:

```

```

; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro

```

```

; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069.60)
US-10-371-069-376

```

```

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 YOEP 7
Db      2 YOEP 5

```

## RESULT 41

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US-10-371-069-382

```

```

; Sequence 382, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:

```

```

; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.

```

```

; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same

```

```

; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069.59)
US-10-371-069-382

```

```

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 YOEP 7
Db      5 YOEP 8

```



```
RESULT 42
US-10-371-645-376
; Sequence 376, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069..60)
US-10-371-645-376

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      2 YQEP 5

RESULT 43
US-10-371-645-382
; Sequence 382, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069..59)
US-10-371-645-382

Query Match      30.8%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      2 YQEP 5

RESULT 44
US-10-133-210-112
; Sequence 112, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-112

Query Match      30.8%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      5 YQEP 8

RESULT 45
US-10-133-210-113
; Sequence 113, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-113

Query Match      30.8%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YQEP 7
Db      5 YQEP 8
```

QY 4 YQEP 7  
|||  
Db 2 YQEP 5

## RESULT 46

US-10-254-446A-122  
; Sequence 122, Application US/10254446A  
; Publication No. US20030113714A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela M  
; APPLICANT: Smalley, Richard E.  
; APPLICANT: Ryan, Esther  
; APPLICANT: Lee, Seung-Wuk  
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES  
; FILE REFERENCE: 119927-1066  
; CURRENT APPLICATION NUMBER: US/10/254,446A  
; CURRENT FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: 60/325,664  
; PRIOR FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 245  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 122  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan

US-10-254-446A-122

Query Match 30.8%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
|||  
Db 3 PVLG 6

## RESULT 47

US-09-572-404B-1421  
; Sequence 1421, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1421  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in CACNA13 OR CACNA1 OR CACNA1 at 1707  
; OTHER INFORMATION: and may interact with Sequence 1422 in this patent.  
US-09-572-404B-1421

Query Match 30.8%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
|||  
Db 4 VLGP 7

## RESULT 48

US-09-572-404B-1423  
; Sequence 1423, Application US/09572404B

; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1423  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in CACNA13 OR CACNA1 OR CACNA1 at 170  
; OTHER INFORMATION: and may interact with Sequence 1424 in this patent.  
US-09-572-404B-1423

Query Match 30.8%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
|||  
Db 3 VLGP 6

## RESULT 49

US-09-572-404B-2039  
; Sequence 2039, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2039  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in CNTFR at 109-118 and may interact with Sequ  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-2039

Query Match 30.8%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9  
|||  
Db 3 EPVL 6

## RESULT 50

US-09-572-404B-2945  
; Sequence 2945, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2945  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens

```
;
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4
; OTHER INFORMATION: CORD6 at 52-61 and may interact with Sequence 2946 in this patent
US-09-572-404B-2945

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLGP 11
Db 7 VLGP 10

RESULT 51
US-09-572-404B-3866
; Sequence 3866, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3866
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 394-403 and may interact with S
US-09-572-404B-3866

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 6 LGPV 9

RESULT 52
US-09-572-404B-3867
; Sequence 3867, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3867
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 394-403 and may interact with S
US-09-572-404B-3867

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 6 LGPV 9

RESULT 53
US-09-572-404B-3868
; Sequence 3868, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3868
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 395-404 and may interact with
US-09-572-404B-3868

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 5 LGPV 8

RESULT 54
US-09-572-404B-3869
; Sequence 3869, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3869
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 393-402 and may interact with
US-09-572-404B-3869

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 7 LGPV 10

RESULT 55
US-09-572-404B-3870
; Sequence 3870, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3870
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 393-402 and may interact with
US-09-572-404B-3870

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 7 LGPV 10
```

```
; SEQ ID NO 3870
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in AGL OR GDE at 396-405 and may interact with s
; OTHER INFORMATION: 3871 in this patent.
US-09-572-404B-3870

Query Match          30.8%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGPV 12
Db 4 LGPV 7
|||||

RESULT 56
US-09-793-451-183
; Sequence 183, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-183

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 2 LLYQ 5
|||||

RESULT 57
US-09-793-451-206
; Sequence 206, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
```

```
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-206

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 6 LLYQ 9
|||||

RESULT 58
US-09-793-451-272
; Sequence 272, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-272

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
Db 1 LLYQ 4
|||||

RESULT 59
US-09-793-451-303
; Sequence 303, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
```

```

; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-303

```

```

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LLYQ 5
Db      2 LLYQ 5

```

```

RESULT 60
US-09-793-451-474
; Sequence 474, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-474

```

```

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LLYQ 5
Db      2 LLYQ 5

```

```

RESULT 61
US-09-793-451-502
; Sequence 502, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano

```

```

; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-502

```

```

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LLYQ 5
Db      6 LLYQ 9

```

```

RESULT 62
US-09-793-451-594
; Sequence 594, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-594

```

```

Query Match          30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LLYQ 5
Db      2 LLYQ 5

```

```

RESULT 63

```

US-09-793-451-596  
; Sequence 596, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 596  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-596

Query Match 30.8%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 LLYQ 5  
Db 6 LLYQ 9

RESULT 64  
US-09-793-451-691  
; Sequence 691, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 691  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-691

Query Match 30.8%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 LLYQ 5

Db 5 LLYQ 8  
||||

RESULT 65  
US-10-239-313A-433  
; Sequence 433, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR FILING DATE: FR 00/03711  
; PRIOR APPLICATION NUMBER: 2000-03-23  
; PRIOR FILING DATE: PCT 01/70772  
; PRIOR APPLICATION NUMBER: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 433  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-239-313A-433

Query Match 30.8%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7  
Db 3 YQEP 6  
||||

RESULT 66  
US-10-200-708-132  
; Sequence 132, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR FILING DATE: US/09/351,036  
; PRIOR APPLICATION NUMBER: 1999-07-09  
; PRIOR FILING DATE: 60/092,346  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 132  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-132

Query Match 30.8%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7  
Db 2 YQEP 5  
||||

RESULT 67  
 US-10-200-708-564  
 ; Sequence 564, Application US/10200708  
 ; Publication No. US200301803141  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeGroot, Anne S.  
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
 ; FILE REFERENCE: 17999-001  
 ; CURRENT APPLICATION NUMBER: US/10/200,708  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US/09/351,036  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/092,346  
 ; PRIOR FILING DATE: 1998-07-10  
 ; PRIOR APPLICATION NUMBER: 60/115,145  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 60/130,677  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 564  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-200-708-564

Query Match 30.8%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7  
 ||||  
 Db 6 YQEP 9

RESULT 68  
 US-10-200-708-662  
 ; Sequence 662, Application US/10200708  
 ; Publication No. US200301803141  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeGroot, Anne S.  
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
 ; FILE REFERENCE: 17999-001  
 ; CURRENT APPLICATION NUMBER: US/10/200,708  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US/09/351,036  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/092,346  
 ; PRIOR FILING DATE: 1998-07-10  
 ; PRIOR APPLICATION NUMBER: 60/115,145  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 60/130,677  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 662  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-200-708-662

Query Match 30.8%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YQEP 7  
 ||||  
 Db 2 YQEP 5

RESULT 69

US-10-283-722-183  
 ; Sequence 183, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 183  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-183

Query Match 30.8%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQ 5  
 ||||  
 Db 2 LLYQ 5

RESULT 70  
 US-10-283-722-206  
 ; Sequence 206, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 206  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-206

Query Match 30.8%; Score 4; DB 12; Length 10;

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Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 LLYQ 5
   ||||
Db 6 LLYQ 9

RESULT 71
US-10-283-722-272
; Sequence 272, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-272

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 1 LLYQ 4

RESULT 72
US-10-283-722-303
; Sequence 303, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
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; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-303

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 2 LLYQ 5

RESULT 73
US-10-283-722-474
; Sequence 474, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-474

Query Match 30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5
   ||||
Db 2 LLYQ 5

RESULT 74
US-10-283-722-502
; Sequence 502, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
```



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; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-502

```

```

Query Match      30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LLYQ 5
Db      6 LLYQ 9

```

```

RESULT 75
US-10-283-722-594
; Sequence 594, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-594

```

```

Query Match      30.8%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 LLYQ 5
Db      2 LLYQ 5

```

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Search completed: November 25, 2003, 20:37:08
Job time : 21.8605 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 10.5058 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-32

Perfect score: 13

Sequence: 1 FLLVQEPVLGPR 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	4	US-09-641-803-32
2	7	53.8	7	4	US-09-492-766-12
3	6	46.2	7	4	US-09-641-803-28
4	5	38.5	10	2	US-08-617-929-14
5	5	38.5	13	5	PCT-US94-10257A-16
6	5	38.5	14	2	US-08-617-923-16
7	5	38.5	20	1	US-08-399-646-6
8	5	38.5	20	1	US-08-399-646-10
9	5	38.5	20	1	US-08-607-321-6
10	5	38.5	20	1	US-08-607-321-10
11	5	38.5	20	2	US-08-961-240-6
12	5	38.5	20	2	US-08-961-240-10
13	5	38.5	20	2	US-08-605-501-6
14	5	38.5	20	2	US-08-605-501-10
15	5	38.5	20	5	PCT-US94-10257A-91
16	4	30.8	6	4	US-09-155-613A-48
17	4	30.8	6	4	US-09-465-901-49
18	4	30.8	7	1	US-08-212-433A-46
19	4	30.8	7	3	PCT-US95-03239-46
20	4	30.8	7	5	US-08-159-339A-366
21	4	30.8	9	3	US-08-159-339A-516
22	4	30.8	9	3	US-08-159-339A-517
23	4	30.8	9	3	US-08-660-092-110
24	4	30.8	9	3	US-08-660-092-121
25	4	30.8	9	3	US-08-660-092-125
26	4	30.8	9	3	US-08-704-344-11
27	4	30.8	9	3	US-08-704-344-11

28	4	30.8	9	4	US-09-160-513-110	Sequence 110, App
29	4	30.8	9	4	US-09-160-513-121	Sequence 121, App
30	4	30.8	9	4	US-09-160-513-125	Sequence 125, App
31	4	30.8	9	4	US-09-311-784A-376	Sequence 376, App
32	4	30.8	9	4	US-09-311-784A-382	Sequence 382, App
33	4	30.8	10	1	US-08-203-716-17	Sequence 17, Appl
34	4	30.8	10	1	US-08-440-179-17	Sequence 17, Appl
35	4	30.8	10	3	US-08-159-339A-375	Sequence 375, App
36	4	30.8	10	3	US-09-039-657-17	Sequence 17, Appl
37	4	30.8	10	4	US-08-980-523-1	Sequence 1, Appl
38	4	30.8	10	4	US-08-403-459-18	Sequence 18, Appl
39	4	30.8	11	3	US-08-159-339A-641	Sequence 641, App
40	4	30.8	11	3	US-08-159-339A-1159	Sequence 1159, App
41	4	30.8	11	6	5177197-24	Patent No. 5177197
42	4	30.8	12	1	US-08-260-582-63	Sequence 63, Appl
43	4	30.8	12	2	US-08-442-063A-23	Sequence 23, Appl
44	4	30.8	12	2	US-08-750-856A-9	Sequence 9, Appl
45	4	30.8	12	2	US-08-617-929-17	Sequence 17, Appl
46	4	30.8	12	2	US-08-659-984A-8	Sequence 8, Appl
47	4	30.8	12	3	US-09-075-257A-20	Sequence 20, Appl
48	4	30.8	12	3	US-09-133-341-11	Sequence 11, Appl
49	4	30.8	12	3	US-08-660-531-8	Sequence 8, Appl
50	4	30.8	12	3	US-09-534-639-20	Sequence 20, Appl
51	4	30.8	12	4	US-09-739-852-11	Sequence 11, Appl
52	4	30.8	12	4	US-09-692-170C-11	Sequence 11, Appl
53	4	30.8	12	5	PCT-US95-05471-63	Sequence 63, Appl
54	4	30.8	13	1	US-08-064-400B-16	Sequence 16, Appl
55	4	30.8	13	1	US-08-291-601-1	Sequence 1, Appl
56	4	30.8	13	1	US-08-291-601-2	Sequence 2, Appl
57	4	30.8	13	1	US-08-291-601-3	Sequence 3, Appl
58	4	30.8	13	4	US-09-227-357-439	Sequence 439, App
59	4	30.8	14	1	US-07-956-700B-82	Sequence 82, Appl
60	4	30.8	14	1	US-07-956-700B-92	Sequence 92, Appl
61	4	30.8	14	1	US-08-476-537-82	Sequence 82, Appl
62	4	30.8	14	1	US-08-476-537-92	Sequence 92, Appl
63	4	30.8	14	1	US-08-485-607-82	Sequence 82, Appl
64	4	30.8	14	2	US-08-485-607-92	Sequence 92, Appl
65	4	30.8	14	2	US-08-659-984A-11	Sequence 11, Appl
66	4	30.8	14	2	US-08-475-873-82	Sequence 82, Appl
67	4	30.8	14	2	US-08-475-873-92	Sequence 92, Appl
68	4	30.8	14	3	US-08-660-531-11	Sequence 11, Appl
69	4	30.8	14	4	US-09-433-043B-82	Sequence 82, Appl
70	4	30.8	14	4	US-09-433-043B-92	Sequence 92, Appl
71	4	30.8	15	1	US-07-794-288D-20	Sequence 20, Appl
72	4	30.8	15	1	US-09-501-612A-6	Sequence 6, Appl
73	4	30.8	16	1	US-07-794-288D-19	Sequence 19, Appl
74	4	30.8	16	1	US-08-077-797A-36	Sequence 36, Appl
75	4	30.8	16	3	US-08-602-999A-207	Sequence 207, App
76	4	30.8	16	4	US-09-009-953-36	Sequence 36, Appl
77	4	30.8	16	4	US-09-500-124-207	Sequence 207, App
78	4	30.8	16	5	PCT-US94-01238-36	Sequence 36, Appl
79	4	30.8	17	1	US-07-794-288D-18	Sequence 18, Appl
80	4	30.8	18	1	US-07-794-288D-17	Sequence 17, Appl
81	4	30.8	18	1	US-07-794-288D-214	Sequence 214, App
82	4	30.8	18	1	US-08-244-116B-9	Sequence 9, Appl
83	4	30.8	18	2	US-08-816-105A-11	Sequence 11, Appl
84	4	30.8	18	6	5258287-50	Patent No. 5258287
85	4	30.8	19	1	US-07-794-288D-16	Sequence 16, Appl
86	4	30.8	19	1	US-07-794-288D-126	Sequence 126, App
87	4	30.8	19	1	US-08-507-124-5	Sequence 5, Appl
88	4	30.8	19	3	US-08-928-213B-35	Sequence 35, Appl
89	4	30.8	20	1	US-07-794-288D-15	Sequence 15, Appl
90	4	30.8	20	1	US-07-794-288D-118	Sequence 118, App
91	4	30.8	20	1	US-07-794-288D-125	Sequence 125, App
92	4	30.8	20	1	US-08-484-635-140	Sequence 140, App
93	4	30.8	20	2	US-08-484-635-140	Sequence 140, App
94	4	30.8	20	2	US-08-617-929-1	Sequence 1, Appl
95	4	30.8	20	2	US-08-827-570-140	Sequence 140, App
96	4	30.8	20	3	US-09-247-527-17	Sequence 17, Appl
97	4	30.8	20	5	PCT-US94-10257A-90	Sequence 90, Appl
98	3	23.1	4	1	US-07-657-769B-14	Sequence 14, Appl
99	3	23.1	4	1	US-07-657-769B-54	Sequence 54, Appl
100	3	23.1	4	1	US-07-729-353-7	Sequence 7, Appl

## ALIGNMENTS

```
RESULT 1
US-09-641-803-32
; Sequence 32, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-32

Query Match          100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQEPVLGPVR 13
Db 1 FLLYQEPVLGPVR 13

RESULT 2
US-09-492-766-12
; Sequence 12, Application US/09492766
; Patent No. 6506732
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"
; CURRENT APPLICATION NUMBER: US/09/492,766
; CURRENT FILING DATE: 2000-01-27
; EARLIER APPLICATION NUMBER: 60/117,661
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
; OTHER INFORMATION: proteins
US-09-492-766-12

Query Match          53.8%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQEPVL 9
Db 1 LYQEPVL 7

RESULT 3
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US-09-641-803-28
; Sequence 28, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-28

Query Match          46.2%; Score 6; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLYQE 6
Db 2 FLLYQE 7

RESULT 4
US-08-617-929-14
; Sequence 14, Application US/08617929
; Patent No. 5895771
; GENERAL INFORMATION:
; APPLICANT: KUMAZAWA, Toshiaki
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
; TITLE OF INVENTION: IMMUNOASSAY
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
```

```

; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-14

Query Match 38.5%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQE 6
Db 3 LLYQE 7

RESULT 5
PCT-US94-10257A-16
; Sequence 16, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-16

Query Match 38.5%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLGP 11
Db 7 PVLGP 11

```

```

Db 8 PVLGP 12

RESULT 6
US-08-617-929-16
; Sequence 16, Application US/08617929
; Patent No. 5885771
; GENERAL INFORMATION:
; APPLICANT: KUMAZAWA, Toshiaki
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
; TITLE OF INVENTION: IMMUNOASSAY
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-16

Query Match 38.5%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLYQE 6
Db 10 LLYQE 14

RESULT 7
US-08-399-646-6
; Sequence 6, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE

```

NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,646  
FILING DATE: 07-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA=5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-399-646-6

Query Match 38.5%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
DB 11 PVLGP 15

RESULT 8  
US-08-399-646-10  
Sequence 10, Application US/08399646  
Patent No. 5556781  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuo  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,646  
FILING DATE: 07-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA=5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-399-646-10

Query Match 38.5%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
DB 1 PVLGP 5

RESULT 9  
US-08-607-321-6  
Sequence 6, Application US/08607321  
Patent No. 5716813  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuo  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,321  
FILING DATE: 26-FEB-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA=5  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-607-321-6

Query Match 38.5%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
Db 11 PVLGP 15

## RESULT 10

US-08-607-321-10  
Sequence 10, Application US/08607321  
Patent No. 5715813

## GENERAL INFORMATION:

APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,321  
FILING DATE: 26-FEB-1996  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA=5

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-607-321-10

Query Match 38.5%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
Db 1 PVLGP 5

## RESULT 11

US-08-961-240-6  
Sequence 6, Application US/08961240  
Patent No. 5830715

## GENERAL INFORMATION:

APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,240  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA=5

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid

## STRANDEDNESS: single

## TOPOLOGY: linear

## MOLECULE TYPE: peptide

## US-08-961-240-6

Query Match 38.5%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
Db 1 PVLGP 5

Db 11 PVLGP 15

# RESULT 12

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US-08-961-240-10
; Sequence 10, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,240
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-961-240-10

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Query Match 38.5%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
 Db 1 PVLGP 5

# RESULT 13

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US-08-605-501-6
; Sequence 6, Application US/08605501
; Patent No. 5834287
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko

```

```

; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,501
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-605-501-6

```

Query Match 38.5%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11  
 Db 11 PVLGP 15

# RESULT 14

```

US-08-605-501-10
; Sequence 10, Application US/08605501
; Patent No. 5834287
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,501
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,646
; FILING DATE: 07-MAR-1995
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA=5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-605-501-10

Query Match 38.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 1 PVLGP 5

RESULT 15
PCT-US94-10257A-91
; Sequence 91, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824

```

```

; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US94-10257A-91

Query Match 38.5%; Score 5; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLGP 11
DB 7 PVLGP 11

RESULT 16
US-09-155-613A-48
; Sequence 48, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-09-155-613A-48

Query Match 30.8%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LGPV 12
DB 1 LGPV 4

RESULT 17
US-09-465-901-49
; Sequence 49, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries

```



```

; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-49

```

```

Query Match          30.8%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 FLYY 4
        ||||
Db      2 FLYY 5

```

```

RESULT 18
US-08-212-433A-46
; Sequence 46, Application US/08212433A
; Patent No. 5538897
; GENERAL INFORMATION:
; APPLICANT: Yates, III, John R.
; APPLICANT: Eng, James K.
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
; TITLE OF INVENTION: DATABASES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,433A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Hughes, Richard L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: 16336-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-433A-46

```

```

Query Match          30.8%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 FVLG 10

```

```

Db      3 FVLG 6
        ||||
US-08-716-256-46
; Sequence 46, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,256
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-256-46

```

```

Query Match          30.8%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 FVLG 10
        ||||
Db      3 FVLG 6

```

```

RESULT 20
PCT-US95-03239-46
; Sequence 46, Application PC/TUS9503239
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:

```



```

Db      5 YQEP 8
|||||
RESULT 23
US-08-159-339A-517
; Sequence 517, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 517:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-517

Query Match      30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 YQEP 7
|||||
Db      2 YQEP 5

RESULT 24
US-08-660-092-110
; Sequence 110, Application US/08660092
; Patent No. 6207160
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; TITLE OF INVENTION:
; TITLE OF INVENTION: PATHOLOGIES
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

Query Match      30.8%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      7 PVLG 10
|||||
Db      3 PVLG 6

RESULT 25
US-08-660-092-121
; Sequence 121, Application US/08660092
; Patent No. 6207160
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION:
; TITLE OF INVENTION: PATHOLOGIES
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/660,092  
FILING DATE: 06-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Park, Freddie K.  
REGISTRATION NUMBER: 35,636  
REFERENCE/DOCKET NUMBER: 25231-20061.20  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-660-092-121

Query Match 30.8%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
Db 3 PVLG 6

RESULT 26  
US-08-660-092-125  
Sequence 125, Application US/08660092  
Patent No. 6207160  
GENERAL INFORMATION:  
APPLICANT: Victoria, Edward J.  
APPLICANT: Marquis, David M.  
APPLICANT: Jones, David S.  
APPLICANT: Yu, Lin  
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
TITLE OF INVENTION: THREEOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED  
TITLE OF INVENTION: PATHOLOGIES  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,092  
FILING DATE: 06-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Park, Freddie K.  
REGISTRATION NUMBER: 35,636  
REFERENCE/DOCKET NUMBER: 25231-20061.20  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 125:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-660-092-125

Query Match 30.8%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
Db 4 VLGP 7

RESULT 27  
US-08-704-344-11  
Sequence 11, Application US/08704344  
Patent No. 6218363  
GENERAL INFORMATION:  
APPLICANT: BASERGA, Renato L.  
APPLICANT: RESNICOFF, Mariana  
APPLICANT: HUANG, Ziwei  
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE and DORR LLP  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,344  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, Henry N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.196  
TELEPHONE: (202) 942-8459  
TELEFAX: (202) 942-8484  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-704-344-11

Query Match 30.8%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13  
Db 5 GPVR 8

RESULT 28  
US-09-160-513-110  
Sequence 110, Application US/09160513  
Patent No. 6410775  
GENERAL INFORMATION:  
APPLICANT: Victoria, Edward J.  
APPLICANT: Marquis, David M.  
APPLICANT: Jones, David S.  
APPLICANT: Yu, Lin

```
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-110

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 29
US-09-160-513-121
; Sequence 121, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 30
US-09-160-513-125
; Sequence 125, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLG 11
```

```
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-121

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
DB 3 PVLG 6

RESULT 30
US-09-160-513-125
; Sequence 125, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-160-513-125

Query Match 30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVLG 11
```

```
Db          4 VLGP 7
|||||
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
US-09-311-784A-376
; Sequence 376, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 376
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1036 (peptide 1069.60)
US-09-311-784A-376

Query Match          30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 YOEP 7
|||||
Db          2 YOEP 5
|||||

RESULT 32
US-09-311-784A-382
; Sequence 382, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 382
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV pol 1033 (peptide 1069.59)
US-09-311-784A-382

Query Match          30.8%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 YOEP 7
|||||
Db          2 YOEP 5
|||||

RESULT 33
US-08-203-716-17
; Sequence 17, Application US/08203716
; Patent No. 5416013
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,716
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/750,644
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L. 25011
; REGISTRATION NUMBER: IMMUNEX2108
; REFERENCE/DOCKET NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165460
; TELEX: 9102211206
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-203-716-17

Query Match          30.8%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          10 GPVR 13
|||||
Db          6 GPVR 9
|||||

RESULT 34
US-08-440-179-17
; Sequence 17, Application US/08440179
; Patent No. 5756465
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
```

ADDRESSEE: MILNAMOW  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,179  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,644  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-17

Query Match 30.8%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13  
Db 6 GPVR 9

RESULT 35  
US-08-159-339A-375  
Sequence 375, Application US/08159339A  
Patent No. 6037135  
GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 375:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-375

Query Match 30.8%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
Db 2 LLYQ 5

RESULT 36  
US-09-039-657-17  
Sequence 17, Application US/09039657  
Patent No. 6136787  
GENERAL INFORMATION:  
APPLICANT: Black, Roy A.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRADEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-17

Query Match 30.8%; Score 4; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVR 13  
 ||||  
 Db 6 GPVR 9

## RESULT 37

US-08-980-523-1  
 ; Sequence 1, Application US/08980523  
 ; Patent No. 6310181  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kouhara, Haruhiko  
 ; APPLICANT: Spivak-kroizman, Taly  
 ; APPLICANT: Lax, Irit  
 ; APPLICANT: Schlensing, Joseph  
 ; TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND  
 ; TITLE OF INVENTION: RELATED PRODUCTS AND METHODS  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/980,523  
 FILING DATE: December 1, 1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/21851  
 FILING DATE: December 1, 1997

APPLICATION NUMBER: 60/032,093  
 FILING DATE: December 3, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/045  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-980-523-1

Query Match 30.8%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
 ||||  
 Db 2 VLGP 5

## RESULT 38

US-08-403-459-18

; Sequence 18, Application US/08403459  
 ; Patent No. 6514942  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ioannides, Constantin G.  
 ; APPLICANT: Fisk, Bryan A.  
 ; APPLICANT: Ioannides, Maria G.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
 ; TITLE OF INVENTION: T-LYMPHOCYTES  
 ; NUMBER OF SEQUENCES: 68  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: United States of America  
 ; ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/403,459  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: UTSC:390/KIT

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-403-459-18

Query Match 30.8%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLYQ 5  
 ||||  
 Db 2 LLYQ 5

## RESULT 39

US-08-159-339A-641  
 ; Sequence 641, Application US/08159339A  
 ; Patent No. 6037135

## GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.  
 APPLICANT: Grey, Howard M.  
 APPLICANT: Sette, Alessandro  
 APPLICANT: Celis, Esteban  
 TITLE OF INVENTION: HLA Binding peptides and Their  
 TITLE OF INVENTION: Uses  
 NUMBER OF SEQUENCES: 1254  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible



```

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 641:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-641

Query Match 30.8%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YOEP 7
Db 6 YOEP 9

RESULT 40
US-08-159-339A-1159
; Sequence 1159, Application US/08/159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396

```

```

; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1159

Query Match 30.8%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YOEP 7
Db 3 YOEP 6

RESULT 41
5177197-24
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUO;OLOFSSON, ANDERS;MOREN, ANITA;
; WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
; LENA;HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO:24:
; LENGTH: 11
5177197-24

Query Match 30.8%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10
Db 5 PVLG 8

RESULT 42
US-08-260-582-63
; Sequence 63, Application US/08260582
; Patent No. 5635182
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M.
; APPLICANT: Lu, Zhijian
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/260,582
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-260-582-63

Query Match 30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLPV 11
Db 3 VLPV 6

RESULT 43
US-08-442-063A-23
; Sequence 23, Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHBACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE
; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MULLEN, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,063A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1454
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-442-063A-23

Query Match 30.8%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LGPV 12
Db 5 LGPV 8

RESULT 44
US-08-750-856A-9
; Sequence 9, Application US/08750856A
; Patent No. 5858672
; GENERAL INFORMATION:
; APPLICANT: SONIGO, PIERRE
; APPLICANT: PANCINO, GIANFRANCO
; APPLICANT: PETERHANS, ERNST
; APPLICANT: BERTONI, GIUSEPPE
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND CORRESPONDING
; TITLE OF INVENTION: PEPTIDE FRAGMENTS FROM THE CAPRINE ARTHRITIS-ENCEPHALITIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,856A
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION INFORMATION:
; APPLICATION NUMBER: FR 94/07933
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 917-052-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-750-856A-9

Query Match 30.8%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LYQE 6
Db 9 LYQE 12
```

RESULT 45  
 US-08-617-929-17  
 ; Sequence 17, Application US/08617929  
 ; Patent No. 5885771  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KUMAZAWA, Toshiaki  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND  
 ; TITLE OF INVENTION: IMMUNOSSAY  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/617,929  
 ; FILING DATE: 24-APR-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/JP94/01823  
 ; FILING DATE: 28-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 6/207695  
 ; FILING DATE: 31-AUG-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 5/272864  
 ; FILING DATE: 29-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SAXE, Bernhard D.  
 ; REGISTRATION NUMBER: 28,665  
 ; REFERENCE/DOCKET NUMBER: 77384/109  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-617-929-17  
 Query Match 30.8%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Qy 2 LLYQ 5  
 Db 9 LLYQ 12

RESULT 46  
 US-08-659-984A-8  
 ; Sequence 8, Application US/08659984A  
 ; Patent No. 5942400  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, John P.  
 ; APPLICANT: Sinha, Sukanto  
 ; APPLICANT: Jacobson-Croak, Kirsten L.  
 ; TITLE OF INVENTION: Assays for Detecting Beta-Secretase  
 ; TITLE OF INVENTION: Inhibition  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/659,984A  
 ; FILING DATE: 07-JUN-1996  
 ; CLASSIFICATION: 436  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/485,152  
 ; FILING DATE: 07-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Heslin, James M.  
 ; REGISTRATION NUMBER: 29,541  
 ; REFERENCE/DOCKET NUMBER: 15270-002810US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-659-984A-8  
 Query Match 30.8%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 Qy 6 EPVL 9  
 Db 6 EPVL 9

RESULT 47  
 US-09-075-257A-20  
 ; Sequence 20, Application US/09075257A  
 ; Patent No. 6074645  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIAMOND, DON JEFFREY  
 ; APPLICANT: YORK, JOANNE  
 ; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES  
 ; TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BART G. NEWMAN  
 ; STREET: 555 13TH STREET, NW SUITE 701E  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/075,257A  
 ; FILING DATE: 11-MAY-1998  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 09/021,298  
 ; FILING DATE: 10-FEB-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/950,064

;  
; FILING DATE: 14-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/747,488  
; FILING DATE: 12-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NEWLAND, BART G  
; REGISTRATION NUMBER: 31,282  
; REFERENCE/DOCKET NUMBER: 1954-112CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-075-257A-20

Query Match 30.8%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VLPG 11  
Db 2 VLPG 5

## RESULT 48

US-09-133-341-11  
; Sequence 11, Application US/09133341A  
; Patent No. 6162440  
; GENERAL INFORMATION:  
; APPLICANT: Hayward, Diane S.  
; APPLICANT: Ling, Paul D.  
; TITLE OF INVENTION: EBNA2 PEPTIDES AND METHODS OF USING SAME  
; FILE REFERENCE: 87512  
; CURRENT APPLICATION NUMBER: US/09/133,341A  
; CURRENT FILING DATE: 1998-08-13  
; EARLIER APPLICATION NUMBER: WO 97US2243  
; EARLIER FILING DATE: 1997-02-12  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Epstein-Barr Virus  
; US-09-133-341-11

Query Match 30.8%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PVLG 10  
Db 8 PVLG 11

## RESULT 49

US-08-660-531-8  
; Sequence 8, Application US/08660531  
; Patent No. 6221645  
; GENERAL INFORMATION:  
; APPLICANT: Chrysier, Susanna M.S.  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Keim, Pamela S.  
; APPLICANT: Anderson, John P.  
; TITLE OF INVENTION: Beta-Secretase  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

;  
; STREET: Two Embarcadero Ctr., 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,531  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/480,498  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/DOCKET NUMBER: 15270-002210US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-660-531-8

Query Match 30.8%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EPVL 9  
Db 6 EPVL 9

## RESULT 50

US-09-534-639-20  
; Sequence 20, Application US/09534639  
; Patent No. 6251399  
; GENERAL INFORMATION:  
; APPLICANT: Diamond, Don J  
; APPLICANT: York, Joanne  
; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN  
; TITLE OF INVENTION: CYTOMEGALOVIRUS  
; FILE REFERENCE: 1954-343  
; CURRENT APPLICATION NUMBER: US/09/534,639  
; CURRENT FILING DATE: 2000-03-27  
; EARLIER APPLICATION NUMBER: 09/075,257  
; EARLIER FILING DATE: 1998-05-11  
; EARLIER APPLICATION NUMBER: 09/021,298  
; EARLIER FILING DATE: 1998-02-10  
; EARLIER APPLICATION NUMBER: 08/950,064  
; EARLIER FILING DATE: 1997-10-14  
; EARLIER APPLICATION NUMBER: 08/747,488  
; EARLIER FILING DATE: 1996-11-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Human Cytomegalovirus  
; US-09-534-639-20

Query Match 30.8%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
 Db 2 VLGP 5

RESULT 51  
 US-09-739-852-11  
 ; Sequence 11, Application US/09739852  
 ; Patent No. 6495144  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hayward, Diane S.  
 ; APPLICANT: Ling, Paul D.  
 ; TITLE OF INVENTION: ENNA2 PEPTIDES AND METHODS OF USING SAME  
 ; FILE REFERENCE: 87512  
 ; CURRENT APPLICATION NUMBER: US/09/739,852  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: 09/133,341  
 ; PRIOR FILING DATE: 2000-12-18  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Epstein-Barr Virus  
 US-09-739-852-11

Query Match 30.8%; Score 4; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PVLG 10  
 Db 8 PVLG 11

RESULT 52  
 US-09-692-170C-11  
 ; Sequence 11, Application US/09692170C  
 ; Patent No. 6562345  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Diamond, Don J.  
 ; TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS  
 ; FILE REFERENCE: 1954-346  
 ; CURRENT APPLICATION NUMBER: US/09/692,170C  
 ; CURRENT FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: US 09/534,639  
 ; PRIOR FILING DATE: 2000-03-27  
 ; PRIOR APPLICATION NUMBER: US 09/075,257  
 ; PRIOR FILING DATE: 1998-05-11  
 ; PRIOR APPLICATION NUMBER: US 09/021,298  
 ; PRIOR FILING DATE: 1998-02-10  
 ; PRIOR APPLICATION NUMBER: US 08/950,064  
 ; PRIOR FILING DATE: 1997-10-14  
 ; PRIOR APPLICATION NUMBER: US 08/747,488  
 ; PRIOR FILING DATE: 1996-11-12  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 11  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Human cytomegalovirus  
 US-09-692-170C-11

Query Match 30.8%; Score 4; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
 Db 2 VLGP 5

RESULT 53  
 PCT-US95-05471-63  
 ; Sequence 63, Application PC/TUS9505471  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS  
 ; NUMBER OF SEQUENCES: 76  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/05471  
 ; INFORMATION FOR SEQ ID NO: 63:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 PCT-US95-05471-63

Query Match 30.8%; Score 4; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLGP 11  
 Db 3 VLGP 6

RESULT 54  
 US-08-064-400B-16  
 ; Sequence 16, Application US/08064400B  
 ; Patent No. 5559028  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E.  
 ; TITLE OF INVENTION: Regulation of Antigen Presentation  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: ME  
 ; COUNTRY: USA  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/064,400B  
 ; FILING DATE: May 19, 1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Farrell, Kevin M.  
 ; REGISTRATION NUMBER: 35,505  
 ; REFERENCE/DOCKET NUMBER: REH93-01  
 ; TELEPHONE: 207-363-0558  
 ; TELEFAX: 207-363-0528  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-064-400B-16

Query Match 30.8%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6  
|||  
DB 1 LYQE 4

RESULT 55  
US-08-291-601-1  
; Sequence 1, Application US/08291601  
; Patent No. 5679527  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: Maine  
; COUNTRY: US  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,601  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9401M  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-291-601-1

Query Match 30.8%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6  
|||  
DB 1 LYQE 4

RESULT 56  
US-08-291-601-2  
; Sequence 2, Application US/08291601  
; Patent No. 5679527  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: Maine  
; COUNTRY: US  
; ZIP: 03911

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,601  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9401M  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-291-601-2

Query Match 30.8%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 LYQE 6  
|||  
DB 1 LYQE 4

RESULT 57  
US-08-291-601-3  
; Sequence 3, Application US/08291601  
; Patent No. 5679527  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: Maine  
; COUNTRY: US  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,601  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9401M  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-291-601-3

Query Match 30.8%; Score 4; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 3 LYQE 6  
|||  
Db 1 LYQE 4

RESULT 58  
US-09-227-357-439  
; Sequence 439, Application US/09227357  
; Patent No. 6342581  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: P2010P1  
; CURRENT APPLICATION NUMBER: US/09/227,357  
; CURRENT FILING DATE: 1999-01-08  
; EARLIER APPLICATION NUMBER: PCT/US98/13684  
; EARLIER FILING DATE: 1998-07-07  
; EARLIER APPLICATION NUMBER: 60/051,926  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,793  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,925  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,929  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,803  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,732  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,931  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,932  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,916  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,930  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,918  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,920  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,733  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,795  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,919  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,928  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/055,722  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,723  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,948  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,949  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,953  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,950  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,947  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,964  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/056,360  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,684  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,984

; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,954  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/058,785  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,664  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,660  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,661  
; EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 439  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-227-357-439

Query Match 30.8%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 FILLY 4  
|||  
Db 7 FILLY 10

RESULT 59  
US-07-956-700B-82  
; Sequence 82, Application US/07956700B  
; Patent No. 5539092  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Arnold, White & Durkee  
; STREET: 321 No. 5539092th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/956,700B  
; FILING DATE: 19921002  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5539092thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-07-956-700B-82

Query Match 30.8%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

Qy      4 YOEP 7
Db      1 YOEP 4

RESULT 60
US-07-956-700B-92
; Sequence 92, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956.700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-07-956-700B-92

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YOEP 7
Db      1 YOEP 4

RESULT 61
US-08-476-537-82
; Sequence 82, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-07-956-700B-92

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YOEP 7
Db      1 YOEP 4

RESULT 62
US-08-476-537-92
; Sequence 92, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

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; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YOEP 7
Db      1 YOEP 4

RESULT 62
US-08-476-537-92
; Sequence 92, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-476-537-82

```



```

; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-92

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YQEP 7
Db      1 YQEP 4

```

```

RESULT 63
US-08-485-607-82
; Sequence 82, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-82

```

```

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 YQEP 7
Db      1 YQEP 4

```

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RESULT 64
US-08-485-607-92
; Sequence 92, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:

```

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; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-485-607-92

```

```

Query Match      30.8%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      4 YQEP 7
Db      1 YQEP 4

```

```

RESULT 65
US-08-659-984A-11
; Sequence 11, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659.984A

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; FILING DATE: 07-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,152  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/DOCKET NUMBER: 15270-002810US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 14  
; OTHER INFORMATION: /note="C-terminal Lys is  
; OTHER INFORMATION: amidated."  
US-08-659-984A-11

Query Match 30.8%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 BPVL 9  
Db 8 BPVL 11

RESULT 66  
US-08-475-879-82  
; Sequence 92, Application US/08475879  
; Patent No. 5972644  
; Patent No. 5972644 5786170  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5972644 5786170th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,879  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/956,700  
; FILING DATE: 10/21/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5972644 5786170thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-08-475-879-82

Query Match 30.8%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YQEP 7  
Db 1 YQEP 4

RESULT 67  
US-08-475-879-92  
; Sequence 92, Application US/08475879  
; Patent No. 5972644  
; Patent No. 5972644 5786170  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5972644 5786170th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,879  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/956,700  
; FILING DATE: 10/21/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5972644 5786170thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-08-475-879-92

Query Match 30.8%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 YQEP 7  
Db 1 YQEP 4

RESULT 68  
US-08-660-531-11  
; Sequence 11, Application US/08660531

; Patent No. 6221645  
; GENERAL INFORMATION:  
; APPLICANT: Chrysler, Susanna M.S.  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Keim, Pamela S.  
; APPLICANT: Anderson, John P.  
; TITLE OF INVENTION: Beta-Secretase  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Ctr., 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,531  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/480,498  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heslin, James M.  
; REGISTRATION NUMBER: 29,541  
; REFERENCE/DOCKET NUMBER: 15270-002210US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: one-of(14)  
; OTHER INFORMATION: /note= "C-terminal Lys is  
; OTHER INFORMATION: amidated."  
US-08-660-531-11

Query Match 30.8%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred.No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPVL 9  
Db 8 EPVL 11

RESULT 69  
US-09-433-043B-82  
; Sequence 82, Application US/09433043B  
; Patent No. 6399342  
; GENERAL INFORMATION:  
; APPLICANT: HASELKORN, ROBERT  
; APPLICANT: GORNICKI, PIOTR  
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
; FILE REFERENCE: ARCD:338US  
; CURRENT APPLICATION NUMBER: US/09/433,043B  
; CURRENT FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/475,879  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/956,700  
; PRIOR FILING DATE: 1992-10-02  
; NUMBER OF SEQ ID NOS: 128

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-433-043B-82

Query Match 30.8%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred.No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7  
Db 1 YQEP 4

RESULT 70  
US-09-433-043B-92  
; Sequence 92, Application US/09433043B  
; Patent No. 6399342  
; GENERAL INFORMATION:  
; APPLICANT: HASELKORN, ROBERT  
; APPLICANT: GORNICKI, PIOTR  
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
; FILE REFERENCE: ARCD:338US  
; CURRENT APPLICATION NUMBER: US/09/433,043B  
; CURRENT FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 08/475,879  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/956,700  
; PRIOR FILING DATE: 1992-10-02  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-433-043B-92

Query Match 30.8%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred.No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YQEP 7  
Db 1 YQEP 4

RESULT 71  
US-07-794-288D-20  
; Sequence 20, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700

```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; MEDIUM TYPE: Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA: US/07/794,288D
; APPLICATION NUMBER: 07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duft, Bradford, J.
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 193/153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
; US-07-794-288D-20

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Query Match 30.8%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 9 LGPV 12
Db 1 LGPV 4

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```

RESULT 72
US-09-501-612A-6
; Sequence 6, Application US/09501612A
; Patent No. 6544765
; GENERAL INFORMATION:
; APPLICANT: Hjoert, Carsten M.
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells
; FILE REFERENCE: 5789.200-US
; CURRENT APPLICATION NUMBER: US/09/501.612A
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-501-612A-6

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Query Match 30.8%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 5 QEPV 8
Db 4 QEPV 7

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RESULT 73
US-07-794-288D-19
; Sequence 19, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S. L. GAFTA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEAUMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; MEDIUM TYPE: Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duft, Bradford, J.
; REGISTRATION NUMBER: 32,219
; REFERENCE/DOCKET NUMBER: 193/153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
; US-07-794-288D-19

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Query Match 30.8%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 9 LGPV 12
Db 2 LGPV 5

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RESULT 74
US-08-077-797A-36
; Sequence 36, Application US/08077797A
; Patent No. 5679548
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Rosenblum, Jonathan
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL

```

;/ TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF  
;/ NUMBER OF SEQUENCES: 65  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: The Scripps Research Institute, Office of  
;/ ADDRESSEE: Patent Counsel  
;/ STREET: 10666 No. 5679548th Torrey Pines Road, TPC8  
;/ CITY: La Jolla  
;/ STATE: CA  
;/ COUNTRY: USA  
;/ ZIP: 92037  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/077,797A  
;/ FILING DATE: 14-JUN-1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/012,566  
;/ FILING DATE: 02-FEB-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Fitting, Thomas  
;/ REGISTRATION NUMBER: 34,163  
;/ REFERENCE/DOCKET NUMBER: SCRI276P  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 619-554-2937  
;/ TELEFAX: 619-554-6312  
;/ INFORMATION FOR SEQ ID NO: 36:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 16 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ FRAGMENT TYPE: internal  
;/ US-08-077-797A-36

Query Match 30.8%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 GPCR 13  
Db 1 GPCR 4

RESULT 75  
US-08-602-999A-207  
;/ Sequence 207, Application US/08602999A  
;/ Patent No. 6184205  
;/ GENERAL INFORMATION:  
;/ APPLICANT: SPARKS, Andrew B.  
;/ APPLICANT: KAY, Brian K.  
;/ APPLICANT: THORN, Judith M.  
;/ APPLICANT: QUILLIAM, Lawrence A.  
;/ APPLICANT: DER, Channing J.  
;/ APPLICANT: FOWLKES, Dana M.  
;/ APPLICANT: RIDER, James E.  
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
;/ TITLE OF INVENTION: ISOLATING AND USING SAME  
;/ NUMBER OF SEQUENCES: 467  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: Patent In Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/602,999A  
;/ FILING DATE: 16-FEB-1996  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Misrock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 1101-202  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 790-9090  
;/ TELEFAX: (212) 869-9741/8864  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 207:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 16 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: peptide  
;/ US-08-602-999A-207

Query Match 30.8%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 VLGP 11  
Db 3 VLGP 6

Search completed: November 25, 2003, 20:30:08  
Job time : 11.5058 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 2.05814 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:\*\*

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	100.0	8	2	Ac1348
2	3	100.0	8	2	A43976
3	3	100.0	8	2	B43976
4	3	100.0	9	2	A61230
5	3	100.0	10	2	C39398
6	3	100.0	11	2	S23364
7	3	100.0	12	2	B80228
8	3	100.0	15	2	C36198
9	3	100.0	16	2	A24099
10	3	100.0	16	2	PH1770
11	3	100.0	17	2	B48943
12	3	100.0	18	2	C32537
13	3	100.0	20	2	A53875
14	2	66.7	6	2	A43129
15	2	66.7	7	2	S71867
16	2	66.7	7	2	B44787
17	2	66.7	7	2	A34026
18	2	66.7	7	2	PN0649
19	2	66.7	7	2	PC2370
20	2	66.7	8	2	A28004
21	2	66.7	8	2	S08995
22	2	66.7	8	2	S10596
23	2	66.7	8	2	A49823
24	2	66.7	8	2	A44960
25	2	66.7	8	2	S15422
26	2	66.7	8	2	S55310
27	2	66.7	8	2	A58641
28	2	66.7	8	2	A58620
29	2	66.7	8	2	PL0184
30	2	66.7	8	2	A05169
31	2	66.7	8	2	S21663
32	2	66.7	8	2	A39892
33	2	66.7	9	2	AL4683
34	2	66.7	9	2	AKLQIM
35	2	66.7	9	2	S19523
36	2	66.7	9	2	A57444
37	2	66.7	9	2	B57444
38	2	66.7	9	2	S78420
39	2	66.7	10	2	A60421
40	2	66.7	10	2	S08997
41	2	66.7	10	2	S08998
42	2	66.7	10	2	A26381
43	2	66.7	10	2	C60788
44	2	66.7	10	2	A60787
45	2	66.7	10	2	A60787
46	2	66.7	10	2	A60527
47	2	66.7	10	2	G60527
48	2	66.7	10	2	G60589
49	2	66.7	10	2	I60527
50	2	66.7	10	2	S42282
51	2	66.7	10	2	F44644
52	2	66.7	10	2	B39308
53	2	66.7	10	2	S38304
54	2	66.7	10	2	PN0165
55	2	66.7	10	2	C44787
56	2	66.7	10	2	C39111
57	2	66.7	10	2	PT0289
58	2	66.7	10	2	PT0284
59	2	66.7	10	2	S36849
60	2	66.7	10	2	A47364
61	2	66.7	10	2	S53789
62	2	66.7	11	2	I41138
63	2	66.7	11	2	S35490
64	2	66.7	11	2	S71304
65	2	66.7	11	2	PN0664
66	2	66.7	12	2	A29169
67	2	66.7	12	2	I64829
68	2	66.7	12	2	S29859
69	2	66.7	12	2	B58502
70	2	66.7	12	2	S71034
71	2	66.7	12	2	B61497
72	2	66.7	12	2	A56878
73	2	66.7	12	2	F61308
74	2	66.7	12	2	PH1567
75	2	66.7	12	2	PH1454
76	2	66.7	12	2	S23168
77	2	66.7	12	4	PC2123
78	2	66.7	13	1	NTKXAS
79	2	66.7	13	1	G44644
80	2	66.7	13	2	S29488
81	2	66.7	13	2	B28810
82	2	66.7	13	2	G56046
83	2	66.7	13	2	PH0787
84	2	66.7	13	2	S54344
85	2	66.7	13	4	I70076
86	2	66.7	14	1	QMVHP2
87	2	66.7	14	2	C60414
88	2	66.7	14	2	B60842
89	2	66.7	14	2	A60840
90	2	66.7	14	2	S00172
91	2	66.7	14	2	A42473
92	2	66.7	14	2	A41589
93	2	66.7	14	2	B56919
94	2	66.7	14	2	PA0007
95	2	66.7	14	2	F61497
96	2	66.7	14	2	PS0252
97	2	66.7	14	2	S29486
98	2	66.7	14	2	I56493
99	2	66.7	14	2	S41601
100	2	66.7	14	2	

neuropeptide M-I -  
neuropeptide - flo  
P element, P cytot  
aspartate transami  
locustamycininhibi  
orf AB protein - S  
neuropeptide Grb-A  
neuropeptide Grb-A  
gene NF2 protein -  
ribosomal protein  
hypertrehalosemic  
hypertrehalosemic  
hypertrehalosemic  
hypertrehalosemic  
sperm-activating p  
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sperm-activating p  
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sperm-activating p  
sperm-activating p  
parasporal crystal  
neurotoxin-associa  
glycine reductase  
lectin GNL1 alpha  
triester-phosphate i  
caillifMRamide 12  
Ig heavy chain C r  
Ig heavy chain CRD  
Ig heavy chain CRD  
Ig heavy chain v r  
placental lactogen  
neuropeptide pec-H  
acetyl ornithine d  
type II site-speci  
amine oxidase (cop  
dystrophin-associa  
phospholipase A2 (  
gene HEXA protein  
gene p10 protein -  
43.2K bile stone p  
potB protein - Sal  
seed protein ws-17  
light yellow cell  
hemocyanin chain 5  
cerebrin 28 - huma  
T-cell receptor al  
Z protein - Guinea  
aminotransferase c  
alpha-conotoxin SI  
neurotoxin-associa  
GTP-binding protei  
glutathione transf  
urinary tract ston  
T-cell receptor al  
glyceraldhyde-3-p  
glycophorin B/glyc  
mastoparan C - Eur  
somatostatin - sli  
somatostatin I - c  
somatostatin I - E  
somatostatin I - s  
ermK leader peptid  
25K elastin-bindin  
PS I complex subun  
lectin B1 - Psopho  
seed protein ws-21  
16K protein 5404 -  
GTP-binding protei  
endothelial growth  
interferon alpha r

## ALIGNMENTS

## RESULT 1

A61348  
red pigment-concentrating hormone - northern shrimp  
N/Alternate names: blanching hormone  
C/Species: Pandanus borealis (northern shrimp)  
C/Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C/Accession: A61348; S07139  
R/Fernlund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A/Reference number: A61348; MUID:7228738; PMID:5041363  
A/Accession: A61348  
A/Molecule type: protein  
A/Residues: 1-8 <PER1>  
R/Fernlund, P.  
Biochim. Biophys. Acta 371, 304-311, 1974  
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandanus borealis  
A/Reference number: S07139; MUID:75054965; PMID:4433569  
A/Accession: S07139  
A/Molecule type: protein  
A/Residues: E', 2-8 <FER2>  
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-  
zed pigment-containing cells.  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami  
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 2

A43976  
hypertrehalosemic hormone - yellow mealworm  
C/Species: Tenebrio molitor (yellow mealworm)  
C/Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
C/Accession: A43976  
R/Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be  
A/Reference number: A43976; MUID:90341081; PMID:2381871  
A/Accession: A43976  
A/Molecule type: protein  
A/Residues: 1-8 <GAE>  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 3

B43976  
hypertrehalosemic hormone - beetle (Zophobas rugipes)  
C/Species: Zophobas rugipes  
C/Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999

C/Accession: B43976  
R/Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be  
A/Reference number: A43976; MUID:90341081; PMID:2381871  
A/Accession: B43976  
A/Molecule type: protein  
A/Residues: 1-8 <GAE>  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 100.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 4

A61230  
calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)  
N/Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin  
C/Species: Rana pipiens (northern leopard frog)  
C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Jul-1999  
C/Accession: A61230  
R/McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.  
Circ. Res. 69, 344-359, 1991  
A/Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular  
rdium.  
A/Reference number: A61230; MUID:91316784; PMID:1860177  
A/Accession: A61230  
A/Molecule type: protein  
A/Residues: 1-9 <MCL>  
C/Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding prote  
C/Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to  
C/Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in v  
C/Superfamily: calsequestrin  
C/Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 100.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

## RESULT 5

C39398  
Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 20-Mar-1998  
C/Accession: C39398  
R/Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
A/Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1  
A/Reference number: A39398; MUID:91219496; PMID:2023945  
A/Accession: C39398  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <CAM>

Query Match 100.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 LNF 3  
|||

Db . 6 LNF 8

## RESULT 6

S23364  
T-cell receptor alpha chain J region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S23364  
R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman  
Eur. J. Immunol. 21, 2749-2754, 1991  
A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu  
A:Reference number: S23364; MUID:92037820; PMID:1657615  
A:Accession: S23364  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-11 <PLU>  
A:Cross-references: EMBL:X58164  
C:Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 9 LNF 11

## RESULT 7

B60228  
Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)  
N:Alternate names: membrane protein B29  
C:Species: Mus musculus (house mouse)  
C>Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Mar-1998  
C:Accession: B60228; B39398  
R:Hombach, J.; Lottspeich, F.; Reth, M.  
Eur. J. Immunol. 20, 2795-2799, 1990  
A:Title: Identification of the genes encoding the IgM-alpha and Ig-beta components of th  
A:Reference number: A60228; MUID:91099432; PMID:2269334  
A:Accession: B60228  
A:Molecule type: protein  
A:Residues: 1-12 <HOM>  
R:Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
A:Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g  
A:Reference number: A39398; MUID:91219496; PMID:2023945  
A:Accession: B39398  
A:Molecule type: protein  
A:Residues: 'XX', 3-10 <CAM>  
C:Keywords: membrane protein

Query Match 100.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 6 LNF 8

## RESULT 8

C36198  
T-cell receptor beta chain J region - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 21-Jul-2000  
C:Accession: C36198  
R:Tjoelker, L.W.; Carlson, L.M.; Lee, K.; Lahti, J.; McCormack, W.T.; Leiden, J.M.; Chen  
Proc. Natl. Acad. Sci. U.S.A. 87, 7856-7860, 1990  
A:Title: Evolutionary conservation of antigen recognition: the chicken T-cell receptor b  
A:Reference number: A36198; MUID:91045896; PMID:2236002  
A:Accession: C36198  
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <TJO>

A:Cross-references: EMBL:M37799; NID:g212737; PIDN:AAA62754.1; PID:g555475

C:Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 4 LNF 6

## RESULT 9

A24099  
crystal protein, 28K - Bacillus thuringiensis (fragment)  
C:Species: Bacillus thuringiensis  
C>Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Jun-2000  
C:Accession: A24099  
R:Chetukhina, G.G.; Zalunin, I.A.; Kostina, L.I.; Bormatova, M.E.; Klepikova, F.S.; Kl  
FEBS Lett. 190, 345-348, 1985  
A:Title: Structural features of crystal-forming proteins produced by Bacillus thuringie  
A:Reference number: A91347  
A:Accession: A24099  
A:Molecule type: protein  
A:Residues: 1-16 <CHE>

Query Match 100.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 4 LNF 6

## RESULT 10

PH1770  
T cell receptor alpha chain V region (clone 2V alpha 23-1) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1770  
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057

A:Accession: PH1770

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-16 <POR>

Query Match 100.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

Db 13 LNF 15

## RESULT 11

B48943  
phage antigenic determinant (clone pOA79) - phage phi-197 (fragment)  
C:Species: phage phi-197  
C>Date: 13-Aug-1997 #sequence\_revision 19-Dec-1997 #text\_change 19-Dec-1997  
C:Accession: B48943  
R:Schouler, C.; Bouet, C.; Ritzenhaler, P.; Drouet, X.; Mata, M.  
Appl. Environ. Microbiol. 58, 2479-2484, 1992  
A:Title: Characterization of Lactococcus lactis phage antigens.  
A:Reference number: A48943; MUID:92384563; PMID:1514794  
A:Contents: Lactococcus lactis



A;Accession: B48943  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-17 <SCH>

A;Note: sequence modified after extraction from NCBI backbone  
A;Note: sequence extracted from NCBI backbone (NCBIN:114551)

Query Match 100.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
DB 5 LNF 7

## RESULT 12

C32537  
T-cell receptor alpha chain J region (HAJTL17) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 30-May-1997  
C;Accession: C32537

R;Kimura, N.; Toyonaga, B.; Yoshikai, Y.; Du, R.P.; Mak, T.W.  
Eur. J. Immunol. 17, 375-383, 1987

A;Title: Sequences and repertoire of the human T cell receptor alpha- and beta-chain variable regions  
A;Reference number: A91263; MUID:87190670; PMID:3494611

A;Accession: C32537

A;Molecule type: mRNA

A;Residues: 1-18 <KIM>

A;Cross-references: GB:M27378

C;Keywords: T-cell receptor

Query Match 100.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
DB 2 LNF 4

## RESULT 13

A53875  
creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)  
C;Species: Oncorhynchus kisutch (coho salmon)  
C;Date: 26-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1997  
C;Accession: A53875

R;White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.

J. Protein Chem. 11, 489-494, 1992

A;Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB islet  
A;Reference number: A53875; MUID:93080727; PMID:1449598

A;Accession: A53875

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-20 <WHI>

A;Experimental source: Brockmann body, principal islet

A;Note: sequence extracted from NCBI backbone (NCBIP:120599)

C;Superfamily: creatine kinase; creatine kinase repeat homology

C;Keywords: phosphotransferase

Query Match 100.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
DB 11 LNF 13

## RESULT 14

A43129  
neuropeptide GNFRamide - tapeworm (Moniezia expansa)  
C;Species: Moniezia expansa

C;Date: 10-Nov-1997 #sequence\_revision 14-Nov-1997 #text\_change 14-Nov-1997  
C;Accession: A43129  
R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.  
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993  
A;Title: GNFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep  
A;Reference number: A43129; MUID:93312289; PMID:8323531

A;Accession: A43129

A;Molecule type: protein

A;Residues: 1-6 <MAU>

C;Keywords: amidated carboxyl end; neuropeptide

F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 66.7%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
|||  
DB 2 NF 3

## RESULT 15

S71867

glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)

N;Alternate names: glutathione S-transferase class alpha 5

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999

C;Accession: S71867

R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospr.

A;Reference number: S71864; MUID:96332484; PMID:8760377

A;Accession: S71867

A;Molecule type: protein

A;Residues: 1-7 <ROU>

C;Comment: At least five species-independent classes of cytosolic glutathione transferases

s mitochondrial form are known.

C;Complex: dimer

C;Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a

A;Pathway: detoxification; xenobiotics metabolism

A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 66.7%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
|||  
DB 3 LN 4

## RESULT 16

B44787

calliphoramide 11 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999

C;Accession: B44787

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorp,

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (des

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: B44787

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <DUV>

C;Keywords: amidated carboxyl end; neuropeptide

F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0

QY 2 NF 3  
||  
3 NF 4

Db

RESULT 17  
A34026  
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)  
C:Species: Torpedo californica (Pacific electric ray)  
C>Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 08-Nov-1996  
C:Accession: A34026  
R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedwick, T.; Low, M.G.; Taylor, S.S.; T  
J. Biol. Chem. 263, 1140-1145, 1988  
A:Title: Divergence in primary structure between the molecular forms of acetylcholinester  
A:Reference number: A34026; PMID:88087239; PMID:3335534  
A:Accession: A34026  
A:Molecule type: protein  
A:Residues: 1-7 <GIB>  
C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 66.7%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
2 LN 3

Db

RESULT 18  
PN0649  
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)  
C:Species: Bacillus sp.  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 03-Jun-2002  
C:Accession: PN0649  
R:Kim, C.H.; Choi, H.I.; Lee, D.S.  
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993  
A:Title: Purification and biochemical properties of an alkaline pullulanase from alkalop  
A:Reference number: PN0649; PMID:94080025; PMID:7764261  
A:Accession: PN0649  
A:Molecule type: protein  
A:Residues: 1-7 <KIM>  
C:Comment: This enzyme is used together with glucoamylase to improve the efficiency of st  
nent in high maltose syrups.  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 66.7%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
2 LN 3

Db

RESULT 19  
PC2370  
probable H<sup>+</sup>-transporting two-sector ATPase (EC 3.6.3.14) alpha chain [similarity] - Baci  
N:Alternate names: unidentified 78K protein  
C:Species: Bacillus cereus  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 03-Jun-2002  
C:Accession: PC2370  
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.  
Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
A:Title: Identification of DNA-binding proteins changed after induction of sporulation i  
A:Reference number: PC2369; PMID:95218265; PMID:7766022  
A:Accession: PC2370  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MAS>

C:Keywords: ATP biosynthesis; hydrolase

Query Match 66.7%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
3 LN 4

Db

RESULT 20  
A28004  
adipokinetic hormone G - two-spotted cricket  
N:Alternate names: AKI-G  
C:Species: Gryllus bimaculatus (two-spotted cricket)  
C>Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 24-Oct-1997  
C:Accession: A28004  
R:Gaede, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pept  
A:Reference number: A28004; PMID:88106553; PMID:3426616  
A:Accession: A28004  
A:Molecule type: protein  
A:Residues: 1-8 <GAE>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we hav  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
||  
3 NF 4

Db

RESULT 21  
S08995  
hypertrehalosemic hormone I - oriental cockroach  
N:Alternate names: Pea-CAH-I  
C:Species: Blatta orientalis (oriental cockroach)  
C>Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: S08995  
R:Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corp  
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombai  
A:Reference number: S08995; PMID:90253659; PMID:2340112  
A:Accession: S08995  
A:Molecule type: protein  
A:Residues: 1-8 <GAE>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we hav  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
||  
3 NF 4

Db

RESULT 22  
S10596  
adipokinetic hormone - pond skimmer

C;Species: Libellula auripennis  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 14-Nov-1997  
 C;Accession: S10596  
 R;Gaede, G.  
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990  
 A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone  
 A;Reference number: S10596; MUID:90359055; PMID:2390213  
 A;Accession: S10596  
 A;Molecule type: protein  
 A;Residues: 1-8 <BIO>  
 C;Comment: This peptide has both adipokinetic and hypertrhalosemic activities.  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 23  
 A49823  
 adipokinetic hormone I - American cockroach  
 N;Alternate names: periplanetin CC-1  
 C;Species: Periplaneta americana (American cockroach)  
 C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C;Accession: A49823  
 R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp  
 A;Reference number: A49823; MUID:84298179; PMID:6591205  
 A;Accession: A49823  
 A;Molecule type: protein  
 A;Residues: 1-8 <SCA>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 24  
 A44960  
 neuropeptide Led-CC-I - Colorado potato beetle  
 C;Species: Leptinotarsa decemlineata (Colorado potato beetle)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: A44960  
 R;Gaede, G.; Kellner, R.  
 Peptides 10, 1287-1289, 1989  
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and  
 A;Reference number: A44960; MUID:90160053; PMID:2576128  
 A;Accession: A44960  
 A;Molecule type: protein  
 A;Residues: 1-8 <GAE>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 25  
 S15422  
 adipokinetic hormone - cockchafer  
 C;Species: Melolontha melolontha (cockchafer)  
 C;Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
 C;Accession: S15422  
 R;Gaede, G.  
 Biochem. J. 275, 671-677, 1991  
 A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red-p  
 A;Reference number: S15422; MUID:91248100; PMID:2039445  
 A;Accession: S15422  
 A;Molecule type: protein  
 A;Residues: 1-8 <BIO>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 2 LN 3

RESULT 26  
 S55310  
 adipokinetic hormone - damselfly (Pseudagrion inconspicuum)  
 N;Alternate names: Psi-AKH  
 C;Species: Pseudagrion inconspicuum  
 C;Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-May-1999  
 C;Accession: S55310  
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
 Biochem. J. 302, 539-543, 1994  
 A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspi  
 A;Reference number: S55310; MUID:94379987; PMID:8093008  
 A;Accession: S55310  
 A;Molecule type: protein  
 A;Residues: 1-8 <JAN>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 27  
 A58641  
 adipokinetic hormone - dor beetle  
 C;Species: Geotrupes stercorosus (dor beetle)  
 C;Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
 C;Accession: A58641  
 R;Gaede, G.  
 Biochem. J. 275, 671-677, 1991  
 A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red-p  
 A;Reference number: S15422; MUID:91248100; PMID:2039445  
 A;Accession: A58641

A;Molecule type: protein

A;Residues: 1-8 <BIO>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

||

2 LN 3

RESULT 28

A58620

adipokinetic hormone - damselfly (*Ischnura senegalensis*)

C;Species: *Ischnura senegalensis*

C;Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-May-1999

C;Accession: A58620

R;Janssens, M.P.E.; Kellner, R.; Gaede, G.

Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies *Pseudagrion inconspicu*

A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: A58620

A;Molecule type: protein

A;Residues: 1-8 <JAN>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

||

3 NF 4

RESULT 29

PL0184

capsid protein VP-1 - murine poliovirus (fragment)

C;Species: murine poliovirus, Theiler's encephalomyelitis virus

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995

C;Accession: PL0184

R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.

J. Exp. Med. 170, 2037-2049, 1989

A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicity

A;Reference number: PL0184; MUID:90063468; PMID:2479706

A;Accession: PL0184

A;Molecule type: genomic RNA

A;Residues: 1-8 <ZUR>

C;Keywords: capsid protein

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

||

6 NF 7

RESULT 30

A05169

neuropeptide M-I - American cockroach

C;Species: *Periplaneta americana* (American cockroach)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993

C;Accession: A05169

R;Witten, J.L.; Schafer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment ma

A;Reference number: A90118; MUID:85046530; PMID:6548628

A;Accession: A05169

A;Molecule type: protein

A;Residues: 1-8 <WIT>

C;Keywords: neuropeptide

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

||

3 NF 4

RESULT 31

S21663

neuropeptide - flower beetle (*Pachnoda marginata*)

C;Species: *Pachnoda marginata*

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S21663

R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 373, 133-142, 1992

A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of vari

ectrometry.

A;Reference number: S21663; MUID:92265187; PMID:1586453

A;Accession: S21663

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <GAE>

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

||

2 LN 3

RESULT 32

A39892

P element, P cytotype-determining - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Feb-1997

C;Accession: A39892

R;Nitasaka, E.; Mukai, T.; Yamazaki, T.

Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987

A;Title: Repressor of P elements in *Drosophila melanogaster*: cytotype determination by

A;Reference number: A39892

A;Accession: A39892

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 <NIT>

C;Genetics:

A;Gene: *FlyBase:P-element*

A;Cross-references: *FlyBase:FBgn0003055*

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

||

4 NF 5

RESULT 33

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (frag

N;Alternate names: aspartate aminotransferase, mitochondrial  
C;Species: Gallus gallus (chicken)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
C;Accession: A14683  
R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
FEBS Lett. 108, 98-102, 1979  
A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
A;Reference number: A14683; MUID:80092116; PMID:520566  
A;Accession: A14683  
A;Molecule type: protein  
A;Residues: 1-8 <WIL>  
C;Keywords: aminotransferase; mitochondrion

Query Match 66.7%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
||  
Db 4 NF 5

RESULT 34  
AKLQIM  
locustamyo-inhibiting peptide - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 20-Mar-1998  
C;Accession: A60065  
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.  
Regul. Pept. 36, 111-119, 1991  
A;Title: Isolation, identification and synthesis of locustamyo-inhibiting peptide (LOM-MI)  
A;Reference number: A60065; MUID:92179466; PMID:1796179  
A;Accession: A60065  
A;Molecule type: protein  
A;Residues: 1-9 <SCH>  
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and c  
C;Superfamily: locustamyo-inhibiting peptide  
C;Keywords: amidated carboxyl end; hormone  
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 66.7%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 5 LN 6

RESULT 35  
S19523  
orf AB protein - Shigella dysenteriae insertion sequence IS911  
C;Species: Shigella dysenteriae  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1998  
C;Accession: S19523  
R;Polard, P.; Prere, M.F.; Chandler, M.; Fayet, O.  
J. Mol. Biol. 222, 465-477, 1991  
A;Title: Programmed translational frameshifting and initiation at an AUU codon in gene e  
A;Reference number: S19523; MUID:92085268; PMID:1660923  
A;Accession: S19523  
A;Molecule type: protein  
A;Residues: 1-9 <POL>  
C;Genetics:  
A;Mobile element: insertion sequence IS911

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
||  
Db 5 NF 6

RESULT 36  
A57444  
neuropeptide Grb-AST B1 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 26-Jan-1996  
C;Accession: A57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: A57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 5 LN 6

RESULT 37  
B57444  
neuropeptide Grb-AST B2 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 26-Jan-1996  
C;Accession: B57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: B57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 5 LN 6

RESULT 38  
I54379  
gene NF2 protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C;Accession: I54379  
R;Arai, E.; Ikeuchi, T.; Nakamura, Y.  
Hum. Mol. Genet. 3, 937-939, 1994  
A;Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a pa  
A;Reference number: I54379; MUID:95038750; PMID:7951241  
A;Accession: I54379  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <RES>  
A;Cross-references: GB:S75841; NID:G861532; PIDN:AAI4190.1; PID:G4261890  
C;Genetics:  
A;Gene: GDB:NF2  
A;Cross-references: GDB:120232; OMIM:101000  
A;Map position: 22q12.2-22q12.2

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 1 LN 2

## RESULT 39

S08997  
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
C:Accession: S78420  
R:Goldschmidt-Reisin, S.; Graack, H.R.  
submitted to the Protein Sequence Database, February 1998  
A:Reference number: S78411  
A:Accession: S78420  
A:Molecule type: protein  
A:Residues: 1-9 <GOL>  
A:Note: the protein is designated as mitochondrial ribosomal protein L41  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 1 LN 2

## RESULT 40

A60421  
hypertrehalosemic hormone - German cockroach  
N:Alternate names: Bld-HrTH  
C:Species: Blattella germanica (German cockroach)  
C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 31-Oct-1997  
C:Accession: A60421; S09137  
R:Veenstra, J.A.; Camps, F.  
Neuropeptides 15, 107-109, 1990  
A:Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica  
A:Reference number: A60421; MUID:91179584; PMID:2080017  
A:Accession: A60421  
A:Molecule type: protein  
A:Residues: 1-10 <VEE>  
R:Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A:Reference number: S08995; MUID:90253659; PMID:2340112  
A:Accession: S09137  
A:Molecule type: protein  
A:Residues: 1-10 <GAE>  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 3 NF 4

## RESULT 41

S08997  
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)  
C:Species: Gromphadorina portentosa  
C:Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 24-Oct-1997  
C:Accession: S08997  
R:Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A:Reference number: S08995; MUID:90253659; PMID:2340112  
A:Accession: S08997  
A:Molecule type: protein  
A:Residues: 1-10 <GAE>  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 3 NF 4

RESULT 42  
S08998  
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach  
C:Species: Leucophaea maderae (Madeira cockroach)  
C:Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 24-Oct-1997  
C:Accession: S08998  
R:Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A:Reference number: S08995; MUID:90253659; PMID:2340112  
A:Accession: S08998  
A:Molecule type: protein  
A:Residues: 1-10 <GAE>  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 3 NF 4

## RESULT 43

A26381  
hypertrehalosemic hormone - gray cockroach  
C:Species: Nauphoeta cinerea (gray cockroach)  
C:Date: 31-Mar-1988 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: A26381  
R:Gaede, G.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 141, 774-781, 1986  
A:Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiaca of the cockroach Nauphoeta cinerea  
A:Reference number: A26381; MUID:87100208; PMID:3801028  
A:Accession: A26381  
A:Molecule type: protein  
A:Residues: 1-10 <GAD>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used the sequence of the amidated form  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||

Db 3 NF 4

## RESULT 44

C60788  
 sperm-activating peptide (speract) - sea urchin (Pseudocentrotus depressus)  
 C;Species: Pseudocentrotus depressus  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 18-Aug-2000  
 C;Accession: C60788  
 R;Suzuki, N.; Kajiuura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus depressus  
 A;Reference number: A60787; PMID:88242184; PMID:3378407  
 A;Accession: C60788  
 A;Molecule type: protein  
 A;Residues: 1-10 <SUZ>  
 C;Comment: This oligopeptide from egg jelly is one of several from this species, all of which show some, but not absolute, species restriction.  
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2

||

Db 4 LN 5

## RESULT 45

C60787  
 sperm-activating peptide (Ser-3,10 speract) - sea urchin (Hemicentrotus pulcherrimus)  
 C;Species: Hemicentrotus pulcherrimus  
 C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 18-Aug-2000  
 C;Accession: C60787  
 R;Suzuki, N.; Kajiuura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus pulcherrimus  
 A;Reference number: A60787; PMID:88242184; PMID:3378407  
 A;Accession: C60787  
 A;Molecule type: protein  
 A;Residues: 1-10 <SUZ>  
 C;Comment: This oligopeptide from egg jelly is one of several from this species, all of which show some, but not absolute, species restriction.  
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2

||

Db 4 LN 5

## RESULT 46

A60787  
 sperm-activating peptide (speract) - sea urchin (Hemicentrotus pulcherrimus)  
 C;Species: Hemicentrotus pulcherrimus  
 C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 18-Aug-2000  
 C;Accession: A60787  
 R;Suzuki, N.; Kajiuura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus pulcherrimus  
 A;Reference number: A60787; PMID:88242184; PMID:3378407  
 A;Accession: A60787  
 A;Molecule type: protein  
 A;Residues: 1-10 <SUZ>  
 C;Comment: This oligopeptide from egg jelly is one of several from this species, all of which show some, but not absolute, species restriction.  
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2

||

Db 4 LN 5

## RESULT 47

A60527  
 sperm-activating peptide (Br-Phe-2 SAP-I) - sea urchin (Tripneustes gratilla)  
 N;Alternate names: SAP-a; speract; TG-1; TG-9  
 C;Species: Tripneustes gratilla  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C;Accession: A60527; A39572; A60973; H60527; H60572  
 R;Yoshino, K.I.; Kajiuura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related p  
 otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.  
 A;Reference number: A60527

A;Accession: A60527  
 A;Molecule type: protein  
 A;Residues: 1-10 <YOS>  
 R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; S  
 Biochemistry 30, 6203-6209, 1991  
 A;Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associat  
 A;Reference number: A39572; PMID:91283461; PMID:2059627

A;Accession: A39572  
 A;Molecule type: protein  
 A;Residues: 1-10 <YOS>  
 R;Takao, T.; Yoshino, K.; Suzuki, N.; Shimonishi, Y.  
 Biomed. Environ. Mass Spectrom. 19, 705-712, 1990  
 A;Title: Analysis of post-translational modifications of proteins by accurate mass meas  
 A;Reference number: A60973; PMID:91167743; PMID:2076468  
 A;Accession: A60973  
 A;Molecule type: protein  
 A;Residues: 1-10 <TRAX>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: bromine  
 F;2;Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2

||

Db 4 LN 5

## RESULT 48

G60527  
 sperm-activating peptide (Br-Phe-2, Asn-3 SAP-I) - sea urchin (Tripneustes gratilla)  
 N;Alternate names: speract homolog TG-2; TG-10  
 N;Contains: sperm-activating peptide (Asn-3 SAP-I)  
 C;Species: Tripneustes gratilla  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C;Accession: G60527; B39572; A40051; B60527  
 R;Yoshino, K.I.; Kajiuura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A;Title: A halogenated amino acid-containing sperm activating peptide and its related p  
 otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.  
 A;Reference number: A60527

A;Accession: G60527  
 A;Molecule type: protein  
 A;Residues: 1-10 <YOS>  
 A;Note: this peptide was found both with both phenylalanine and bromophenylalanine  
 R;Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; S  
 Biochemistry 30, 6203-6209, 1991  
 A;Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associat  
 A;Reference number: A39572; PMID:91283461; PMID:2059627  
 A;Accession: B39572  
 A;Molecule type: protein

Mol. Gen. Genet. 242, 365-368, 1994  
A;Title: Use of an operon fusion to induce expression and crystallisation of a Bacillus  
A;Reference number: S42282; MUID:94150472; PMID:7906381  
C;Keywords: bromine  
F;2/Modified site: 2'-bromophenylalanine or 4'-bromophenylalanine (Phe) (partial) #status

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
4 LN 5

Db

RESULT 49  
G60589  
sperm-activating peptide (Tyr-2, Asn-3, Asp-7,10, Arg-8, Ile-9 SAP-I) - Echinomera math  
C;Species: Echinomera mathaei  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C;Accession: G60589  
R;Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe  
otus nudus, Echinomera mathaei and Heterocentrotus mammillatus.  
A;Reference number: A60527  
A;Accession: G60589  
A;Molecule type: protein  
A;Residues: 1-10 <YOS>  
C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
4 LN 5

Db

RESULT 50  
I60527  
sperm-activating peptide (SAP-I) - sea urchin (Strongylocentrotus nudus)  
N;Alternate names: speract  
C;Species: Strongylocentrotus nudus  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C;Accession: I60527  
R;Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe  
otus nudus, Echinomera mathaei and Heterocentrotus mammillatus.  
A;Reference number: A60527  
A;Accession: I60527  
A;Molecule type: protein  
A;Residues: 1-10 <YOS>  
C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
4 LN 5

Db

RESULT 51  
S42282  
parasporal crystal protein cryIIB - Bacillus thuringiensis plasmid (fragment)  
N;Alternate names: delta-endotoxin  
C;Species: Bacillus thuringiensis  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 24-Jul-1998  
C;Accession: S42282  
R;Crickmore, N.; Wheeler, V.C.; Ellar, D.J.

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
4 LN 5

Db

RESULT 52  
F44644  
neurotoxin-associated protein type B Hn+ 35K chain, band 3a - Clostridium botulinum (fr  
C;Species: Clostridium botulinum  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: F44644  
R;Somers, E.; DasGupta, B.R.  
J. Protein Chem. 10, 415-425, 1991  
A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h  
A;Reference number: A44644; MUID:92143938; PMID:1781887  
A;Contents: type B  
A;Accession: F44644  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SOM>  
A;Note: sequence extracted from NCBI backbone (NCBIP:83787)  
C;Keywords: hemagglutinin

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
5 LN 6

Db

RESULT 53  
B39308  
glycine reductase (EC 1.4.99.-) sulphydryl protein C, beta chain - Clostridium sticklan  
C;Species: Clostridium sticklandii  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997  
C;Accession: B39308  
R;Stadtman, T.C.; Davis, J.N.  
J. Biol. Chem. 266, 22147-22153, 1991  
A;Title: Glycine reductase protein C. Properties and characterization of its role in th  
A;Reference number: A39308; MUID:92042141; PMID:1939235  
A;Accession: B39308  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <STA>  
C;Function:  
A;Description: glycine reductase complex catalyzes the reductive deamination of glycine  
C;Keywords: ATP; oxido-reductase

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
3 LN 4

Db



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Db          ||
           6 NF 7

RESULT 54
S38304
lectin GNLI alpha chain - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C>Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:Accession: S38304
R;Kamemura, K.; Furuichi, Y.; Umekawa, H.; Takahashi, T.
Biochim. Biophys. Acta 1158, 181-188, 1993
A:Title: Purification and characterization of novel lectins from Great Northern bean, Phaseolus communis
A:Reference number: S38304; MUID:94002183; PMID:8399319
A:Accession: S38304
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <KAM>

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
Db      7 NF 8

RESULT 55
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PN0160
A:Accession: PN0165
A:Molecule type: protein
A:Residues: 1-10 <FUK>
A:Experimental source: strain M-1-1
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
Db      9 NF 10

RESULT 56
C44787
Calliphora vomitoria 12 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: C44787
R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe, R.;
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (deserpin)
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: C44787
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <DUV>
A:Keywords: amidated carboxyl end; neuropeptide
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3

Db      2 NF 3

RESULT 57
C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C:Species: Eptatretus stoutii (Pacific hagfish)
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity to immunoglobulin heavy chain
A:Reference number: A39111; MUID:91156684; PMID:2000382
A:Accession: C39111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAR>
C:Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      1 LN 2

RESULT 58
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0289
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      2 LN 3

RESULT 59
PT0284
Ig heavy chain CRD3 region (clone 4-97) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0284
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0284
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match          66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
Db      2 NF 3

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```
Qy      2 NF 3
      ||
Db      7 NF 8

RESULT 60
S36849
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36849
R:Jacob, J.; Kelsoe, G.
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A:Reference number: S25024
A:Accession: S36849
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-10 <JAC>
A:Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:gl333861
C:Keywords: heterotetramer; immunoglobulin

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      9 NF 10

RESULT 61
A47364
Placental lactogen-I precursor - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: A47364
R:Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A:Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro
A:Reference number: A47364; MUID:93225959; PMID:8469232
A:Accession: A47364
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <RES>
A:Cross-references: GB:S58124; NID:G299449

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      5 LN 6

RESULT 62
S53789
neuropeptide Pec-HrTH - Platypus capensis
C:Species: Platypus capensis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S53789
R:Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A:Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalo
A:Reference number: S53789; MUID:95225985; PMID:7710694
A:Accession: S53789
A:Molecule type: protein
A:Residues: 1-10 <GAE>
C:Keywords: blocked amino end; blocked carboxyl end

Query Match      66.7%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      5 LN 6

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      10 NF 11

RESULT 65
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999
C:Accession: S71304
R:Frederick, I.; Tanaka, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asar
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the my
A:Reference number: S71303; MUID:96203933; PMID:8620862
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
```

```
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      3 NF 4

RESULT 63
I41138
acetyl ornithine deacetylase (argE) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 08-Oct-1999
C:Accession: I41138
R:Charlier, D.; Piette, J.; Glansdorff, N.
Nucleic Acids Res. 10, 5935-5948, 1982
A:Title: 183 can function as a mobile promoter in e.coli.
A:Reference number: I41137; MUID:83064529; PMID:16292860
A:Accession: I41138
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:J01589; NID:G145346; PIDN:AAA23485.1; PID:G551788

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LN 2
      ||
Db      2 LN 3

RESULT 64
S35490
type II site-specific deoxyribonuclease (EC 3.1.21.4) PvuI - Proteus vulgaris
A:Alternate names: PvuI endonuclease
C:Species: Proteus vulgaris
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S35490
R:Smith, M.D.; Longo, M.; Gerard, G.F.; Chatterjee, D.K.
Nucleic Acids Res. 20, 5743-5747, 1992
A:Title: Cloning and characterization of genes for the PvuI restriction and modificati
A:Reference number: S35490; MUID:93087186; PMID:1454536
A:Accession: S35490
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-11 <SMI>
A:Cross-references: EMBL:L04163; NID:G150901; PIDN:AAA25660.1; PID:G150902
C:Keywords: hydrolase

Query Match      66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 NF 3
      ||
Db      10 NF 11

RESULT 65
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999
C:Accession: S71304
R:Frederick, I.; Tanaka, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asar
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the my
A:Reference number: S71303; MUID:96203933; PMID:8620862
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
```

C;Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinone

Query Match 66.7%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 6 LN 7

## RESULT 66

PN0664

dystrophin-associated glycoprotein A3a-III - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0664

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A;Reference number: PN0662; MUID: 94156881; PMID: 8113213

A;Accession: PN0664

A;Molecule type: protein

A;Residues: 1-11 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 66.7%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 4 LN 5

## RESULT 67

A29169

phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 31-Oct-1997

C;Accession: A29169

R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.

Eur. J. Biochem. 53, 91-97, 1975

A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.

A;Reference number: A94661

A;Accession: A29169

A;Molecule type: protein

A;Residues: 1-12 <DUT>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 4 LN 5

## RESULT 68

I64829

gene HEXA protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I64829

R;Boles, D.J.; Proia, R.L.

Am. J. Hum. Genet. 56, 716-724, 1995

A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs

A;Reference number: I51882; MUID: 95193801; PMID: 7887427

A;Accession: I64829

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-12 <RES>

A;Cross-references: GB:S76984; NID:G912781; PIDN:AADI4243.1; PID:G4261943

C;Genetics:

A;Gene: GDB:HEXA

A;Cross-references: GDB:120040; OMIM:272800

A;Map position: 15q23-15q24

C;Superfamily: beta-hexosaminidase

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 4 LN 5

## RESULT 69

S29859

gene p10 protein - Choristoneura fumiferana nuclear polyhedrosis virus (fragment)

C;Species: Choristoneura fumiferana nuclear polyhedrosis virus, CFMNPV

C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

C;Accession: S29859

R;Hill, J.E.; Kuzio, J.; Wilson, J.A.; MacKinnon, E.A.; Faulkner, P.

Biochim. Biophys. Acta 1172, 187-189, 1993

A;Title: Nucleotide sequence of the p74 gene of a baculovirus pathogenic to the spruce

A;Reference number: S29849; MUID: 93176808; PMID: 8439559

A;Accession: S29859

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-12 <HIL>

A;Experimental source: strain Ireland

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 5 LN 6

## RESULT 70

E58502

43.2K bile stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C;Accession: E58502

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: E58502

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <BIN>

A;Experimental source: human bile with stones

A;Note: a secondary sequence DVKIGVAGS was also found

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
||  
Db 5 LN 6

## RESULT 71

S71034

potB protein - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999  
C;Accession: S71034  
R;Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, F.; Finlay, B.B.  
Mol. Microbiol. 20, 151-164, 1996  
A;Title: Identification of a Salmonella virulence gene required for formation of filamen  
A;Reference number: S71033; MUID:97014378; PMID:8861213  
A;Accession: S71034  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-12 <STE>  
A;Cross-references: EMBL:U51867; NID:gl272352; PIDN:AAA97466.1; PID:gl272353  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996  
C;Genetics:  
A;Gene: potB

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 3 LN 4

RESULT 72  
B61497  
seed protein ws-17 - winged bean (fragment)  
C;Species: Psophocarpus tetragonolobus (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: B61497  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electroblooded from two-dim  
A;Reference number: A61491; MUID:89351606; PMID:2765119  
A;Accession: B61497  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <HIR>  
C;Keywords: seed

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 6 NF 7

RESULT 73  
A56878  
light yellow cell peptide A - great pond snail  
N;Contains: light yellow cell peptide B  
C;Species: Lymnaea stagnalis (great pond snail)  
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Aug-1999  
C;Accession: A56878  
R;Hoek, R.M.; Li, K.W.; van Minnen, J.; Geraerts, W.P.  
Brain Res. Mol. Brain Res. 16, 71-74, 1992  
A;Title: Chemical characterization of a novel peptide from the neuroendocrine light yell  
A;Reference number: A56878; MUID:93095719; PMID:1334202  
A;Accession: A56878  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <HOE>  
A;Cross-references: PIDN:AB24433.1; PID:G261422  
A;Note: sequence extracted from NCBI backbone (NCBIP:120090)  
C;Keywords: neuropeptide  
F;1-12/Product: light yellow cell peptide A #status experimental <YCPA>  
F;12-12/Product: light yellow cell peptide B #status experimental <YCPB>

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LN 2  
||  
Db 9 LN 10  
RESULT 74  
F61308  
hemocyanin chain 5B - Sahara scorpion (fragment)  
C;Species: Androctonus australis (Sahara scorpion)  
C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C;Accession: F61308  
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 289-291, 1979  
A;Title: Structural characterization of seven different subunits in Androctonus austral  
A;Reference number: A61308; MUID:80047238; PMID:499512  
A;Accession: F61308  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <JOL>

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 2 LN 3

RESULT 75  
PH1567  
cerebrin 28 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C;Accession: PH1567  
R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.  
J. Neurochem. 61, 533-540, 1993  
A;Title: Micropurification of two human cerebrospinal fluid proteins by high performanc  
A;Reference number: PH1566; MUID:93329419; PMID:8336140  
A;Accession: PH1567  
A;Molecule type: protein  
A;Residues: 1-12 <LEO>

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 11 NF 12

Search completed: November 25, 2003, 19:36:14  
Job time : 2.05814 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 1.06395 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	100.0	8	1	HTF TENMO
2	3	100.0	8	1	RPCX PANBO
3	2	66.7	6	1	FARP MONEX
4	2	66.7	7	1	FAR1 MACRS
5	2	66.7	7	1	FAR1 PROCL
6	2	66.7	7	1	FAR2 PROCL
7	2	66.7	7	1	FAR4 PANRE
8	2	66.7	7	1	FARB CALVO
9	2	66.7	8	1	AKHG GRBYI
10	2	66.7	8	1	AKH LIBAU
11	2	66.7	8	1	AKH MELML
12	2	66.7	8	1	ALL1 CYDPO
13	2	66.7	8	1	ALL6 CYDPO
14	2	66.7	8	1	FAR1 PANRE
15	2	66.7	8	1	FAR1 PENMO
16	2	66.7	8	1	FAR2 MACRS
17	2	66.7	8	1	FAR3 HOMAM
18	2	66.7	8	1	FAR4 HOMAM
19	2	66.7	8	1	HTF1 PERAM
20	2	66.7	9	1	FAR2 PANRE
21	2	66.7	9	1	FAR3 MACRS
22	2	66.7	9	1	FAR6 MACRS
23	2	66.7	9	1	FAR8 MACRS
24	2	66.7	9	1	LMP1 LOCHI
25	2	66.7	9	1	PTSP BOMMO
26	2	66.7	9	1	UPA6 HUMAN
27	2	66.7	10	1	FAR2 PENMO
28	2	66.7	10	1	FAR7 MACRS
29	2	66.7	10	1	FARC CALVO
30	2	66.7	10	1	HTF1 ROMMI
31	2	66.7	10	1	HTF NAUCI
32	2	66.7	10	1	URA7 HUMAN
33	2	66.7	10	1	UXA6 CHLTR

34	2	66.7	11	1	CS15 BACSU
35	2	66.7	11	1	RRPL CHAV
36	2	66.7	11	1	T2P1 PROVU
37	2	66.7	11	1	ULAG HUMAN
38	2	66.7	12	1	FIF1 SARBU
39	2	66.7	12	1	UR2 SCYCA
40	2	66.7	13	1	CXAA CONST
41	2	66.7	13	1	FARB ASCSU
42	2	66.7	13	1	ITB5 BOVIN
43	2	66.7	13	1	ORCK ORCLI
44	2	66.7	13	1	RPOC MCGA
45	2	66.7	13	1	TEJA RANGA
46	2	66.7	13	1	TEMC RANTE
47	2	66.7	13	1	TEMD RANTE
48	2	66.7	13	1	TEME RANTE
49	2	66.7	13	1	YENP PHOLU
50	2	66.7	14	1	LECB PSOSC
51	2	66.7	14	1	LPER BACLI
52	2	66.7	14	1	MAST VESCR
53	2	66.7	14	1	PSAG CUCSA
54	2	66.7	14	1	SMS1 MYOSC
55	2	66.7	14	1	SMS ALLMI
56	2	66.7	15	1	ECDA LYMDI
57	2	66.7	15	1	FRE2 LITIN
58	2	66.7	15	1	LEC1 PSOSC
59	2	66.7	15	1	LEC2 PSOSC
60	2	66.7	15	1	LEC3 AXIPO
61	2	66.7	15	1	LEC3 PSOSC
62	2	66.7	15	1	MAOX CHICK
63	2	66.7	15	1	PC20 BRANA
64	2	66.7	15	1	UBL1 MONDO
65	2	66.7	15	1	UC17 MAIZE
66	2	66.7	15	1	UC28 MAIZE
67	2	66.7	15	1	UE15 HORVU
68	2	66.7	16	1	ALL1 CALVO
69	2	66.7	16	1	MDH SYN14
70	2	66.7	16	1	ODPB SOLTU
71	2	66.7	17	1	PATS ANASP
72	2	66.7	17	1	PSBL SYNNU
73	2	66.7	18	1	A2M OCTVU
74	2	66.7	18	1	AHD2 TETPY
75	2	66.7	18	1	ALL2 CYDPO
76	2	66.7	18	1	LCTN LANGL
77	2	66.7	18	1	LUXB KRYAS
78	2	66.7	19	1	HI70 RAT
79	2	66.7	19	1	ITHA PERAM
80	2	66.7	19	1	LCRP PETMA
81	2	66.7	19	1	LPGE ECOLI
82	2	66.7	19	1	MIFH TRISP
83	2	66.7	19	1	RL10 CITFR
84	2	66.7	20	1	ARQQ AMYME
85	2	66.7	20	1	CATA ACIRA
86	2	66.7	20	1	FLA VIBAL
87	2	66.7	20	1	ITRA ALBUU
88	2	66.7	20	1	PSBH SYNNU
89	2	66.7	20	1	RL10 PROVU
90	2	66.7	20	1	STVA STYCL
91	2	66.7	20	1	STYB STYCL
92	2	66.7	20	1	THIO CANFA
93	2	66.7	20	1	TRYL STREX
94	1	33.3	4	1	ACH1 ACHFU
95	1	33.3	4	1	FAR3 HIRME
96	1	33.3	4	1	FAR4 HIRME
97	1	33.3	4	1	FFKA ANTEL
98	1	33.3	4	1	FLRF HIRME
99	1	33.3	4	1	FLRN ANTEL
100	1	33.3	4	1	FMRF MACNI

ALIGNMENTS

RESULT 1

HTF TENMO  
ID \_HTF TENMO STANDARD; PRT; 8 AA.  
AC P25419;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).  
OS Tenebrio molitor (Yellow mealworm), and  
OS Zophobas rugipes.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Tenebrionidae; Tenebrio.  
OX NCBI\_TaxID=7067, 7075;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=T.molitor, and Z.rugipes;  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90341081; PubMed=2381871;  
RA Gaede G., Rosinski G.;  
RT "The primary structure of the hypertrehalosemic neuropeptide from  
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";  
RL Peptides 11:455-459(1990).  
CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A43976; B43976.  
DR PIR; B43976; B43976.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;  
  
Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LNF 3  
Db |||  
2 LNF 4

RESULT 2  
RPCH\_PANBO  
ID \_RPCH\_PANBO STANDARD; PRT; 8 AA.  
AC P08939;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Red pigment concentrating hormone (RPCH).  
OS Pandanus borealis (Northern red shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;  
OC Pandallidae; Pandalus.  
OX NCBI\_TaxID=6703;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75054965; PubMed=4433569;  
RA Fernlund P.;  
RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
RT Pandalus borealis.";  
RL Biochim. Biophys. Acta 371:304-311(1974).  
CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY  
CC STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-  
CC CHROMATOPHORES.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A61348; A61348.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;  
  
Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LNF 3  
Db |||  
2 LNF 4

RESULT 3  
FARP\_MONEX  
ID \_FARP\_MONEX STANDARD; PRT; 6 AA.  
AC F41966;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE FMRamide-like neuropeptide GNFRP-amide.  
OS Moniezia expansa (Sheep tapeworm)  
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
OC Cyclophyllidae; Anoplocephalidae; Moniezia.  
OX NCBI\_TaxID=28841;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93312289; PubMed=8323531;  
RA Maule A.G., Shaw C., Halton D.W., Thim L.;  
RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from  
RT the sheep tapeworm, Moniezia expansa.";  
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A43129; A43129.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 NF 3  
Db |||  
2 NF 3

RESULT 4  
FARI\_MACRS  
ID \_FARI\_MACRS STANDARD; PRT; 7 AA.  
AC P8327A;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLPI (DRNFLRP-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eye stalk;  
RA Sithigongul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
RA Sithigongul W.;  
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn Macrobrachium rosenbergii.";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -1- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.

FT MOD RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NF 3  
Db 3 NF 4  
RESULT 5  
FAR1\_PROCL STANDARD; PRT; 7 AA.  
ID FAR1\_PROCL STANDARD; PRT; 7 AA.  
AC P38498;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardioexcitatory FMRFamide homolog NF1.  
OS Procamburus clarkii (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Procamburus.  
OX NCBI\_TaxID=6728;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J.; Orchard I.; Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRFamide-related peptides from crayfish  
pericardial organs."  
RL Peptides 14:137-143(1993).  
CC -I- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NF 3  
Db 3 NF 4  
RESULT 6  
FAR2\_PROCL STANDARD; PRT; 7 AA.  
ID FAR2\_PROCL STANDARD; PRT; 7 AA.  
AC P38498;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardioexcitatory FMRFamide homolog DF2.  
OS Procamburus clarkii (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Procamburus.  
OX NCBI\_TaxID=6728;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J.; Orchard I.; Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRFamide-related peptides from crayfish  
pericardial organs."  
RL Peptides 14:137-143(1993).  
CC -I- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS

CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NF 3  
Db 3 NF 4  
RESULT 7  
FAR4\_PANRE STANDARD; PRT; 7 AA.  
ID FAR4\_PANRE STANDARD; PRT; 7 AA.  
AC P41875;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RN SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=95232026; PubMed=7716079;  
RA Maule A.G.; Shaw C.; Bowman J.W.; Halton D.W.; Thompson D.P.;  
Thim L.; Kubiak T.M.; Martin R.A.; Geary T.G.;  
RT "Isolation and preliminary biological characterization of  
KPNFIRFamide, a novel FMRFamide-related peptide from the free-living  
nematode, Panagrellus redivivus."  
RL Peptides 16:87-93(1995).  
CC -I- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT  
CC MUSCLE TENSION INCREASE.  
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NF 3  
Db 3 NF 4  
RESULT 8  
FARB\_CALVO STANDARD; PRT; 7 AA.  
ID FARB\_CALVO STANDARD; PRT; 7 AA.  
AC P41866;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallifMRFamide 11.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphrinamides) from the blowfly  
 RL Calliphora vomitoria.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR; B44787;  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 926 MW; 69D40693C44AB700 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 9  
 AKHG GRVBI STANDARD; PRT; 8 AA.  
 ID AKHG GRVBI  
 AC P14086;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone G (AKH-G) (RO II).  
 OS Gryllus bimaculatus (Two-spotted cricket), and  
 OS Romalea microptera (Lubber grasshopper).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 OC Gryllus.  
 OX NCBI\_TaxID=6993, 7007;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=88106553; PubMed=3426616;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
 RT of a peptide with adipokinetic activity from the corpora cardiaca of  
 RT the cricket Gryllus bimaculatus.";  
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
 RL [2]

SEQUENCE.  
 RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;  
 RX MEDLINE=89145002; PubMed=3226948;  
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
 RT the lubber grasshopper, Romalea microptera.";  
 RL Peptides 9:681-688(1988).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.

DR PIR; A28004; A28004.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 10  
 AKH LIBAU STANDARD; PRT; 8 AA.  
 ID AKH LIBAU  
 AC P25418;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH).  
 OS Libellula auripennis (Skimmer dragonfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Palaepodera; Odonata; Anisoptera; Libellulidae; Libellula.  
 OX NCBI\_TaxID=6966;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90359055; PubMed=2390213;  
 RA Gaede G.;  
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-  
 RT concentrating hormone family isolated and sequenced from a  
 RT dragonfly.";  
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.  
 DR PIR; S10596; S10596.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
 ||  
 Db 3 NF 4

RESULT 11  
 AKH MELML STANDARD; PRT; 8 AA.  
 ID AKH MELML  
 AC P25423;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH).  
 OS Melolontha melolontha (Cockchafer),  
 OS Geotrupes stercorarius (Dor beetle), and  
 OS Pachnoda marginata (Flower beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;  
 OC Scarabaeidae; Melolonthinae; Melolontha.  
 OX NCBI\_TaxID=7061, 7087, 7058;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=M.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;  
 RX MEDLINE=91248100; PubMed=2039445;  
 RA Gaede G.;  
 RT "A unique charged tyrosine-containing member of the adipokinetic  
 RT hormone/red-pigment-concentrating hormone peptide family isolated and  
 RT sequenced from two beetle species.";  
 RL Biochem. J. 275:671-677(1991).  
 RL [2]

RP SEQUENCE.  
 RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;  
 RX MEDLINE=92265187; PubMed=1586453;  
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;



RT "Primary structures of neuropeptides isolated from the corpora  
 RT cardiaca of various cetonid beetle species determined by  
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass  
 RT spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A58641; A58641.  
 DR PIR; S15422; S15422.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 2 LN 3

RESULT 12  
 ALL1 CYDPO STANDARD; PRT; 8 AA.  
 ID -FAR1 PANRE  
 AC P41872;  
 DT 01-NOV-1995 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Cydiaastatin 1.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OK NCBI\_TaxID=82600;  
 [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -!- FUNCTION: MYOACTIVE.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 5 NF 6

RESULT 13  
 ALL6 CYDPO STANDARD; PRT; 8 AA.  
 ID -FAR1 PANRE  
 AC P8316;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Cydiaastatin 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OK NCBI\_TaxID=82600;  
 [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC -!- FUNCTION: MYOACTIVE.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 5 NF 6

RESULT 14  
 FAR1 PANRE STANDARD; PRT; 8 AA.  
 ID -FAR1 PANRE  
 AC P41872;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide PF1 (SDENFLRP-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OK NCBI\_TaxID=6233;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=3027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRamide-like peptides from the free-living nematode  
 RT Panagrellus redivivus.";  
 RL Peptides 13:209-214(1992).  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
 CC CAUDALLY TO THE BASE OF THE PHARYNX.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 4 NF 5

RESULT 15  
 FAR1 PENMO STANDARD; PRT; 8 AA.  
 ID -FAR1 PENMO  
 AC P8316;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE FMRamide-like neuropeptide FLPI1 (GDRNFLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=1199015;  
 RA Sithigorngul P., Pupum J., Krungkasek C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 Db ||  
 4 NF 5

RESULT 16  
 FAR2 MACRS  
 ID FAR2\_MACRS STANDARD; PRT; 8 AA.  
 AC P83275;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP2 (ADKNFURF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Sarathongkum W., Jai-dechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
 DR Neuropeptide; Amidation.  
 KW MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 Db ||  
 4 NF 5

RESULT 17,  
 FAR3 HOMAM  
 ID FAR3\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamide-like immunoreactive  
 substances from the lobster nervous system: isolation and sequence  
 analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM  
 POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 Db ||  
 4 NF 5

RESULT 18  
 FAR4 HOMAM  
 ID FAR4\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41487;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamide-like immunoreactive  
 substances from the lobster nervous system: isolation and sequence  
 analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC  
 CC NEUROMUSCULAR JUNCTIONS.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 Db ||  
 4 NF 5

RESULT 19

HTF1 PERAM  
ID HTF1 PERAM STANDARD; PRT; 8 AA.  
AC P04548;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, last sequence update)  
DT 28-FEB-2003 (Rel. 41, last annotation update)  
DE Hypertrichaloseamic factor I (Neuropeptide M-I) (Periplaneta CC-I)  
DE (PeA-CAH-I) (Led-CC-I) (Hypertrichaloseamic neuropeptide I).  
OS Periplaneta americana (American cockroach).  
OS Lepidoptera decemlineata (Colorado potato beetle), and  
OC Blattella orientalis (Oriental cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 7539, 6976;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry.";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=L.americana;  
RX MEDLINE=84298179; PubMed=6591205;  
RA Scarborough R.M., Jamieson G.C., Kalish P., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioacceleratory and hyperglycemic activity from the corpora  
RT cardiaca of Periplaneta americana.";  
RL proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; PubMed=2576128;  
RA Gaede G., Kellner R.;  
RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrichaloseamic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portuosa, Blattella germanica and Blattella orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC -!- FUNCTION: HYPERTRICHALOSEAMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR: A44960; A44960.  
DR PIR: A49823; A49823.  
DR PIR: S08995; S08995.  
DR PROSITE: PS002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 931 MW; 86745775B9C452D6 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 NF 4  
RESULT 20  
FAR2 PANRE STANDARD; PRT; 9 AA.  
ID FAR2 PANRE  
AC P41873;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, last sequence update)  
DT 01-NOV-1995 (Rel. 32, last annotation update)  
DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRFamide-like peptides from the free-living nematode  
RT Panagrellus redivivus.";  
RL Peptides 13:209-214(1992).  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CC CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
Db 5 NF 6  
RESULT 21  
FAR3 MACRS STANDARD; PRT; 9 AA.  
ID FAR3 MACRS  
AC P83276; 2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, last sequence update)  
DT 28-FEB-2003 (Rel. 41, last annotation update)  
DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk; Sarathongkum W., Jaidechoey S., Longyant S.,  
RA Sithigornkul P., Sarathongkum W.;  
RA Sithigornkul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn Macrobrachium rosenbergii.";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SQ SEQUENCE 9 AA; 1133 MW; 845A0729C4441F5 CRC64;
Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 5 NF 6

RESULT 24
LMIP LOCM
ID LMIP LOCM STANDARD; PRT; 9 AA.
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyo-inhibiting peptide (LOM-MIP).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
SEQUENCE.
RP MEDLINE=92179466; PubMed=1796179;
RX Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyo-inhibiting
RT peptide (LOM-MIP), a novel biologically active neuro-peptide from
RT Locusta migratoria."
RL Regul. Pept. 36:111-119(1991).
CC -1- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
CC OVIDUCT.
CC -1- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
CC IN THE SUBESOPHAGEAL GANGLION.
DR PIR; A60065; AKLQIM.
KW Amidation; Neuro-peptide.
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 5 LN 6

RESULT 25
PTSP BOMMO
ID PTSP BOMMO STANDARD; PRT; 9 AA.
AC P82003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prothoracicostatic peptide (Bom-PTSP).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
SEQUENCE.
RP STRAIN=C145 X N140; TISSUE=Brain;
RX MEDLINE=2002634; PubMed=10531308;
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA Kataoka H.;
RT "Identification of a prothoracicostatic peptide in the larval brain of
RT the silkworm, Bombyx mori."
RL J. Biol. Chem. 274:31169-31173(1999).
RN [2]

```

RP ERRATUM.  
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
RA Kataoka H.,  
RL J. Biol. Chem. 275:9892-9892(2000).  
CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic  
CC gland.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.  
KW Hormone; Amidation.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LN 2  
||  
Db 5 LN 6  
RESULT 26  
UPA6 HUMAN  
ID \_UPA6 HUMAN STANDARD; PRT; 9 AA.  
AC P30092;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 14) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Plasma;  
RC MEDLINE=9302937; PubMed=1459097;  
RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5, ITS MW IS: 48 kDa.  
CC SWISS-2DPAGE; P30092; HUMAN.  
FT NON\_TER 1 9  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 935 MW; 5282F2CAA8676447 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

||

Db 2 LN 3

RESULT 27  
FAR2 PENMO  
ID \_FAR2 PENMO STANDARD; PRT; 10 AA.  
AC P8317;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP2 (AYSNLNLRF-amide).  
OS Penaeus monodon (Pencoid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigornkul P., Pupum J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigornkul W., Petsom A.,  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;  
Query Match 66.7%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

||

Db 5 LN 6

RESULT 28  
FAR7 MACRS  
ID \_FAR7 MACRS STANDARD; PRT; 10 AA.  
AC P83280;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP7 (GYGRNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21107394; PubMed=11179812;  
RA Sithigornkul P., Saraithongkum W., Longyant S., Panchan N.,  
RA Sithigornkul W., Petsom A.;  
RT "Three more novel FMRamide-like neuropeptide sequences from the  
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";  
RL Peptides 22:191-197(2001).  
CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3

||

Db 6 NF 7

RESULT 29  
FARC CALVO  
ID \_FARC CALVO STANDARD; PRT; 10 AA.  
AC P41867;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRamide 12.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion; PubMed=1549595;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliFMRFamides) from the blowfly  
 RT Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC PIR; C44787;  
 DR Neuropeptide; Amidation.  
 KW MOD RES 10 10  
 FT SEQUENCE 10 AA; 1156 MW; 2281039C4AB6D8 CRC64;  
 SQ  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 DB 6 NF 7  
 RESULT 30  
 HTF1\_ROMMI STANDARD; PRT; 10 AA.  
 ID P18110;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE RO I (Hypertrehaloseamic factor).  
 OS Romalea microptera (Lubber grasshopper).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Romaleidae; Romalea.  
 OX NCBI\_TaxID=7007;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89145002; PubMed=3226948;  
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
 RT the lubber grasshopper, Romalea microptera.";  
 RL Peptides 9:681-688(1988).  
 CC -!- FUNCTION: HYPERTREHALOSEAMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 DB 3 NF 4  
 RESULT 31  
 HTF1\_NAUCI STANDARD; PRT; 10 AA.  
 ID HTF1\_NAUCI

AC P10939;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertrehaloseamic hormone (HTH) (Hypertrehaloseamic neuropeptide).  
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
 OS Leucophaea maderae (Madeira cockroach),  
 OS Blattella germanica (German cockroach), and  
 OS Gromphadorhina portentosa (Madagascan hissing cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Nauphoeta.  
 OX NCBI\_TaxID=6990, 6988, 6973, 36953;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;  
 RX MEDLINE=87100208; PubMed=3801028;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Amino acid sequence of a hypertrehaloseamic neuropeptide from the  
 RT corpus cardiacum of the cockroach, Nauphoeta cinerea.";  
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=L.maderae, G.portentosa, and B.germanica;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehaloseamic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 RT atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=B.germanica;  
 RX MEDLINE=91179584; PubMed=2080017;  
 RA Veenstra J.A., Camps F.;  
 RT "Structure of the hypertrehalosemic neuropeptide of the German  
 RT cockroach, Blattella germanica.";  
 RL Neuropeptides 15:107-109(1990).  
 CC -!- FUNCTION: HYPERTREHALOSEAMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A26381; A26381.  
 DR PIR; A60421; A60421.  
 DR PIR; S08997; S08997.  
 DR PIR; S08998; S08998.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NF 3  
 DB 3 NF 4  
 RESULT 32  
 UR7\_HUMAN STANDARD; PRT; 10 AA.  
 ID UR7\_HUMAN  
 AC P34990;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)  
 DE (Fragment).

OS Homo sapiens (Human) .  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Erythrocyte;  
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
 RA Balant L., Hochstrasser D.F.;  
 RL Submitted (FEB-1994) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.77, ITS MW IS: 26 kDa.  
 DR SWISS-2DPAGE; P34990; HUMAN.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NF 3  
 ||  
 Db 6 NF 7

RESULT 33  
 UXA6\_CHLTR STANDARD; PRT; 10 AA.  
 AC P38007;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Unknown protein from 2D-page from elementary body (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=L2/434/Bu;  
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,  
 RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,  
 RA Pallini V.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.  
 DR Siena-2DPAGE; P38007; -.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NF 3  
 ||  
 Db 2 NF 3

RESULT 34  
 CS15\_BACSU STANDARD; PRT; 11 AA.  
 AC P81095;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=168 / JH642;

RA Graumann P.L., Schmid R., Marahiel M.A.;  
 RL Submitted (OCT-1997) to the SWISS-PROT data bank.  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=168 / JH642;  
 RX MEDLINE=96345629; PubMed=8755892;  
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";  
 RL J. Bacteriol. 178:4611-4619(1996).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: In response to low temperature.  
 CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEEE6322C330 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LN 2  
 ||  
 Db 10 LN 11

RESULT 35  
 RRPL\_CHAV STANDARD; PRT; 11 AA.  
 AC P13179;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
 DE (L protein) (Fragment).  
 GN L.  
 OS Chandipura virus (strain 1653514).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; Vesiculovirus.  
 OX NCBI\_TaxID=11273;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89299473; PubMed=2741347;  
 RA Masters P.S., Shella R.S., Butcher M., Patel B., Ghosh H.P.,  
 RA Banerjee A.K.;  
 RT "Structure and expression of the glycoprotein gene of Chandipura  
 RT virus."; 171:285-290(1989).  
 RL Virology 171:285-290(1989).  
 CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE  
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS  
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC {RNA}(N).  
 CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE  
 CC NUCLEOCASID (N) PROTEIN.  
 CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND  
 CC PARAMYXOVIRUSES.

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EMBL; J04350; AAA42917.1; -.  
 KW Transferase; RNA-directed RNA polymerase.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 36
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
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CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
      ||
Db     10 NF 11

RESULT 37
ULAG_HUMAN
ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,

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RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Sienna-2DPAGE; P31933; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      8 LN 9

RESULT 38
FIF1_SARBU
ID FIF1_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
CC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FWRamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FWRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
      ||
Db      8 NF 9

RESULT 39
UR2_SCYCA
ID UR2_SCYCA STANDARD; PRT; 12 AA.
AC P35490;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]

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RP SEQUENCE.
RC TISSUE=Spinal cord;
RX MEDLINE=92319231; PubMed=1620290;
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazon N.;
RT "Purification and characterization of urotensin II and parvalbumin
RL from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
RL Neuroendocrinology 55:230-235(1992).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW HORMONE.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; 804729F9D579CEBA CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 2 NF 3

RESULT 40
CXAA CONST STANDARD; PRT; 13 AA.
AC P28878;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin SIA (SIA).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91369955; PubMed=1892838;
RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Olivera B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RL receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A40312; NTKAS.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 10 NF 11

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RESULT 41
FARB ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RL Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 9 NF 10

RESULT 42
ITB5 BOVIN STANDARD; PRT; 13 AA.
AC P80747;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-5 (Fragment).
GN ITGB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=97299777; PubMed=9154926;
RA Andersen M.H., Berglund L., Rasmussen J.T., Petersen T.E.;
RT "Bovine PAS-6/7 binds alpha v beta 5 integrins and anionic
RT phospholipids through two domains.";
RL Biochemistry 36:5441-5446(1997).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
DR InterPro; IPR001169; Integrin beta C.
DR PROSITE; PS00243; INTEGRIN_BETA; PARTIAL.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1299 MW; 844197D005B9B865 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LN 2
Db      1 LN 2

RESULT 43
ORCK ORCLI STANDARD; PRT; 13 AA.
AC P37086; 1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Orcokinin.
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal nerve cord;
RX MEDLINE=93126144; PubMed=1480511;
RA Scanglier J., Hilbich C., Burdick S., Keller R.;
RT "Orcokinin: a novel myotropic peptide from the nervous system of the
RT crayfish, Orconectes limosus.";
RL Peptides 13:859-864(1992).
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC -!- AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS.
CC -!- TISSUE SPECIFICITY: ABDOMINAL NERVE CORD AND HINDGUT.
KW Neuropeptide.
SQ SEQUENCE 13 AA; 1518 MW; 8A318D7B4A93A40A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
Db      1 NF 2

RESULT 44
RPOC MYCGA STANDARD; PRT; 13 AA.
AC P47716; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).
GN RPOC.
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5969Var B;
RA Skarmov A.V., Feoktistova E.S., Gol'dman M.A., Feoktistova E.S.,
RA Bibilashvili R.S.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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CC -----
CC EMBL: L38402; AAB40952.1; -
KW Transferase; DNA-directed RNA polymerase; Transcription.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1630 MW; 4BEC27C7480D4333 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      4 LN 5

RESULT 45
TEJA_RANJA STANDARD; PRT; 13 AA.
AC P83307; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin-1Ja.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RT skin of the Japanese brown frog Rana japonica.";
RL Peptides 23:419-425(2002).
CC -!- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the temporin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1407 MW; 3EF713EA610A2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
Db      9 LN 10

RESULT 46
TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP TISSUE=Skin secretion;

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RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1363 MW; 2201403AG55B2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
DB 9 LN 10

RESULT 47
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]_TaxID=8407;
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has no antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1379 MW; 3BF35DFA655B2448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
DB 9 LN 10

RESULT 48
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

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OX NCBI_TaxID=8407;
RN [1]_TaxID=8407;
RP SEQUENCE.
RT TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporaria,";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
DB 9 LN 10

RESULT 49
YPNP_PHOLU
ID YPNP_PHOLU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3'region (ORF3) (Fragment).
OS Photobacterium luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=29488;
RN [1]_TaxID=29488;
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photobacterium sp. strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
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CC -----
CC EMBL; X76069; CAA53672.1; -.
KW Hypothetical protein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
DB 2 NF 3

RESULT 50
LECB_PSOSC

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ID LSCB\_PSOSC STANDARD; PRT; 14 AA.  
 AC P22584;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Basic lectin B1 (Fragment).  
 OS Psophocarpus scandens.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OX NCBI\_TaxID=3890;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Kortt A.A.;  
 RT "Isolation and characterization of the lectins from the seeds of  
 RT Psophocarpus scandens.";  
 RL Phytochemistry 27:2847-2855(1988).  
 CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF  
 CC ABOUT 32000 APPARENT MW.  
 CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE  
 CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.  
 CC -!- SIMILARITY: WITH P-TETRAONOLOBUS BASIC LECTINS IN N-TERMINAL  
 CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.  
 DR PIR; PA0007; PA0007.  
 KW Lectin; Glycoprotein.  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1732 MW; D804CE43B487C549 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 NF 3  
 Db 6 NF 7  
  
 RESULT 51  
 LPER\_BACLI STANDARD; PRT; 14 AA.  
 ID LPER\_BACLI STANDARD; PRT; 14 AA.  
 AC Q04303;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader  
 DE peptide).  
 OS Bacillus licheniformis, and  
 OS Bacillus anthracis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1402, 1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.licheniformis;  
 RX MEDLINE=84245158; PubMed=6429477;  
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;  
 RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-  
 RT streptogramin B resistance element from Bacillus licheniformis.";  
 RL Mol. Gen. Genet. 194:349-356(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.licheniformis; STRAIN=EMR-1;  
 RX MEDLINE=91310580; PubMed=1713206;  
 RA Kwak J.-K., Choi E.-C., Weisblum B.;  
 RT "Transcriptional attenuation control of ermK, a  
 RT macrolide-lincosamide-streptogramin B resistance determinant from  
 RT Bacillus licheniformis.";  
 RL J. Bacteriol. 173:4725-4735(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.anthraxis; STRAIN=590;  
 RX MEDLINE=913232776; PubMed=8473865;

RA Kim H.-S., Choi E.-C., Kim B.-K.;  
 RT "A macrolide-lincosamide-streptogramin B resistance determinant from  
 RT Bacillus anthracis 590: cloning and expression of ermJ.";  
 RL J. Gen. Microbiol. 139:601-607(1993).  
 CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF  
 CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B  
 CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.  
 CC -----  
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 CC -----  
 DR EMBL; L08389; AAA22596.1; -;  
 DR EMBL; M29832; AAA22598.1; -;  
 DR PIR; A42473; A42473.  
 KW Antibiotic resistance; Leader peptide.  
 SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 LN 2  
 Db 12 LN 13  
  
 RESULT 52  
 MAST\_VESCR STANDARD; PRT; 14 AA.  
 ID MAST\_VESCR STANDARD; PRT; 14 AA.  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.  
 OS Vespa crabro (European hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7445;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Venom;  
 RX MEDLINE=84289390; PubMed=6206053;  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 RT crabrolin, from the venom of the European hornet, Vespa crabro.";  
 RL J. Biol. Chem. 259:10106-10111(1984).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins  
 CC that couple to phospholipase C.  
 DR PIR; A01779; QMVHP2.  
 KW Mast cell degranulation; Amidation.  
 FT MOD RES 14  
 SQ SEQUENCE 14 AA; 1508 MW; 550C05CA1D6AB1D7 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 LN 2  
 Db 1 LN 2  
  
 RESULT 53  
 PSAG\_CUCSA STANDARD; PRT; 14 AA.  
 ID PSAG\_CUCSA STANDARD; PRT; 14 AA.  
 AC P42049;  
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem I reaction center subunit V (PSI-G) (Photosystem I 6.8 kDa  
 DE protein) (PS I subunit 10) (Fragment).  
 GN PSAG.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=3659;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Cotyledon;  
 RX MEDLINE=91355209; PubMed=1883835;  
 RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;  
 RT "Characterization of genes that encode subunits of cucumber PS I  
 RT complex by N-terminal sequencing.";  
 RL Biochim. Biophys. Acta 1059:141-148(1991).  
 CC -!- FUNCTION: NOT YET KNOWN.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST  
 CC THYLAKOID MEMBRANE; ASSOCIATED WITH THE STROMAL SIDE OF THE  
 CC THYLAKOID MEMBRANE.  
 CC -!- SIMILARITY: Belongs to the psag / psak family.  
 CC PIR; B56819;  
 DR InterPro; IPR000549; PSI Psag/K.  
 DR PROSITE; PS01026; PHOTOSYSTEM\_I\_PSAKG; PARTIAL.  
 KW Photosynthesis; Photosystem I; Transmembrane; Chloroplast; Thylakoid.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1452 MW; D712F0B91F1CA142 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 LN 2  
 Db ||  
 2 LN 3  
  
 RESULT 54  
 SMS1 MYOSC  
 ID SMS1 MYOSC STANDARD; PRT; 14 AA.  
 AC P20750;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Somatostatin I.  
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),  
 OS Oncorhynchus kisutch (Coho salmon), and  
 OS Anguilla anguilla (European freshwater eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;  
 OC Cottidae; Cottidae; Myoxocephalus.  
 OX NCBI\_TaxID=8097, 8019, 7936;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=M.scorpius; TISSUE=Pancreas;  
 RX MEDLINE=88029486; PubMed=2889597;  
 RA Conlon J.M., Davis M.S., Falkner S., Thim L.;  
 RT "Structural characterization of peptides derived from  
 RT prosomatostatins I and II isolated from the pancreatic islets of two  
 RT species of teleostean fish: the daddy sculpin and the flounder.";  
 RL Eur. J. Biochem. 168:647-652(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=O.kisutch; TISSUE=Pancreas;  
 RX MEDLINE=87055212; PubMed=2877919;  
 RA Flisetkaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,  
 RA Kimmel J.R., Andrews P.C., Gorman A.;  
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet  
 RT somatostatins.";  
 RL Gen. Comp. Endocrinol. 63:252-263(1986).

RN [3]  
 RP SEQUENCE.  
 RC SPECIES=A.anguilla; TISSUE=Pancreas;  
 RX MEDLINE=89065329; PubMed=2904391;  
 RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;  
 RT "Somatostatin-related and glucagon-related peptides with unusual  
 RT structural features from the European eel (Anguilla anguilla).";  
 RL Gen. Comp. Endocrinol. 72:181-189(1988).  
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.  
 DR PIR; A60840; A60840.  
 DR PIR; B60842; B60842.  
 DR PIR; S00172; S00172.  
 DR InterPro; IPR004250; Somatostatin.  
 DR Pfam; PF03002; Somatostatin; 1.  
 KW Hormone; Multigene family.  
 FT DISULFID 3 14  
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 NF 3  
 Db ||  
 5 NF 6  
  
 RESULT 55  
 SMS ALLMI  
 ID SMS ALLMI STANDARD; PRT; 14 AA.  
 AC P31885;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Somatostatin-14.  
 OS Alligator mississippiensis (American alligator), and  
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496, 34903;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=A.mississippiensis; TISSUE=Stomach;  
 RX MEDLINE=93324451; PubMed=8101369;  
 RA Wang Y., Conlon J.M.;  
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
 RT and stomach of the alligator.";  
 RL Peptides 14:573-579(1993).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=T.scripta;  
 RX MEDLINE=90341082; PubMed=1974347;  
 RA Conlon J.M., Hicks J.W.;  
 RT "Isolation and structural characterization of insulin, glucagon and  
 RT somatostatin from the turtle, Pseudemys scripta.";  
 RL Peptides 11:461-466(1990).  
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.  
 DR PIR; C60414; C60414.  
 DR InterPro; IPR004250; Somatostatin.  
 DR Pfam; PF03002; Somatostatin; 1.  
 KW Hormone.  
 FT DISULFID 3 14  
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 NF 3

```

Db          1 LN 2
           ||
           5 NF 6
           ||
           10 LN 11

RESULT 56
ECDA_LYMDI
ID _ECDA_LYMDI STANDARD; PRT; 15 AA.
AC P80938;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide A (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=37387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -I- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 15 AA; 1712 MW; 12EBD8246B74EE26 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LN 2
           ||
           11 LN 12

RESULT 57
PRE2_LITIN
ID _PRE2_LITIN STANDARD; PRT; 15 AA.
AC P82022;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Frenatin 2.
OS Litoria infraenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
RT the giant tree frog Litoria infraenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -I- FUNCTION: Wide spectrum antimicrobial peptide.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 15
SQ SEQUENCE 15 AA; 1425 MW; 06ED4B7BB1650CBF CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 LN 2
           ||
           10 LN 11

RESULT 58
LEC1_PSOSC
ID _LEC1_PSOSC STANDARD; PRT; 15 AA.
AC P22582;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acidic lectin A1 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -I- SUBUNIT: DIMER. THE SUBUNITS SHOW APPARENT MW HETEROGENEITY
CC (32000-35000 MW). WHICH MAY RESULT FROM DIFFERENT CARBOHYDRATE
CC CONTENT, AA SEQUENCE, OR POLYPEPTIDE LENGTH.
CC -I- PTM: CONTAINS 5-6% CARBOHYDRATE.
CC -I- SIMILARITY: WITH P.TETRAGONOLOBUS ACIDIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
DR PIR; PA0005; PA0005.
KW Lectin; Glycoprotein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1743 MW; D6EB9FE9C6B0254D CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 NF 3
           ||
           7 NF 8

RESULT 59
LEC2_PSOSC
ID _LEC2_PSOSC STANDARD; PRT; 15 AA.
AC P22585;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Basic lectin B2 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -I- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF
CC ABOUT 32000 APPARENT MW.
CC -I- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE
CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
CC -I- SIMILARITY: WITH P.TETRAGONOLOBUS BASIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.

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DR PIR; PA0008; PA0008.
KW Lectin; Glycoprotein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1847 MW; D194CE400C832796 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
Db 7 NF 8

RESULT 60
LEC3 AXIPO
ID LEC3 AXIPO STANDARD; PRT; 15 AA.
AC P28588;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Lectin III (Fragment).
OS Axinella polyoides (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Halichondrida; Axinellidae; Axinella.
OX NCBI_TaxID=12959;
[1] _
RN SEQUENCE.
RX MEDLINE=93003351; PubMed=1390906;
RA Buck F., Luth C., Strupat K., Bretting H.;
RT "Comparative investigations on the amino-acid sequences of different
RL isolectins from the sponge Axinella polyoides (Schmidt).";
RL Biochim. Biophys. Acta 1159:1-8(1992).
CC -!- FUNCTION: POSSESSES D-GALACTOSE BINDING SPECIFICITY.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: STORED IN SPHERULOUS CELLS IN THE SPONGE
CC TISSUE.
DR PIR; S29174; S29174.
KW Lectin.
FT NON TER 15
SQ SEQUENCE 15 AA; 1744 MW; DC05E47E3F8DC5F3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 13 LN 14

RESULT 61
LEC3 PSOSC
ID LEC3 PSOSC STANDARD; PRT; 15 AA.
AC P22583;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acidic lectin A3 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
[1] _
RN SEQUENCE.
RP TISSUE=Seed;
RA Kott A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER. THE SUBUNITS SHOW APPARENT MW HETEROGENEITY
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PC20_BRANA
ID PC20_BRANA STANDARD; PRT; 15 AA.
AC P81096;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 20 kDa pollen coat protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Topas; TISSUE=Pollen;
RX MEDLINE=98345939; PubMed=9680961;
RA Murphy D.J., Ross J.H.;
RT "Biosynthesis, targeting and processing of oleosin-like proteins,
RT which are major pollen coat components in Brassica napus.";
RL Plant J. 13:1-16(1998).
CC -1- FUNCTION: MAJOR COMPONENT OF THE POLLEN COAT.
CC -1- TISSUE SPECIFICITY: POLLEN.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1756 MW; 4C9B7C58ED18A442 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db ||
8 LN 9

RESULT 64
UBLL MONDO
ID USLL MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thioesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
DE UCHL1.
GN Monodelphis domestica (Short-tailed grey opossum).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
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CC
CC -----
CC ENBL: U32208; AAA9059.1; -
CC InterPro; IPR001578; UCH_1.
CC PROSITE; PS00140; UCH_1; PARTIAL.
CC KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
CC FT NON_TER 15
CC SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db ||
13 LN 14

RESULT 65
UC17_MAIZE
ID UC17_MAIZE STANDARD; PRT; 15 AA.
AC P80623;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 42.7 kDa.
CC Maize-2DPAGE; P80623; COLEOPTILE.
CC MaizeDB; 123949; -
CC FT NON_TER 15
CC FT NON_TER 15
CC SQ SEQUENCE 15 AA; 1554 MW; COAFFP15FFCECEC8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db ||
12 LN 13

RESULT 66
UC28_MAIZE
ID UC28_MAIZE STANDARD; PRT; 15 AA.
AC P80634;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (spot 984)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]

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Db          2 LN 3
RESULT 70
ODPB_SOLUTU
ID_ODPB_SOLUTU STANDARD; PRT; 16 AA.
AC P81419;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
DE (EC 1.2.4.1) (PDBE1-B) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
SEQUENCE.
RP STRAIN=cv. Romano; TISSUE=Tuber;
RC MEDLINE=98399821; PubMed=9729464;
RX Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
RA "Plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato.";
RL Biochem. J. 334:571-576 (1998).
CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -1- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC acetylhydrolipoamide + CO(2).
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits (by
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW Phosphorylation; Mitochondrion.
FT NON TER 16
SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
||
Db 13 LN 14

RESULT 71
PATS ANASP
ID_PATS_ANASP STANDARD; PRT; 17 AA.
AC O52748;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heterocyst inhibition signaling peptide.
GN PATS OR ASL2301.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A., AND FUNCTION.
RP MEDLINE=99011350; PubMed=9794762;
RX Yoon H.-S., Golden J.W.;
RA "Heterocyst pattern formation controlled by a diffusible peptide.";
RL Science 282:935-938 (1998).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
RN [3]
FUNCTION
RP MEDLINE=21172878; PubMed=11274121;
RX Yoon H.-S., Golden J.W.;
RA "Pats and products of nitrogen fixation control heterocyst pattern.";
RL J. Bacteriol. 183:2605-2613 (2001).
CC -1- FUNCTION: Inhibits heterocyst differentiation. Seems to control
CC heterocyst pattern formation through intercellular signaling
CC mechanisms. In Anabaena filaments every 10th vegetative cell
CC terminally differentiates into a heterocyst specialized for
CC nitrogen fixation. Pats seems to inhibit the formation of adjacent
CC heterocysts.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable). Seems to diffuse
CC to adjacent cells.
CC -1- DEVELOPMENTAL STAGE: Expressed in proheterocysts.
CC -1- DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 23 of June 2002;
CC WWW="http://www.expasy.org/spotlight/articles/spllt023.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AF046871; AAC03103.1; -.
DR ENBL; AF003589; BAB74000.1; -.
DR PIR; AF2093; AF2093.
SQ Heterocyst; Periplasmic; Complete proteome.
KW SEQUENCE 17 AA; 1927 MW; 192BE168476867F3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3
||
Db 8 NF 9

RESULT 72
PSBL SYNNU
ID_PSBL_SYNNU STANDARD; PRT; 17 AA.
AC P12241;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center L protein (PSII 5 kDa protein)
DE (Fragment).
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
SEQUENCE.
RP Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160 (1989).
CC -1- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -1- SIMILARITY: BELONGS TO THE PSBL FAMILY.
DR PIR; S05033; S05033.
DR InterPro; IPR003372; PSII_Psbl.
DR Pfam; PF02419; Psbl; 1.

```

KW Photosynthesis; Photosystem II.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 12 LN 13

RESULT 73  
 A2M OCTVU STANDARD; PRT; 18 AA.  
 AC P30800;  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).  
 OS Octopus vulgaris (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=6645;  
 RN [1]  
 RP SEQUENCE

RX MEDLINE=92344633; PubMed=1379044;  
 RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Enghild J.J.;  
 RT "Purification and characterization of an alpha-macroglobulin  
 proteinase inhibitor from the mollusc Octopus vulgaris";  
 RL Biochem. J. 285:521-527(1992).  
 CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A  
 UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,  
 CC CALLED THE "BAIT REGION" WHICH CONTAINS SPECIFIC CLEAVAGE SITES  
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT  
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH  
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST  
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR  
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE  
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE  
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.  
 CC -!- SUBUNIT: Homodimer; disulfide-linked.  
 CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,  
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.  
 DR PIR: S23971; S23971.  
 DR GO: GO:0016975; F:alpha-2 macroglobulin; NAS.  
 DR InterPro: IPR001599; MacroglublnA2.  
 DR Pfam: PF00207; A2M; 1.  
 DR PROSITE: PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;  
 KW Thioester bond.  
 FT NON TER 1 1  
 FT CROSSLNK 5 8  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 12 NF 13

RESULT 74  
 AHD2 TETPY STANDARD; PRT; 18 AA.  
 AC P35430;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD  
 (Fragment)).  
 DE Tetrahymena pyriformis.  
 OS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
 OC Tetrahymenina; Tetrahymena.  
 OX NCBI\_TaxID=5908;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=W;  
 RX MEDLINE=94107273; PubMed=8280099;  
 RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;  
 RT "Purification and characterization of a novel dimeric 20 alpha-  
 RT hydroxysteroid dehydrogenase from Tetrahymena pyriformis";  
 RL Biochem. J. 297:195-200(1994).  
 CC -!- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA HYDROXY  
 CC GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-  
 CC HYDROXYPREGNENOLONE.  
 CC -!- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxypregn-4-en-3-one +  
 CC NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.  
 CC -!- SUBUNIT: Homodimer.  
 CC PIR: S40502; S40502.  
 KW Oxidoreductase; NADP.  
 DR NON TER 18 18  
 FT SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;  
 SQ SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 7 LN 8

RESULT 75  
 ALL2 CYDPO STANDARD; PRT; 18 AA.  
 ID \_ALL2 CYDPO  
 AC P82153;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiaastatin 2.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 18 18  
 SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 15 NF 16

Search completed: November 25, 2003, 19:28:28  
 Job time : 2.13538 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 5.63372 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO  
Gapop 60.0 ; Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3	100.0	11	8 Q95E14	Q95E14 dendrochilu
2	3	100.0	12	8 Q95EJ8	Q95EJ8 dendrochilu
3	3	100.0	12	8 Q95E16	Q95E16 dendrochilu
4	3	100.0	12	8 Q95EJ5	Q95EJ5 dendrochilu
5	3	100.0	12	8 Q95E10	Q95E10 dendrochilu
6	3	100.0	12	8 Q95EK0	Q95EK0 dendrochilu
7	3	100.0	12	8 Q95EL6	Q95EL6 dendrochilu
8	3	100.0	12	8 Q95EM2	Q95EM2 dendrochilu
9	3	100.0	12	8 Q95EK8	Q95EK8 dendrochilu
10	3	100.0	12	8 Q95EL2	Q95EL2 dendrochilu
11	3	100.0	12	8 Q95EM0	Q95EM0 dendrochilu
12	3	100.0	12	8 Q95EJ3	Q95EJ3 dendrochilu
13	3	100.0	12	8 Q95EL8	Q95EL8 dendrochilu
14	3	100.0	12	8 Q95EK6	Q95EK6 dendrochilu
15	3	100.0	12	8 Q95EK2	Q95EK2 dendrochilu
16	3	100.0	12	8 Q95EJ1	Q95EJ1 dendrochilu

17	3	100.0	12	8 Q95E12	Q95E12 dendrochilu
18	3	100.0	12	8 Q95E18	Q95E18 dendrochilu
19	3	100.0	12	8 Q95EK4	Q95EK4 dendrochilu
20	3	100.0	15	4 Q16297	Q16297 homo sapien
21	3	100.0	15	6 Q9TRA6	Q9TRA6 bos taurus
22	3	100.0	17	6 Q9TR96	Q9TR96 ovis aries
23	3	100.0	18	2 Q56610	Q56610 vibrio chol
24	3	100.0	18	8 Q9ZYW4	Q9ZYW4 habrobracn
25	3	100.0	18	9 Q9ZX80	Q9ZX80 lactococcus
26	3	100.0	19	8 Q9ZYW3	Q9ZYW3 gnaptodon
27	3	100.0	19	10 Q9S816	Q9S816 oryza sativ
28	3	100.0	20	2 Q9R4D9	Q9R4D9 escherichia
29	3	100.0	20	8 Q9ZY72	Q9ZY72 sathon sp.
30	3	100.0	20	12 Q84858	Q84858 unidentified
31	3	100.0	20	13 Q9PS15	Q9PS15 oncorhynch
32	2	66.7	7	8 Q98866	Q98866 spinacia ol
33	2	66.7	8	2 Q93SR0	Q93SR0 staphylococ
34	2	66.7	8	2 P77556	P77556 escherichia
35	2	66.7	8	2 Q9R5R0	Q9R5R0 shigella dy
36	2	66.7	8	3 P87225	P87225 saccharomyc
37	2	66.7	8	4 Q15889	Q15889 homo sapien
38	2	66.7	8	6 Q8WNS1	Q8WNS1 bos taurus
39	2	66.7	8	8 Q8WGC7	Q8WGC7 petriolithe
40	2	66.7	8	10 Q40659	Q40659 oryza sativ
41	2	66.7	8	11 Q9QVFE4	Q9QVFE4 rattus sp.
42	2	66.7	9	2 Q57328	Q57328 aeromonas s
43	2	66.7	9	2 Q9RSR1	Q9RSR1 shigella dy
44	2	66.7	9	2 Q44377	Q44377 aeromonas t
45	2	66.7	9	2 Q44468	Q44468 aeromonas v
46	2	66.7	9	2 Q43928	Q43928 aeromonas p
47	2	66.7	9	2 Q44001	Q44001 aeromonas e
48	2	66.7	9	4 Q14715	Q14715 homo sapien
49	2	66.7	9	4 Q9UCN5	Q9UCN5 homo sapien
50	2	66.7	9	5 Q96417	Q96417 drosophila
51	2	66.7	9	6 Q9TRS0	Q9TRS0 oryctolagus
52	2	66.7	9	8 Q31653	Q31653 anser caeru
53	2	66.7	9	12 P90359	P90359 barley wild
54	2	66.7	9	12 Q84333	Q84333 simian viru
55	2	66.7	10	2 Q9RSN4	Q9RSN4 clostridium
56	2	66.7	10	2 Q9RSN6	Q9RSN6 clostridium
57	2	66.7	10	2 Q9F5W1	Q9F5W1 vibrio chol
58	2	66.7	10	2 Q47091	Q47091 escherichia
59	2	66.7	10	2 Q8GDC0	Q8GDC0 escherichia
60	2	66.7	10	3 Q8J0C2	Q8J0C2 encephalito
61	2	66.7	10	4 Q9UJ48	Q9UJ48 homo sapien
62	2	66.7	10	5 Q8WPE7	Q8WPE7 skogsbergia
63	2	66.7	10	6 Q9TR49	Q9TR49 bos taurus
64	2	66.7	10	6 Q8SPN8	Q8SPN8 macaca mula
65	2	66.7	10	8 Q8WB87	Q8WB87 chaetophoru
66	2	66.7	10	8 Q8W8Q2	Q8W8Q2 anolis punc
67	2	66.7	10	8 Q8WD18	Q8WD18 anolis tran
68	2	66.7	10	8 Q8W8Q3	Q8W8Q3 anolis nite
69	2	66.7	10	8 Q8W8Q4	Q8W8Q4 anolis punc
70	2	66.7	10	11 Q9QVK8	Q9QVK8 mus sp. mep
71	2	66.7	10	13 Q73588	Q73588 gallus gall
72	2	66.7	10	13 P82080	P82080 limnodynast
73	2	66.7	11	2 Q9A1Z7	Q9A1Z7 carsonella
74	2	66.7	11	2 Q9R4B1	Q9R4B1 streptococc
75	2	66.7	11	2 Q47604	Q47604 escherichia
76	2	66.7	11	2 Q47345	Q47345 escherichia
77	2	66.7	11	2 Q9A1Z8	Q9A1Z8 carsonella
78	2	66.7	11	2 Q47059	Q47059 escherichia
79	2	66.7	11	4 Q9UCF2	Q9UCF2 homo sapien
80	2	66.7	11	5 Q23876	Q23876 dictyosteli
81	2	66.7	11	8 Q35374	Q35374 paramescium
82	2	66.7	11	8 Q9G682	Q9G682 chelosania
83	2	66.7	11	10 Q9T0L9	Q9T0L9 brassica ol
84	2	66.7	11	10 Q941R5	Q941R5 pinus radia
85	2	66.7	11	12 Q86866	Q86866 lymphocytic
86	2	66.7	11	12 Q86864	Q86864 lymphocytic
87	2	66.7	11	12 Q86868	Q86868 lymphocytic
88	2	66.7	11	15 Q83410	Q83410 mouse mamma
89	2	66.7	12	2 Q9X645	Q9X645 unidentified

90 2 66.7 12 2 Q9X638  
 91 2 66.7 12 2 Q9X628  
 92 2 66.7 12 2 Q9WV6  
 93 2 66.7 12 2 Q9WV5  
 94 2 66.7 12 2 Q9X640  
 95 2 66.7 12 2 Q9X643  
 96 2 66.7 12 2 Q9X633  
 97 2 66.7 12 2 Q9X631  
 98 2 66.7 12 2 Q9NTR7  
 99 2 66.7 12 5 Q8MY01  
 100 2 66.7 12 5 Q9TWV4

KW Chloroplast.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;  
 Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 4 LNF 6

## ALIGNMENTS

## RESULT 3

Q95E16 PRELIMINARY; PRT; 12 AA.  
 AC Q95E16; 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Psal (Fragment).  
 OS Dendrochilum glumaceum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=71597;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389215; AAK82407.1; -.  
 KW Chloroplast.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 4

Q95EJ5 PRELIMINARY; PRT; 12 AA.  
 AC Q95EJ5; 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Psal (Fragment).  
 OS Dendrochilum gibbsiae.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79421;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389210; AAK82398.1; -.  
 KW Chloroplast.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

QY 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 2

Q95EJ8 PRELIMINARY; PRT; 12 AA.  
 AC Q95EJ8; 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Psal (Fragment).  
 OS Dendrochilum grandiflorum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79424;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum aciferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389208; AAK82395.1; -.  
 QY 1 LNF 3  
 |||  
 Db 4 LNF 6

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 5

Q95EL0 PRELIMINARY; PRT; 12 AA.  
 AC Q95EL0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Psal (Fragment).  
 OS Dendrochilum corrugatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389202; AAK82383.1; -.  
 KW Chloroplast.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 6

Q95EK0 PRELIMINARY; PRT; 12 AA.  
 AC Q95EK0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Psal (Fragment).  
 OS Dendrochilum joclemensii.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79427;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389207; AAK82393.1; -.  
 KW Chloroplast.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 7

Q95BL6 PRELIMINARY; PRT; 12 AA.  
 AC Q95BL6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Psal (Fragment).  
 OS Dendrochilum muluense.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79434;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389199; AAK82377.1; -.  
 KW Chloroplast.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 8

Q95EM2 PRELIMINARY; PRT; 12 AA.  
 AC Q95EM2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Psal (Fragment).  
 OS Dendrochilum haslamii.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
 OX NCBI\_TaxID=79425;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barkman T.J., Simpson B.B.;  
 RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
 RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
 RT sequence data."  
 RL Syst. Bot. 0:0-0(2001).  
 DR EMBL; AF389196; AAK82371.1; -.  
 KW Chloroplast.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db |||  
4 LNF 6

## RESULT 9

Q95EK8 PRELIMINARY; PRT; 12 AA.  
AC Q95EK8;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Psal (Fragment).  
OS Dendrochilum pseudoscriptum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
OX NCBI\_TaxID=150393;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barkman T.J., Simpson B.B.;  
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
RT sequence data.";  
RL Syst. Bot. 0:0-0(2001).  
DR EMBL; AF389203; AAK82385.1; --  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db |||  
4 LNF 6

## RESULT 10

Q95EL2 PRELIMINARY; PRT; 12 AA.  
AC Q95EL2;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Psal (Fragment).  
OS Dendrochilum alatum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
OX NCBI\_TaxID=79410;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barkman T.J., Simpson B.B.;  
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
RT sequence data.";  
RL Syst. Bot. 0:0-0(2001).  
DR EMBL; AF389201; AAK82381.1; --  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db |||  
4 LNF 6

## RESULT 11

Q95EM0 PRELIMINARY; PRT; 12 AA.  
AC Q95EM0;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Psal (Fragment).  
OS Dendrochilum stachyodes.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
OX NCBI\_TaxID=79441;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barkman T.J., Simpson B.B.;  
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
RT sequence data.";  
RL Syst. Bot. 0:0-0(2001).  
DR EMBL; AF389197; AAK82373.1; --  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db |||  
4 LNF 6

## RESULT 12

Q95EJ3 PRELIMINARY; PRT; 12 AA.  
AC Q95EJ3;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Psal (Fragment).  
OS Dendrochilum dewindtianum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.  
OX NCBI\_TaxID=79419;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barkman T.J., Simpson B.B.;  
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)  
RT inferred in a phylogenetic context using nuclear and chloroplast DNA  
RT sequence data.";  
RL Syst. Bot. 0:0-0(2001).  
DR EMBL; AF389211; AAK82400.1; --  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db |||  
4 LNF 6

## RESULT 13

Q95EL8

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ID Q95EL8 PRELIMINARY; PRT; 12 AA.
AC Q95EL8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Psai (Fragment).
OS Dendrochilum dewildei.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79418;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389198; AAK82375.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 14
Q95EK6 PRELIMINARY; PRT; 12 AA.
ID Q95EK6;
AC Q95EK6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Psai (Fragment).
OS Dendrochilum pterogyne.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79438;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389204; AAK82387.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 15
Q95EK2 PRELIMINARY; PRT; 12 AA.
ID Q95EK2;
AC Q95EK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum trusmiense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79444;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389206; AAK82391.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0F1AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 16
Q95EI1 PRELIMINARY; PRT; 12 AA.
ID Q95EI1;
AC Q95EI1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Psai (Fragment).
OS Dendrochilum tenopokense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79442;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389212; AAK82402.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1393 MW; 1F5AC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 4 LNF 6

RESULT 17
Q95EI2 PRELIMINARY; PRT; 12 AA.
ID Q95EI2;
AC Q95EI2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Psai (Fragment).

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OS Dendrochilum cupulatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79417;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389217; AAK82411.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 18
Q95E18 PRELIMINARY; PRT; 12 AA.
AC Q95E18
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum exasperatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79420;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389214; AAK82405.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 19
Q95EK4 PRELIMINARY; PRT; 12 AA.
AC Q95EK4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Psai (Fragment).
OS Dendrochilum alpinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Coelogyninae; Dendrochilum.
OX NCBI_TaxID=79411;
RN [1]
RP SEQUENCE FROM N.A.
RA Barkman T.J., Simpson B.B.;
RT "Hybridization and parentage of Dendrochilum acuiiferum (Orchidaceae)
RT inferred in a phylogenetic context using nuclear and chloroplast DNA
RT sequence data.";
RL Syst. Bot. 0:0-0(2001).
DR EMBL; AF389205; AAK82389.1; -.
KW Chloroplast.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 0FIAC7B27CA769C4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 20
Q16297 PRELIMINARY; PRT; 15 AA.
AC Q16297
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
DE Kell immunogen (Fragment).
GN KELL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95152088; PubMed=7849312;
RX Lee S., Wu X., Reid M., Zelinski T., Redman C.;
RT "Molecular basis of the Kell (K1) phenotype.";
RL Blood 85:912-916(1995).
DR EMBL; S76770; AAB33389.1; -.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1882 MW; 7316158F0E98614F CRC64;

Query Match 100.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 21
Q9TRA6 PRELIMINARY; PRT; 15 AA.
AC Q9TRA6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PA700 subunit F31=ATP-dependent 20 S proteasome activator
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94342244; PubMed=8063704;

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RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,  
 RA Afendis S.J., Swaffield J.C., Slaughter C.A.;  
 RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an  
 RT ATPase containing multiple members of a nucleotide-binding protein  
 RT family";  
 RL J. Biol. Chem. 269:20878-20884(1994).  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1659 MW; D189812E9389B755 CRC64;

Query Match 100.0%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 6 LNF 8

## RESULT 22

Q9TR96 PRELIMINARY; PRT; 17 AA.  
 AC Q9TR96; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE MEGAPOIETIN=MEGAKARYOCYTE growth and platelet production regulator  
 DE (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 CX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=95062214; PubMed=7972018;  
 RA Kuter D.J., Beeler D.L., Rosenberg R.D.;  
 RT "The purification of megapoietin: a physiological regulator of  
 RT megakaryocyte growth and platelet production.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11104-11108(1994).  
 FT NON TER 1 1  
 FT NON TER 17 17  
 SQ SEQUENCE 17 AA; 1975 MW; DA3A5E835A755C9D CRC64;

Query Match 100.0%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 8 LNF 10

## RESULT 23

Q56610 PRELIMINARY; PRT; 18 AA.  
 AC Q56610; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Acca (Fragment).  
 GN ACCA.

OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.

CX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C6706;

RX MEDLINE=97074686; PubMed=8917113;

RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,

RA Morris J.G.;  
 RT "Cloning and characterization of dnaE, encoding the catalytic subunit

RT of replicative DNA polymerase III, from Vibrio cholerae strain  
 RT C6706";  
 RL Gene 175:281-283(1996).  
 DR EMBL; U30472; AAC44579.1; -.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;

Query Match 100.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 3 LNF 5

## RESULT 24

Q9ZYW4 PRELIMINARY; PRT; 18 AA.  
 AC Q9ZYW4; 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Cytochrome oxidase II (Fragment).  
 OS Habrobracon hebetor.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;  
 OC Braconidae; Braconinae; Habrobracon.  
 CX NCBI\_TaxID=69819;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Downton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 RT the hymenoptera";  
 RL Mol. Biol. Evol. 16:298-309(1999).  
 DR EMBL; AF034597; AAC79745.1; -.  
 KW Mitochondrion.  
 FT NON TER 1 1  
 SQ SEQUENCE 18 AA; 2282 MW; 79721C93C8D5F1D4 CRC64;

Query Match 100.0%; Score 3; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 8 LNF 10

## RESULT 25

Q9ZX80 PRELIMINARY; PRT; 18 AA.  
 AC Q9ZX80; 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Phage antigenic determinant (Fragment).  
 OS Lactococcus lactis phage phi 197.  
 OC Viruses.  
 CX NCBI\_TaxID=12427;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=92384563; PubMed=1514794;  
 RA Schouler C., Bouet C., Ritzenthaler P., Drouet X., Mata M.;  
 RT "Characterization of Lactococcus lactis phage antigens";  
 RL Appl. Environ. Microbiol. 58:2479-2484(1992).  
 DR EMBL; S44895; AAB49317.2; -.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2155 MW; 85601530E6E9DFDA CRC64;

Query Match 100.0%; Score 3; DB 9; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
5 LNF 7

RESULT 26
Q92YW3 PRELIMINARY; PRT; 19 AA.
ID Q9ZYW3
AC Q9ZYW3 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE Cytochrome oxidase II (Fragment).
OS Gnaptodon pumilio.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Gnaptodontinae; Gnaptodon.
OX NCBI_TaxID=64833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309 (1999).
DR EMBL; AF034598; AAC79746.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 19 AA; 2290 MW; 77F1EE77E787BCA CRC64;

Query Match 100.0%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
17 LNF 19

RESULT 27
Q9S8I6 PRELIMINARY; PRT; 19 AA.
ID Q9S8I6
AC Q9S8I6 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCGSSIC acid-induced protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
RT roots of salt-sensitive and salt-tolerant indica rice varieties.";
RL Plant Physiol. 107:177-186 (1995).
DR Gramene; Q9S8I6; -.
SQ SEQUENCE 19 AA; 2039 MW; FE1F0A6872F6F620 CRC64;

Query Match 100.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
1 LNF 3
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RESULT 28
Q9R4D9 PRELIMINARY; PRT; 20 AA.
ID Q9R4D9
AC Q9R4D9 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Fimbrial protein CS20 (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96294774; PubMed=8698489;
RA Valvatne H., Sommerfelt H., Gaastra W., Bhan M.K., Grewal H.M.;
RT "Identification and characterization of CS20, a new putative
RT colonization factor of enterotoxigenic Escherichia coli.";
RL Infect. Immun. 64:2635-2642 (1996).
SQ SEQUENCE 20 AA; 1895 MW; F64DFAE56C8C32CC CRC64;

Query Match 100.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
12 LNF 14

RESULT 29
Q9ZY72 PRELIMINARY; PRT; 20 AA.
ID Q9ZY72
AC Q9ZY72 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE Cytochrome oxidase II (Fragment).
OS Sathon sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgastrinae; Sathon.
OX NCBI_TaxID=81091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309 (1999).
DR EMBL; AF082929; AAD17789.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 20 AA; 2436 MW; DAE6F367B8E4A6BC CRC64;

Query Match 100.0%; Score 3; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
17 LNF 19

RESULT 30
Q84858 PRELIMINARY; PRT; 20 AA.
ID Q84858
AC Q84858 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
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DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DS Hypothetical 2.1 kba protein (Fragment).
OS Unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
CX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30215; AAA66824.1; -.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 20
SQ SEQUENCE 20 AA; 2105 MW; CED4BCA72BF73D77 CRC64;

Query Match 100.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 1 LNF 3

RESULT 31
Q9PSI5 PRELIMINARY; PRT; 20 AA.
AC Q9PSI5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Creatine kinase (EC 2.7.3.2) (Fragment).
OS Oncorhynchus kisutch (Coho salmon)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93080727; PubMed=1449598;
RA White K.C., Babbitt P.C., Buechter D.D., Kenyon G.L.;
RT "The principal islet of the Coho salmon (Oncorhynchus kisutch) contains
RT the BB isoenzyme of creatine kinase.";
RL J. Protein Chem. 11:489-494(1992).
SQ SEQUENCE 20 AA; 2425 MW; BFBCT71D6D2A86E11 CRC64;

Query Match 100.0%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 11 LNF 13

RESULT 32
Q98866 PRELIMINARY; PRT; 7 AA.
AC Q98866;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
CX NCBI_TaxID=3562;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
KW Chloroplast.
FT NON TER 1
FT NON TER 6
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 6 LN 7

RESULT 33
Q93SR0 PRELIMINARY; PRT; 8 AA.
AC Q93SR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-lactamase repressor Blai (Fragment).
GN Blai.
OS Staphylococcus epidermidis.
OG Plasmid pST6.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6;
RA Sidhu M.S., Heir E., Sorum H., Holck A.L.;
RT "Genetic linkage between quaternary ammonium compound and beta-lactam
RT resistance in Staphylococci isolated from food.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028779; AAK38453.1; -.
KW Plasmid.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 930 MW; 4E3325B05AA44720 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 2 LN 3

RESULT 34
P77556 PRELIMINARY; PRT; 8 AA.
AC P77556;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE TRAY (Fragment).
GN TRAY.
OS Escherichia coli.
OG Plasmid IncPII R1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ECOR11;
MEDLINE=96400908; PubMed=8807284;

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RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;  
 RT "Mosaic structure of plasmids from natural populations of Escherichia  
 RL coli.";  
 RL Genetics 143:1091-1100(1996).  
 DR EMBL; U50661; AAC44245.1; -;  
 DR EMBL; U50650; AAC44234.1; -;  
 DR EMBL; U50651; AAC44235.1; -;  
 DR EMBL; U50652; AAC44236.1; -;  
 DR EMBL; U50653; AAC44237.1; -;  
 DR EMBL; U50654; AAC44238.1; -;  
 DR EMBL; U50655; AAC44239.1; -;  
 DR EMBL; U50656; AAC44240.1; -;  
 DR EMBL; U50657; AAC44241.1; -;  
 DR EMBL; U50658; AAC44242.1; -;  
 DR EMBL; U50659; AAC44243.1; -;  
 DR EMBL; U50660; AAC44244.1; -;  
 KW Plasmid.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 834 MW; D335A5B0544735A1 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
 ||  
 Db 3 LN 4

RESULT 35  
 Q9R5R0 PRELIMINARY; PRT; 8 AA.  
 AC Q9R5R0  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 11,500 DA product of ORFA (Fragment).  
 OS Shigella dysenteriae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OX NCBI\_TaxID=622;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92085268; PubMed=1660923;  
 RA Polard P., Prete M.F., Chandler M., Fayet O.;  
 RT "Programmed translational frameshifting and initiation at an AUU codon  
 RL in gene expression of bacterial insertion sequence IS911.";  
 FT J. Mol. Biol. 222:465-477(1991).  
 NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
 ||  
 Db 5 NF 6

RESULT 36  
 P87225 PRELIMINARY; PRT; 8 AA.  
 AC P87225  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE GIN11 protein (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Wedler H., Wedler E., Scharfe M., Wambutt R.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z73169; CAA97518.2; -;  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 66.7%; Score 2; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NF 3  
 ||  
 Db 5 NF 6

RESULT 37  
 Q15889 PRELIMINARY; PRT; 8 AA.  
 AC Q15889  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Clone XP15H8B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries.";  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32070; AAA73879.1; -;  
 FT NON\_TER 1 1  
 NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 865 MW; 047447325A761E7 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2  
 ||  
 Db 6 LN 7

RESULT 38  
 Q8WNS1 PRELIMINARY; PRT; 8 AA.  
 AC Q8WNS1  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE X-linked zinc finger protein (Fragment).  
 GN ZFX.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poloumienko A., Blecher S.;  
 RT "Comparison between intron-exon structures in ZFX and ZFY genes.";

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF045782; AAL58190.1; -.

FT NON\_TER 1 8

SQ SEQUENCE 8 AA; 904 MW; DF1DC2C4472AAB1A CRC64;

Query Match 66.7%; Score 2; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 4 LN 5

#### RESULT 39

Q8WGC7 PRELIMINARY; PRT; 8 AA.

AC Q8WGC7;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE NADH dehydrogenase subunit 1 (Fragment).

OS Petrolisthes armatus (green porcelain crab).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Anomura;

OC Galatheoidea; Porcellanidae; Petrolisthes.

OX NCBI\_TaxID=84662;

RN [1]

RP SEQUENCE FROM N.A.

RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,

RA Cunningham C.W.;

RT "Mitochondrial gene rearrangements support a hypothesis of parallel

RT evolution to the crab-like form."

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF436049; AAL31623.1; -.

KW Mitochondrion.

FT NON\_TER 8

SQ SEQUENCE 8 AA; 1010 MW; FE20504B54472696 CRC64;

Query Match

Best Local Similarity 100.0%; Score 2; DB 8; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 3 LN 4

#### RESULT 40

Q40659 PRELIMINARY; PRT; 8 AA.

ID Q40659;

AC Q40659;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Alpha-amylase (Fragment).

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Erihartoideae; Oryzoae; Oryza.

OX NCBI\_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91078641; PubMed=2258052;

RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,

RA Rodriguez R.L.;

RT "Expression and secretion of rice alpha-amylase by saccharomyces

RT cerevisiae."

RL Gene 94:209-216(1990).

DR EMBL: M62916; AAA33892.1; -.

DR Gramene; Q40659; -.

FT NON\_TER 8

SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 66.7%; Score 2; DB 10; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 4 LN 5

#### RESULT 41

Q9QVF4 PRELIMINARY; PRT; 8 AA.

ID Q9QVF4;

AC Q9QVF4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE TRANSFERRIN-PEPTIDE 60 (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=92165927; PubMed=1791188;

RA Cavanaugh P.G., Nicolson G.L.;

RT "Lung-derived growth factor that stimulates the growth of lung-

RT metastasizing tumor cells: identification as transferrin."

RL J. Cell. Biochem. 47:261-271(1991).

FT NON\_TER 1

FT NON\_TER 8

SQ SEQUENCE 8 AA; 778 MW; 9D744735B69DDAAD CRC64;

Query Match

Best Local Similarity 100.0%; Score 2; DB 11; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2

Db 6 LN 7

#### RESULT 42

Q57328 PRELIMINARY; PRT; 9 AA.

ID Q57328;

AC Q57328;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

DE Hypothetical protein (Fragment).

GN EXEF.

OS Aeromonas sobria.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;

OC Aeromonadaceae; Aeromonas.

OX NCBI\_TaxID=646;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=132;

RX MEDLINE=97089747; PubMed=8935655;

RA Karylshev A.V., Macintyre S.;

RT "Study of the intergenic *exer-exeG* region and its application as a

RT simple preliminary test for *Aeromonas* spp."

RL FEMS Microbiol. Lett. 137:37-44(1996).

DR EMBL: X89466; CAA61647.1; -.

DR EMBL: X89465; CAA61645.1; -.

FT NON\_TER 1

FT NON\_TER 9

SQ SEQUENCE 9 AA; 1077 MW; 79E852C69444472B CRC64;

Query Match

Best Local Similarity 100.0%; Score 2; DB 2; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LN 2
      ||
Db      3 LN 4

RESULT 43
Q9RSR1 ID Q9RSR1 PRELIMINARY; PRT; 9 AA.
AC Q9RSR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Putative transposase (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE.
RX MEDLINE=92085268; PubMed=1660923;
RA Pollard P., Preere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
RL in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; 5EE4C5B9C45AE333 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NF 3
      ||
Db      5 NF 6

RESULT 44
Q44377 ID Q44377 PRELIMINARY; PRT; 9 AA.
AC Q44377;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE ExeF' protein (Fragment).
GN EXE'F'.
OS Aeromonas trota.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29489;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 49659;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RT simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89468; CAA61651.1; -.
DR EMBL; X89468; CAA61651.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 45
Q44468 ID Q44468 PRELIMINARY; PRT; 9 AA.
AC Q44468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE ExeF' protein (Fragment).
GN EXE'F'.
OS Aeromonas veronii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=654;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1306-83;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RT simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89457; CAA61629.1; -.
DR EMBL; X89457; CAA61629.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 46
Q43928 ID Q43928 PRELIMINARY; PRT; 9 AA.
AC Q43928; Q43918; Q43920; Q43921;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DNA for EXE'F'-EXE'G intergenic region (Fragment).
GN EXE'F'.
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VARIOUS STRAINS;
RX MEDLINE=97089747; PubMed=8935655;
RA Karlyshev A.V., Macintyre S.;
RT "Study of the intergenic exeF-exeG region and its application as a
RT simple preliminary test for Aeromonas spp.";
RL FEMS Microbiol. Lett. 137:37-44(1996).
DR EMBL; X89464; CAA61643.1; -.
DR EMBL; X89462; CAA61639.1; -.
DR EMBL; X89460; CAA61635.1; -.
DR EMBL; X89463; CAA61641.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LN 2
      ||
Db      3 LN 4

RESULT 47
Q44001 ID Q44001 PRELIMINARY; PRT; 9 AA.
AC Q44001;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Exer' protein (Fragment).  
GN EXER'.  
OS Aeromonas eucenophila.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=649;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 9179-79;  
RX MEDLINE=97089747; PubMed=8935655;  
RA Karlyshev A.V., MacIntyre S.;  
RT "Study of the intergenic exef-exeG region and its application as a  
RT simple preliminary test for Aeromonas spp.";  
RL FEMS Microbiol. Lett. 137:37-44(1996).  
DR EMBL; X89461; CAA61637.1; -.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1059 MW; 785852C6944472B CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 3 LN 4

RESULT 48  
Q14715  
ID Q14715 PRELIMINARY; PRT; 9 AA.  
AC Q14715;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Keratin 14 (Fragment).  
GN KRT14.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;  
RT "Point mutations in human keratin 14 genes of epidermolysis bullosa  
RT simplex patients: Genetic and functional analyses.";  
RL Cell 66:1301-1311(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95072587; PubMed=7526926;  
RA Yamaniishi K., Matsuki M., Konishi K., Yasuno H.;  
RT "A novel mutation of Leri22 to phe at a highly conserved hydrophobic  
RT residue in the helix initiation motif of keratin 14 in epidermolysis  
RT bullosa simplex.";  
RL Hum. Mol. Genet. 3:1171-1172(1994).  
DR EMBL; D28807; BAA05967.1; -.  
FT NON TER 1  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1138 MW; BE300AA449C456D6 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 4 NF 5

RESULT 49  
Q9UCN5

ID Q9UCN5 PRELIMINARY; PRT; 9 AA.  
AC Q9UCN5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92291065; PubMed=1601862;  
RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;  
RT "Identification of cell-surface heparin/heparan sulfate-binding  
RT proteins of a human uterine epithelial cell line (RL95).";  
RL J. Biol. Chem. 267:11930-11939(1992).  
SQ SEQUENCE 9 AA; 1008 MW; CB56D0544732C732 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
||  
Db 5 LN 6

RESULT 50  
Q96417  
ID Q96417 PRELIMINARY; PRT; 9 AA.  
AC Q96417;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE SXL E1 form (Fragment).  
GN SXL.  
OS Drosophila virilis (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98337843; PubMed=9671597;  
RA Erickson J.W., Cline T.W.;  
RT "Key aspects of the primary sex determination mechanism are conserved  
RT across the genus Drosophila.";  
RL Development 125:3259-3268(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bell M., Cline T.W.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF046045; AAC97605.1; -.  
DR FlyBase; FBgn0016470; Dvir\Sxl.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1089 MW; 9A8BD1AA9C449CA CRC64;

Query Match 66.7%; Score 2; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
||  
Db 4 NF 5

RESULT 51  
Q9TRSO  
ID Q9TRSO PRELIMINARY; PRT; 9 AA.  
AC Q9TRSO;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)



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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calyculin-associated protein, CAP50=CA2+/phospholipid-binding protein
DE L-7 fragment (Fragment)
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
RT "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
RL NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;

Query Match 66.7%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3
Db 6 NF 7

RESULT 52
Q31653 PRELIMINARY; PRT; 9 AA.
ID Q31653
AC Q31653;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTOCHROME B.
OS Anser caerulescens (Snow goose).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8849;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=94141942; PubMed=8308909;
RA Quinn T.W., Wilson A.C.;
RT "Sequence evolution in and around the mitochondrial control region in
RT birds";
RL J. Mol. Evol. 37:417-425(1993).
RL DR EMBL; X77190; CAA54411.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1095 MW; 4751472693344B17 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 7 LN 8

RESULT 53
P90359 PRELIMINARY; PRT; 9 AA.
ID P90359
AC P90359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Barley mild mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

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OC Bymovirus.
OX NCBI_TaxID=12466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UK-M(R);
RA Peerenboom E., Jacobi V., Cartwright E.J., Adams M.J., Steinbiss H.H.,
RA Antoniw J.F.;
RT "A large duplication in the 3'-untranslated region of a sub-population
RT of RNA2 of the UK-M isolate of barley mild mosaic bymovirus.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL DR EMBL; X96970; CAA65658.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1177 MW; C40404473401F1B6 CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 6 LN 7

RESULT 54
Q84333 PRELIMINARY; PRT; 9 AA.
ID Q84333
AC Q84333;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Defective variant in 1449) with monkey alu-type insert
DE (Fragment).
OS Simian virus 40 (SV40).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10633;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054804; PubMed=6254029;
RA Dhruva B.R., Shenk T., Subramanian K.N.;
RT "Integration in vivo into Simian virus 40 DNA of a sequence that
RT resembles a certain family of genomic interspersed repeated
RT sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).
RL DR EMBL; K01001; AAA47875.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
Db 5 LN 6

RESULT 55
Q9R5N4 PRELIMINARY; PRT; 10 AA.
ID Q9R5N4
AC Q9R5N4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 35 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., Dasgupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or

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RT without hemagglutinating activity: do they share common amino acid  
 RT sequences and genes?;  
 RL J. Protein Chem. 10:415-425(1991).  
 FT NON\_TER 1 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1143 MW; CF3CB4A44735B456 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 6 LN 7

## RESULT 56

ID Q9RSN6 PRELIMINARY; PRT; 10 AA.  
 AC Q9RSN6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Neurotoxin type B HN+ 35 kDa SUBUNIT-BAND 3A (Fragment).  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92143938; PubMed=1781887;  
 RA Somers E.; DasGupta B.R.;  
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
 RT without hemagglutinating activity: do they share common amino acid  
 RT sequences and genes?";  
 RL J. Protein Chem. 10:415-425(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1169 MW; 00CF7E3AA4472054 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 5 LN 6

## RESULT 57

Q9F5W1  
 ID Q9F5W1 PRELIMINARY; PRT; 10 AA.  
 AC Q9F5W1;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE Cep (Fragment).  
 GN CEP.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9803;  
 RA Rui Y.Y., Kan B., Gao S.Y., Liu Y.Q., Qi G.M.;  
 RT "RS region of Vibrio cholerae O139 nct-Ctxphi, includes rstr (Rstr),  
 RT rsta (Rsta) and rstB (rstB) genes.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF302794; AAG27711.1;  
 FT NON\_TER 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1181 MW; 9DC61A34433735A5 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 9 LN 10

## RESULT 58

Q47091 PRELIMINARY; PRT; 10 AA.  
 ID Q47091;  
 AC Q47091;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Colicin E1 (Fragment).  
 OS Escherichia coli.  
 OG Plasmid ColE1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86094231; PubMed=3936034;  
 RA Waleh N.S.; Johnson P.H.;  
 RT "Structural and functional organization of the colicin E1 operon.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).  
 DR EMBL; M12543; AAA23065.1;  
 KW Plasmid.  
 FT NON\_TER 1 1  
 FT NON\_TER 1085 MW; 88F00B32CB144041 CRC64;  
 SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 1 LN 2

## RESULT 59

Q8GDC0 PRELIMINARY; PRT; 10 AA.  
 ID Q8GDC0  
 AC Q8GDC0;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Sulfonamide resistance protein (Fragment).  
 GN SULI.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Neonakis I.K.; Scoulica E.V.; Tselentis Y.J.;  
 RT "First detection of blaVIM-1 in an Escherichia coli clinical  
 RT isolate.";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY152821; AAN77116.1;  
 FT NON\_TER 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1106 MW; 91F57E205879D2D1 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 8 LN 9

RESULT 60  
Q8JOC2 PRELIMINARY; PRT; 10 AA.  
AC Q8JOC2; 2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hsp70 (Fragment).  
OS Encephalitozoon hellem.  
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=27973;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PV6/95, and PV7/95;  
RA Haro M., del Aguila C., Fenoy S., Henriques-Gil N.;  
RT "Genotype variability in the microsporidian Encephalitozoon hellem.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY171238; AAN73415.1; -;  
DR EMBL: AY171239; AAN73417.1; -;  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1100 MW; 107C0D472DD44DD4 CRC64;  
Query Match 66.7%; Score 2; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LN 2  
Db 7 LN 8

RESULT 61  
Q9UJ48 PRELIMINARY; PRT; 10 AA.  
AC Q9UJ48;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Latrophilin-2 (Fragment).  
GN LPHH1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99153747; PubMed=10030676;  
RA White G.R.M., Varley J.M., Heighway J.;  
RT "Isolation and characterisation of a human homologue of the  
latrophilin gene from a region of lp31.1 implicated in breast  
cancer.";  
RL Oncogene 17:3513-3519 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20225451; PubMed=10760572;  
RA White G.R.M., Varley J.M., Heighway J.;  
RT "Genomic structure and expression profile of LPHH1, a 7TM gene  
variably expressed in breast cancer cell lines.";  
RL Biochim. Biophys. Acta 1491:75-92 (2000).  
DR EMBL: AJ244514; CAB60206.1; -;  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;  
Query Match 66.7%; Score 2; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LN 2  
Db 4 LN 5

RESULT 62  
Q8WPE7 PRELIMINARY; PRT; 10 AA.  
AC Q8WPE7;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Opsin (Fragment).  
OS Skogsbergia leneri.  
OC Sukaryota; Metazoa; Arthropoda; Crustacea; Ostracoda; Myodocopa;  
OC Myodocopida; Cypridinoida; Cypridinidae; Skogsbergia.  
OX NCBI\_TaxID=176979;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Entire organism;  
RA Oakley T.H., Huber D.R.;  
RT "Eye-specific expression of multiple opsin loci in ostracod  
crustaceans.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF353372; AAL37547.1; -;  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1035 MW; 1F4B3117672DDDD4 CRC64;  
Query Match 66.7%; Score 2; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LN 2  
Db 2 LN 3

RESULT 63  
Q9TR49 PRELIMINARY; PRT; 10 AA.  
AC Q9TR49;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Amphoterin homolog (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96029671; PubMed=7592757;  
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,  
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.;  
RT "The receptor for advanced glycation end products (RAGE) is a cellular  
binding site for amphoterin. Mediation of neurite outgrowth and co-  
expression of rage and amphoterin in the developing nervous system.";  
RL J. Biol. Chem. 270:25752-25761 (1995).  
SQ SEQUENCE 10 AA; 1106 MW; 88BED1C452DAEDDA CRC64;  
Query Match 66.7%; Score 2; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NF 3  
Db 7 NF 8

RESULT 64  
Q8SPN8 PRELIMINARY; PRT; 10 AA.  
AC Q8SPN8;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Solute carrier family 6 member 4 (Fragment).

GN SLC6A4.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Nergren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;  
 RP "Construction of a targeted rhesus macaque microarray."  
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY083583; AAM11998.1; -.  
 DR EMBL; AY083583; AAM11998.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1043 MW; 3B07C4473412CAA8 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 7 LN 8

## RESULT 65

Q8WB7  
 ID Q8WB7 PRELIMINARY; PRT; 10 AA.  
 AC Q8WB7  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit I (Fragment).  
 GN COI.  
 OS Chaitophorus leucomelas.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 OC Aphidoidea; Drepanosiphidae; Chaitophorus.  
 OX NCBI\_TaxID=136351;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Shingleton A.W., Stern D.L.;  
 RT "Molecular phylogenetic evidence for multiple origins of ant mutualism  
 within the aphid genus Chaitophorus."  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF444288; AAL38565.1; -.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NF 3  
 ||  
 Db 9 NF 10

## RESULT 66

Q8WB2  
 ID Q8WB2 PRELIMINARY; PRT; 10 AA.  
 AC Q8WB2  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit 1 (Fragment).  
 GN COI.  
 OS Anolis punctatus.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
 OX NCBI\_TaxID=174263;

RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Glor R.E., Vitt L.J., Larson A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF337775; AAL72033.1; -.  
 DR EMBL; AF337776; AAL72035.1; -.  
 DR EMBL; AF337777; AAL72037.1; -.  
 KW Mitochondrion.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 3 LN 4

## RESULT 67

Q8WD18  
 ID Q8WD18 PRELIMINARY; PRT; 10 AA.  
 AC Q8WD18  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit 1 (Fragment).  
 GN COI.  
 OS Anolis transversalis.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
 OX NCBI\_TaxID=174264;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Glor R.E., Vitt L.J., Larson A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF337769; AAL72021.1; -.  
 KW Mitochondrion.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match 66.7%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2  
 ||  
 Db 3 LN 4

## RESULT 68

Q8W8Q3  
 ID Q8W8Q3 PRELIMINARY; PRT; 10 AA.  
 AC Q8W8Q3  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit 1 (Fragment).  
 GN COI.  
 OS Anolis nitens.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
 OX NCBI\_TaxID=174262;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Glor R.E., Vitt L.J., Larson A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF337802; AAL72087.1; -.  
 DR EMBL; AF337803; AAL72089.1; -.  
 DR EMBL; AF337804; AAL72091.1; -.

```

KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1349 MW; 4B3480C9D3640447 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 8; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 3 LN 4

RESULT 69
Q8W8Q4 PRELIMINARY; PRT; 10 AA.
AC Q8W8Q4; 20, Created
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Cytochrome oxidase subunit 1 (Fragment).
GN C01
OS Anolis punctatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174263;
RN [1]
RP SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337770; AAL72023.1; -
DR EMBL; AF337771; AAL72025.1; -
DR EMBL; AF337772; AAL72027.1; -
DR EMBL; AF337773; AAL72029.1; -
DR EMBL; AF337774; AAL72031.1; -
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1315 MW; 4B3480C733640447 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 8; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 3 LN 4

RESULT 70
Q9QVK8 PRELIMINARY; PRT; 10 AA.
AC Q9QVK8; 13, Created
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MEPRIN=METALLOENDOPEPTIDASE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=91363409; PubMed=1888759;
RA Flannery A.V., Macadam G.C., Beynon R.J.;
RT "Immunological characterisation of different meprin species in mice.";
RL Biochim. Biophys. Acta 1079:119-122(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1163 MW; DD6436144731B2C9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 11; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 6 LN 7

RESULT 71
O73588 PRELIMINARY; PRT; 10 AA.
AC O73588; 07, Created
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Engrailed-3 (Fragment).
GN EN-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryo;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U26148; AAC06186.1; -
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1118 MW; 73C0BE144735B72B CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 13; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2
Db 6 LN 7

RESULT 72
P82080 PRELIMINARY; PRT; 10 AA.
AC P82080; 13, Created
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DYNASTIN 2.
OS Limnodynastes dumerilii (Eastern Banjo Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=104065;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=TIBIAL GLAND;
RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
Limnodynastes terraereginae";
RL Aust. J. Chem. 46:833-842(1993).
CC -1- MASS SPECTROMETRY: MW=986; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 10 AA; 986 MW; 550FDC287735A5B7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 13; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LN 2

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Db      8 LN 9
||
RESULT 73
Q9AIZ7 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
BA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211132; AAK15377.1; -.
KW Aminoacyl-tRNA synthetase.
FT NON TER 1
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 2 LN 3

RESULT 74
Q9R4B1 PRELIMINARY; PRT; 11 AA.
AC Q9R4B1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE BX protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE.
RX MEDLINE=95252678; PubMed=7734831;
RA Gerlach D., Gunther E., Kohler W., Vettermann S., Fleischer B.,
RA Schmidt K.H.;
RT "Isolation and characterization of a mitogen characteristic of group A
streptococci (Streptococcus pyogenes).";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 282:67-
82(1995).
SQ SEQUENCE 11 AA; 1216 MW; CE527287CAA455A2 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 1 LN 7

Db 10 LN 11
||
RESULT 75
Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LN 2
||
Db 6 LN 7

Search completed: November 25, 2003, 19:34:16
Job time : 7.63372 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 7.65698 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq\_19Jun03.\*

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2: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	3	22	Colostrin derixe
2	3	100.0	4	11	AA074278
3	3	100.0	4	12	AA010879
4	3	100.0	4	12	AA010883
5	3	100.0	4	12	AA011232
6	3	100.0	4	14	AA065692
7	3	100.0	4	19	AA080261
8	3	100.0	4	20	AA015702
9	3	100.0	4	20	AA015671

10	3	100.0	4	21	AA080828	Fluorophore-label
11	3	100.0	4	21	AA080856	Fluorophore-label
12	3	100.0	5	14	AA065691	HIV-1 inhibiting p
13	3	100.0	5	19	AA080256	Oxirane compound w
14	3	100.0	5	19	AA080257	Peptide used to ma
15	3	100.0	5	20	AA015749	Peptide used to ma
16	3	100.0	5	20	AA015699	Peptide used to ma
17	3	100.0	5	21	AA015701	Fluorophore-label
18	3	100.0	5	21	AA080853	Fluorophore-label
19	3	100.0	5	21	AA080855	Fluorophore-label
20	3	100.0	5	21	AA080903	Fluorophore-label
21	3	100.0	5	23	AA015547	Australian taipan
22	3	100.0	5	23	AA085424	Human colon specif
23	3	100.0	6	11	AA066673	Retroviral proteas
24	3	100.0	6	13	AA028733	Protease chromogen
25	3	100.0	6	18	AA042234	Biotinylated S-pro
26	3	100.0	6	19	AA054253	Acylated peptide c
27	3	100.0	6	20	AA015740	Peptide used to ma
28	3	100.0	6	20	AA015698	Peptide used to ma
29	3	100.0	6	20	AA015700	Peptide used to ma
30	3	100.0	6	21	AA080852	Fluorophore-label
31	3	100.0	6	21	AA080854	Fluorophore-label
32	3	100.0	6	21	AA080894	Fluorophore-label
33	3	100.0	7	11	AA066674	Retroviral proteas
34	3	100.0	7	12	AA012883	Retroviral proteas
35	3	100.0	7	14	AA065689	HIV-1 inhibiting p
36	3	100.0	7	19	AA080253	Oxirane compound w
37	3	100.0	7	20	AA015697	Peptide used to ma
38	3	100.0	7	20	AA015651	Peptide used to ma
39	3	100.0	7	21	AA085415	Drosophila Bag pro
40	3	100.0	7	21	AA085416	Blk protein fragme
41	3	100.0	7	21	AA080815	Fluorophore-label
42	3	100.0	7	21	AA080881	Fluorophore-label
43	3	100.0	7	21	AA080881	Core polypeptide f
44	3	100.0	7	22	AB001089	Viral core polypep
45	3	100.0	7	22	AB025338	Dp178-like/Dp107-1
46	3	100.0	7	22	AA013635	H11 binding site c
47	3	100.0	7	22	AA044074	H11 binding site c
48	3	100.0	7	22	AA044079	H11 binding site c
49	3	100.0	7	22	AA044124	H11 binding site c
50	3	100.0	7	22	AA044129	H11 binding site c
51	3	100.0	7	22	AA044134	H11 binding site c
52	3	100.0	7	22	AA044139	H11 binding site c
53	3	100.0	7	22	AA044144	H11 binding site c
54	3	100.0	7	22	AA044150	H11 binding site c
55	3	100.0	7	22	AA044560	H11 binding site c
56	3	100.0	7	22	AA044565	H11 binding site c
57	3	100.0	7	22	AA044570	H11 binding site c
58	3	100.0	7	22	AA044575	H11 binding site c
59	3	100.0	7	22	AA044661	H11 binding site c
60	3	100.0	7	22	AA045665	H11 binding site c
61	3	100.0	7	22	AA045884	H11 binding site c
62	3	100.0	7	22	AA045974	H11 binding site c
63	3	100.0	7	22	AA046173	H11 binding site c
64	3	100.0	7	22	AA046416	H11 binding site c
65	3	100.0	7	22	AA046609	H11 binding site c
66	3	100.0	7	22	AA046895	H11 binding site c
67	3	100.0	7	22	AA078082	Core polypeptide T
68	3	100.0	7	24	ABJ37364	G-protein coupled
69	3	100.0	7	24	ABJ37444	Protease chromogen
70	3	100.0	8	13	AA028732	PR/RT HIV protease
71	3	100.0	8	15	AA063662	Synthetic pMEL17 p
72	3	100.0	8	18	AA038400	Molecular mimetic
73	3	100.0	8	19	AA075537	Mammalian tub prot
74	3	100.0	8	20	AA075463	Human immunodefici
75	3	100.0	8	21	AA070353	HIV A01 super moti
76	3	100.0	8	22	ABP11732	HIV A01 super moti
77	3	100.0	8	22	ABP11733	HIV A24 super moti
78	3	100.0	8	22	ABP15843	HIV A24 super moti
79	3	100.0	8	22	ABP15844	HIV B62 super moti
80	3	100.0	8	22	ABP19130	HIV B62 super moti
81	3	100.0	8	22	ABP19336	HIV A03 motif pol
82	3	100.0	8	22	ABP21231	

83 HIV A03 motif pol  
 84 Peptide #42 for il  
 85 Murine Ob receptor  
 86 HIV peptide SEQ ID  
 87 HIV peptide SEQ ID  
 88 HIV peptide SEQ ID  
 89 Hepatitis C virus  
 90 Hepatitis B virus  
 91 Hepatitis B virus  
 92 Hepatitis B virus  
 93 Hepatitis B virus  
 94 Hepatitis B virus  
 95 Hepatitis B virus  
 96 Hepatitis B virus  
 97 Hepatitis B virus  
 98 Hepatitis B virus  
 99 Hepatitis B virus  
 100 Hepatitis B virus

XX Sequence 3 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 1 LNF 3

RESULT 2  
 AAR04018  
 ID AAR04018 standard; Protein; 4 AA.

XX AAR04018;  
 XX 25-MAR-2003 (updated)  
 DT 19-NOV-1991 (first entry)

XX Peptidase substrate analogues having peptidase inhibition activity.  
 XX Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;  
 KW Angiotensin converting enzyme.  
 XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 4  
 FT /label= Terminal modified from -COOH to -COCOR  
 FT /note= "R = alkyl group or -H"

XX EF363284-A.

XX 11-APR-1990.  
 XX 06-OCT-1989; 89EP-0402762.  
 XX 07-OCT-1988; 88US-0254762.  
 PR 06-OCT-1989; 89EP-0402763.

XX (RICH ) MERRELL DOW PHARM INC.  
 PA (RICH ) MERRELL PHARM INC.  
 XX Bey P, Angelastro M, Mehdi S;  
 PI WPI; 1990-109579/15.

XX New peptidase substrate analogue cpds. - useful as protease  
 PT inhibitors in treatment of disease states.  
 XX Claim 45; Page 31; 33pp; English.

XX The analogues may be useful in treatment of a variety of disease  
 CC states. The scissile amide group is replaced with H or a substituted  
 CC Carbon moiety effectively inhibiting the activity of peptidases such  
 CC as elastase, plasmin thrombin, urokinase etc.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 4 AA;

Query Match 100.0%; Score 3; DB 11; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 3  
 AAR10879

## ALIGNMENTS

RESULT 1  
 AAB72278  
 ID AAB72278 standard; peptide; 3 AA.  
 AC AAB72278;  
 XX 14-MAY-2001 (first entry)  
 DT Colostrin derived cytokine inducing peptide SEQ ID 33.  
 DE Colostrin; immune response; cytokine; blood cell proliferation;  
 XX central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX Synthetic.  
 XX WO200111937-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22818.  
 XX 17-AUG-1999; 99US-0149311.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX Stanton GV, Hughes TK, Boldogh I, Georgiades J;  
 DR WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrin as an immunological  
 PT regulator -  
 XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.



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ID XX AAR10879 standard; Protein; 4 AA.
AC XX AAR10879;
DT XX 10-APR-1991 (first entry)
DE XX Peptide component of pentafluoroethylcarbonyl analogue.
KW XX Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis;
KW XX male contraceptive.
XX OS Synthetic.
XX PN EP410411-A.
XX PD 30-JAN-1991.
XX PF 25-JUL-1990; 90EP-0114250.
XX XX 26-JUL-1989; 89US-0385624.
XX PA (RICH ) MERRELL DOW PHARM INC.
XX PI Bey P, Peet NP, Angelastro MR, Mehdi S;
XX DR WPI; 1991-030811/05.
XX PT Novel serine-, carboxylic acid- and metallo-proteinase-inhibitors
XX - inhibit range of proteinase(s) in treating rheumatoid
XX arthritis, thrombosis and psoriasis, also is a male contraceptive
XX Claim 44; page 28; 40pp; English.
XX CC This peptide is the R1 gp. of the cpd. of formula: RINHCH(R2)-
XX COCF2CF3. This cpd. is a peptidase substrate analogue and is a
XX specific enzyme inhibitor for a range of proteases, e.g. serine-,
XX carboxylic acid-, and metallo-proteases. It is useful in the
XX treatment of rheumatoid arthritis, thrombosis and psoriasis and is
XX also used as a male contraceptive. See also AAR10876-82 and AAR10886-
XX 88.
XX SQ Sequence 4 AA;
XX Query Match 100.0%; Score 3; DB 12; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
DB 2 LNF 4
RESULT 5
AAR11232
ID AAR11232 standard; Protein; 4 AA.
AC AAR11232;
XX DT 24-MAY-1991 (first entry)
XX DE Ketone analogue protease inhibitor #11.
XX KW protease inhibitor; antiinflammatory agent; hypotensive; analgesic;
XX antiproliferative agent; antidemyelinating agent; antithrombotic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /label= carboxyloxalyl-Phe
XX FT
XX EP417721-A.
XX PN
XX XX 20-MAR-1991.
XX XX
XX PF 11-SEP-1990; 90EP-0117461.
XX XX
XX PR 11-SEP-1989; 89US-0405491.
XX XX
XX PA (RICH ) MERRELL DOW PHARM INC.
XX PI Flynn GA, Bey P;
XX XX
XX DR WPI; 1991-081980/12.
XX XX
XX PT New ketone analogue peptidase and isomerase inhibitors - for
XX inhibition of leukocyte elastase, cathepsin G, thrombin,
XX chymotrypsin, plasmin etc.
XX PS Claim 44; Page 30; 50pp; English.
XX XX
XX CC This peptide is a specific example of a highly generic protease

```

CC inhibitor useful for medical purposes. The peptide analogues include  
 CC inhibitors of urokinase, renin, cathepsin D, etc. which can be used  
 CC as anti-proliferative agents and abortifacients, hypotensives,  
 CC antiinflammatory and antidiemvelinating agents, respectively.  
 CC See also AAR11222-R11230 and AAR11231-R11238.

XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 3; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 6  
 AAR65692  
 ID AAR65692 standard; peptide; 4 AA.  
 XX  
 AC AAR65692;

XX 25-MAR-2003 (updated)  
 DT 08-JAN-1995 (first entry)

XX HIV-1 inhibiting pseudopeptide.

XX Aspartic proteinase; reversible inhibitor; pseudopeptide;  
 KW phosphinate methylene ammonium group; exploding transition analogue;  
 HIV-1.

XX Synthetic.

FT Key Location/Qualifiers  
 FT Modified-site 1 /note= "Acetyl-Leu"  
 FT Modified-site 3..4  
 FT Modified-site 4 /note= "CONH linkage replaced by P(O) (OH) CH2NH"  
 FT /label= OTHER  
 FT /note= "piperidine-2(S)-carbonyl tert. butylamide  
 FT or (4aS, 8aS)-decahydro-3(S)-isoquinoline  
 FT carbonyl tert. butylamide"

XX WO9314114-A1.

XX 22-JUL-1993.

XX 11-JAN-1993; 93WO-US00228.

XX 09-JAN-1992; 92US-0819356.

XX (SCRI ) SCRIPPS RES INST.

XX Ikeda S, Janda KD, Wirsching P;

XX WPI; 1993-243142/30.

XX New peptide linkage unit - comprising phosphinate methylene  
 PT ammonium gp., esp. for pseudo-peptide aspartic proteinase  
 PT inhibitors

XX Claims 37,38; Page 71; 76pp; English.

XX The invention relates to a phosphinic acid methylene amine linkage  
 CC PO(OH)CH2NH to be used in place of a peptide linkage CONH at the  
 CC cleavage site in an aspartic proteinase substrate. The linkage is  
 CC resistant to cleavage and serves as an exploding transition state  
 CC analogue of the cleavage site, thus the peptide containing it can  
 CC bind or interfere with the active site of the aspartic proteinase  
 CC enzyme and inhibit its activity.

CC The present sequence is a specifically claimed example of a

CC HIV-1 inhibiting peptide containing the linkage.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4 AA;

Query Match 100.0%; Score 3; DB 14; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 7  
 AAW80261  
 ID AAW80261 standard; peptide; 4 AA.  
 XX  
 AC AAW80261;

XX 06-JAN-1999 (first entry)

XX Oxirane compound which is an inhibitor of HIV-1 protease.

XX Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;  
 KW gag; pol; HIV-1 protease.

XX Synthetic.

XX US5827827-A.

XX 27-OCT-1998.

XX 20-JUN-1996; 96US-0667001.

XX 20-JUN-1996; 96US-0667001.

XX 16-FEB-1995; 95US-0335039.

XX (SCRI ) SCRIPPS RES INST.

XX Janda KD, Wirsching P;

XX WPI; 1998-594033/50.

XX Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used  
 PT as human immunodeficiency virus protease inhibitors

XX Disclosure; Column 10; 29pp; English.

XX The present sequence is part of an oxirane compound which acts as a  
 CC human immunodeficiency virus (HIV) protease inhibitor. The compounds  
 CC have a terminal epoxide moiety. The compounds inhibit HIV protease  
 CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1  
 CC protease.

XX Sequence 4 AA;

Query Match 100.0%; Score 3; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 8  
 AAY15702  
 ID AAY15702 standard; Peptide; 4 AA.  
 XX  
 AC AAY15702;

XX 27-JUL-1999 (first entry)

XX DE Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;

XX KW apoptosis; protease; peptidase; apoptosis cascade; cancer;

XX KW chemotherapeutic agent; cell death; viral protease activity.

OS OS Synthetic.

XX PN WO9918856-A1.

XX PD 22-APR-1999.

XX PF 09-OCT-1998; 98WO-US21231.

XX PR 03-MAR-1998; 98US-0033661.

XX PR 10-OCT-1997; 97US-0061582.

XX PA (CYTO-) CYTOVIA INC.

XX PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX PI WPI; 1999-312448/26.

XX DR New fluorogenic or fluorescent reporter molecules

XX PT Disclosure; Page 183; 202pp; English.

XX PS AAY15618-Y15759 represent peptides used to make the fluorogenic or

XX CC fluorescent reporter molecules of the invention. These molecules

XX CC contain a peptide moiety (e.g. present sequence) which acts as a

XX CC substrate for enzymes involved in apoptosis or protease or peptidase

XX CC enzymes. The compounds can be used as fluorogenic or fluorescent

XX CC substrates for enzymes. Depending on the peptide moiety used, the

XX CC fluorescent molecules can be used for detecting or measuring the

XX CC activity of an enzyme involved in the apoptosis cascade in cells; to

XX CC determine whether a test compound has an effect on an enzyme involved

XX CC in the apoptosis cascade in cells; for determining the sensitivity of

XX CC an animal with cancer to treatment with chemotherapeutic agents or

XX CC enhancing cell death of test cells; for detecting or measuring the

XX CC activity of a viral protease in cells; for determining whether a test

XX CC compound has an effect on the activity of a viral protease in cells;

XX CC and for measuring the activity or determining whether a test substance

XX CC has an effect on the activity of a protease or peptidase in cells.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 1 LNF 3

RESULT 9

AAY15671

ID AAY15671 standard; Peptide; 4 AA.

XX AC AAY15671;

XX DT 27-JUL-1999 (first entry)

XX DE Peptide used to make fluorescent reporter molecules.

XX KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;

XX KW apoptosis; protease; peptidase; apoptosis cascade; cancer;

XX KW chemotherapeutic agent; cell death; viral protease activity.

OS OS Synthetic.

PN WO9918856-A1.

XX PD 22-APR-1999.

XX PF 09-OCT-1998; 98WO-US21231.

XX PR 03-MAR-1998; 98US-0033661.

XX PR 10-OCT-1997; 97US-0061582.

XX PA (CYTO-) CYTOVIA INC.

XX PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX PI WPI; 1999-312448/26.

XX DR New fluorogenic or fluorescent reporter molecules

XX PT Disclosure; Page 174; 202pp; English.

XX PS AAY15618-Y15759 represent peptides used to make the fluorogenic or

XX CC fluorescent reporter molecules of the invention. These molecules

XX CC contain a peptide moiety (e.g. present sequence) which acts as a

XX CC substrate for enzymes involved in apoptosis or protease or peptidase

XX CC enzymes. The compounds can be used as fluorogenic or fluorescent

XX CC substrates for enzymes. Depending on the peptide moiety used, the

XX CC fluorescent molecules can be used for detecting or measuring the

XX CC activity of an enzyme involved in the apoptosis cascade in cells; to

XX CC determine whether a test compound has an effect on an enzyme involved

XX CC in the apoptosis cascade in cells; for determining the sensitivity of

XX CC an animal with cancer to treatment with chemotherapeutic agents or

XX CC enhancing cell death of test cells; for detecting or measuring the

XX CC activity of a viral protease in cells; for determining whether a test

XX CC compound has an effect on the activity of a viral protease in cells;

XX CC and for measuring the activity or determining whether a test substance

XX CC has an effect on the activity of a protease or peptidase in cells.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 20; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 2 LNF 4

RESULT 10

AAY80828

ID AAY80828 standard; peptide; 4 AA.

XX AC AAY80828;

XX DT 22-MAY-2000 (first entry)

XX DE Fluorophore-labelled HIV protease substrate peptide, SEQ ID NO:54.

XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;

XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;

XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.

OS OS Synthetic.

XX PN WO200004914-A1.

XX PD 03-FEB-2000.

XX PF 21-JUL-1999; 99WO-US16423.

XX PR 21-JUL-1998; 98US-0093642.

XX PA (CYTO-) CYTOVIA INC.

PA (ZHAN/) ZHANG H.  
 PA (CAIS/) CAI S X.  
 PA (DREW/) DREWE J A.  
 PA (YANG/) YANG W.  
 XX  
 FI Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI; 2000-195079/17.  
 DR  
 XX  
 XX  
 PT New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group -  
 XX  
 XX  
 PS Disclosure; Page 36; 174pp; English.  
 XX  
 XX  
 CC The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti- angiogenic or anticancer agents. Sequences  
 CC AAY80782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.  
 XX  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 11  
 AAY80856  
 ID AAY80856 standard; peptide; 4 AA.  
 XX  
 AC AAY80856;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:85.  
 XX  
 KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200004914-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-US16423.  
 XX  
 PR 21-JUL-1998; 98US-0093642.  
 XX  
 PA (CYTO-) CYTOVIA INC.  
 FA (ZHAN/) ZHANG H.  
 PA (CAIS/) CAI S X.

PA (DREW/) DREWE J A.  
 PA (YANG/) YANG W.  
 XX  
 FI Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI; 2000-195079/17.  
 DR  
 XX  
 XX  
 PT New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group -  
 XX  
 XX  
 PS Claim 30; Page 109; 174pp; English.  
 XX  
 XX  
 CC The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti- angiogenic or anticancer agents. Sequences  
 CC AAY80782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.  
 XX  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 1 LNF 3

RESULT 12  
 AAR65691  
 ID AAR65691 standard; peptide; 5 AA.  
 XX  
 AC AAR65691;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 08-JAN-1995 (first entry)  
 XX  
 DE HIV-1 inhibiting pseudopeptide.  
 XX  
 KW Aspartic proteinase; reversible inhibitor; pseudopeptide;  
 KW phosphate methylene ammonium group; exploding transition analogue;  
 KW HIV-1.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Acetyl-Ser"  
 FT Modified-site 4..5 /note= "CONH linkage replaced by P(O) (OH) CH2NH"  
 FT Modified-site 5 /label= OTHER  
 FT 21-JUL-1998; 98US-0093642.  
 FT (CYTO-) CYTOVIA INC.  
 FT (ZHAN/) ZHANG H.  
 FT (CAIS/) CAI S X.

```

XX PD 22-JUL-1993.
XX XX
XX PF 11-JAN-1993; 93WO-US00228.
XX XX
XX PR 09-JAN-1992; 92US-0819356.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Ikeda S, Janda KD, Wirsching P;
XX DR WPI; 1993-243142/30.
XX XX
XX PT New peptide linkage unit - comprising phosphinate methylene
XX PT ammonium gp., esp. for pseudo-peptide aspartic proteinase
XX PT inhibitors
XX XX
XX PS Claim 35; Page 70; 76pp; English.
XX XX
XX CC The invention relates to a phosphinic acid methylene amine linkage
XX CC PO(OH)CH2NH to be used in place of a peptide linkage CONH at the
XX CC cleavage site in an aspartic proteinase substrate. The linkage is
XX CC resistant to cleavage and serves as an exploding transition state
XX CC analogue of the cleavage site. Thus the peptide containing it can
XX CC bind or interfere with the active site of the aspartic proteinase
XX CC enzyme and inhibit its activity.
XX CC The present sequence is a specifically claimed example of a
XX CC HIV-1 inhibiting peptide containing the linkage.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX XX
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNF 3
Db |||
2 LNF 4

RESULT 13
AAW80256
ID AAW80256 standard; peptide; 5 AA.
XX XX
XX AC AAW80256;
XX XX
XX DT 06-JAN-1999 (first entry)
XX DE Oxirane compound which is an inhibitor of HIV-1 protease.
XX KW Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
XX KW gag; pol; HIV-1 protease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Ser is linked to CH3C(O) "
XX FT Modified-site 4..5
XX FT Modified-site 5 /note= "these residues are linked by a pseudo
XX FT peptide linkage comprising 1-epoxy-ethylene"
XX FT /note= "PIC-NH-tBu, where
XX FT PIC=piperidine-2-(S)-carboxyl (proline
XX FT analogue), and tBu=tert-butyl"
XX PN US5827827-A.
XX XX
XX PD 27-OCT-1998.
XX XX
XX PF 20-JUN-1996; 96US-0667001.
XX XX
XX PR 20-JUN-1996; 96US-0667001.
XX PR 16-FEB-1995; 95US-0335039.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Janda KD, Wirsching P;
XX DR WPI; 1998-594033/50.
XX XX

Query Match 100.0%; Score 3; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LNF 3
Db |||
2 LNF 4

RESULT 14
AAW80257
ID AAW80257 standard; peptide; 5 AA.
XX XX
XX AC AAW80257;
XX XX
XX DT 06-JAN-1999 (first entry)
XX DE Oxirane compound which is an inhibitor of HIV-1 protease.
XX KW Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
XX KW gag; pol; HIV-1 protease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Ser is linked to CH3C(O) "
XX FT Modified-site 4..5
XX FT Modified-site 5 /note= "these residues are linked by a pseudo
XX FT peptide linkage comprising 1-epoxy-ethylene"
XX FT /note= "PIC-NH-tBu, where
XX FT PIC=(4aS,8aS)-decahydro-3(S)-isoquinoline
XX FT carbonyl (proline analogue),
XX FT and tBu=tert-butyl"
XX PN US5827827-A.
XX XX
XX PD 27-OCT-1998.
XX XX
XX PF 20-JUN-1996; 96US-0667001.
XX XX
XX PR 20-JUN-1996; 96US-0667001.
XX PR 16-FEB-1995; 95US-0335039.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Janda KD, Wirsching P;
XX DR WPI; 1998-594033/50.
XX XX

```

PT Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used  
 PT as human immunodeficiency virus protease inhibitors  
 XX  
 PS Disclosure; Column 9; 29pp; English.

XX The present sequence is part of an oxirane compound which acts as a  
 CC human immunodeficiency virus (HIV) protease inhibitor. The compounds  
 CC have a terminal epoxide moiety. The compounds inhibit HIV protease  
 CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1  
 CC protease.  
 XX  
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 15

AAV15749  
 ID AAY15749 standard; Peptide; 5 AA.

XX AAY15749;

XX 27-JUL-1999 (first entry)

DE Peptide used to make fluorescent reporter molecules.

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX

OS Synthetic.

XX WO9918856-A1.

XX 22-APR-1999.

PF 09-OCT-1998; 98WO-US21231.

XX 03-MAR-1998; 98US-0033661.

PR 10-OCT-1997; 97US-0061582.

XX (CYTO-) CYTOVIA INC.

XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX WPI; 1999-312448/26.

XX New fluorogenic or fluorescent reporter molecules

PS Claim 39; Page 196; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance

CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 16

AAV15699  
 ID AAY15699 standard; Peptide; 5 AA.

XX AAY15699;

XX 27-JUL-1999 (first entry)

DE Peptide used to make fluorescent reporter molecules.

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX

OS Synthetic.

XX WO9918856-A1.

XX 22-APR-1999.

PF 09-OCT-1998; 98WO-US21231.

XX 03-MAR-1998; 98US-0033661.

PR 10-OCT-1997; 97US-0061582.

XX (CYTO-) CYTOVIA INC.

XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX WPI; 1999-312448/26.

XX New fluorogenic or fluorescent reporter molecules

PS Disclosure; Page 182; 202pp; English.

XX AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.

XX Sequence 5 AA;

Query Match 100.0%; Score 3; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

```

Db          |||
            2 LNF 4

RESULT 17
AAV15701
ID  AAV15701 standard; Peptide; 5 AA.
XX
XX  AAV15701;
XX
XX  27-JUL-1999 (first entry)
XX
XX  Peptide used to make fluorescent reporter molecules.
DE
XX
XX  Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW  apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW  chemotherapeutic agent; cell death; viral protease activity.
XX
XX  Synthetic.
XX
XX  WO9918856-A1.
XX
XX  22-APR-1999.
XX
XX  09-OCT-1998; 98WO-US21231.
XX
XX  03-MAR-1998; 98US-0033661.
XX  10-OCT-1997; 97US-0061582.
XX
XX  (CYTO-) CYTOVIA INC.
XX
XX  Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
XX  WPI; 1999-312448/26.
XX
XX  New fluorogenic or fluorescent reporter molecules
XX
XX  Disclosure; Page 182; 202pp; English.
XX
XX  AAV15618-Y1579 represent peptides used to make the fluorogenic or
CC  fluorescent reporter molecules of the invention. These molecules
CC  contain a peptide moiety (e.g. present sequence) which acts as a
CC  substrate for enzymes involved in apoptosis or protease or peptidase
CC  enzymes. The compounds can be used as fluorogenic or fluorescent
CC  substrates for enzymes. Depending on the peptide moiety used, the
CC  fluorescent molecules can be used for detecting or measuring the
CC  activity of an enzyme involved in the apoptosis cascade in cells; to
CC  determine whether a test compound has an effect on an enzyme involved
CC  in the apoptosis cascade in cells; for determining the sensitivity of
CC  an animal with cancer to treatment with chemotherapeutic agents or
CC  determining whether a test substance inhibits, prevents, causes or
CC  enhances cell death of test cells; for detecting or measuring the
CC  activity of a viral protease in cells; for determining whether a test
CC  compound has an effect on the activity of a viral protease in cells;
CC  and for measuring the activity or determining whether a test substance
CC  has an effect on the activity of a protease or peptidase in cells.
XX
XX  Sequence 5 AA;
SQ
Query Match 100.0%; Score 3; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
            |||
Db          1 LNF 3

RESULT 18
AAV80853
ID  AAV80853 standard; peptide; 5 AA.
XX
XX  AAV80853;
AC  AAV80853;

XX  22-MAY-2000 (first entry)
XX
XX  Fluorophore-labelled protease substrate peptide, SEQ ID NO:82.
DE
XX
XX  Protease substrate; fluorescent label; fluorophore; rhodamine;
KW  blocking group; halobenzoyl group; cleavage; caspase; viral protease;
KW  methionine aminopeptidase type 2; MetAP-2; drug screening.
XX
XX  Synthetic.
XX
XX  WO200004914-A1.
XX
XX  03-FEB-2000.
XX
XX  21-JUL-1999; 99WO-US16423.
XX
XX  21-JUL-1998; 98US-0093642.
XX
XX  (CYTO-) CYTOVIA INC.
XX  (ZHAN/) ZHANG H.
XX  (CAIS/) CAI S X.
XX  (DREW/) DREWE J A.
XX  (YANG/) YANG W.
XX
XX  Zhang H, Cai SX, Drewe JA, Yang W;
XX  WPI; 2000-195079/17.
XX
XX  New fluorescently labeled amino acids or peptides, used as substrates
XX  for detecting enzymes or their modulators, e.g. anticancer or antiviral
XX  agents, contains a halobenzoyl N-blocking group -
XX
XX  Claim 30; Page 109; 174pp; English.
XX
XX  The invention relates to fluorescently labelled peptides containing
CC  a halobenzoyl group on the fluorophore. They are of the structure
CC  peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
CC  group, Y is a fluorescent or fluorogenic moiety (preferably a
CC  rhodamine), and the peptide-Y bond is cleavable by the enzyme being
CC  assayed. The labelled peptides are reporters for detecting intracellular
CC  proteolytic enzymes, particularly caspases and other enzymes involved in
CC  apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
CC  cytomegalovirus and hepatitis C virus proteases); and methionine
CC  aminopeptidase type 2 (MetAP-2). The peptides are particularly useful to
CC  identify modulators of these enzymes which may be potentially useful as
CC  agents for treating conditions such as cancer, neurodegeneration,
CC  autoimmune diseases, myocardial infarction and viral infection.
CC  Modulators identified may also be used to prolong the life of cells being
CC  cultured for recombinant protein production, or to monitor the treatment
CC  of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
CC  potential anti- angiogenic or anticancer agents. Sequences
CC  AAY80782-Y80910 represent peptides, some of which are specifically
CC  claimed, which may be used in assay methods according to the invention.
XX
XX  Sequence 5 AA;
SQ
Query Match 100.0%; Score 3; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
            |||
Db          2 LNF 4

RESULT 19
AAV80855
ID  AAV80855 standard; peptide; 5 AA.
XX
XX  AAV80855;
AC  AAV80855;
XX
XX  22-MAY-2000 (first entry)
XX

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XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:84.  
 XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX OS Synthetic.  
 XX PN WO200004914-A1.  
 XX PD 03-FEB-2000.  
 XX PF 21-JUL-1999; 99WO-US16423.  
 XX PR 21-JUL-1998; 98US-0093642.  
 XX PA (CYTO-) CYTOVIA INC.  
 XX PA (ZHAN/) ZHANG H.  
 XX PA (CAIS/) CAI S X.  
 XX PA (DREW/) DREWE J A.  
 XX PA (YANG/) YANG W.  
 XX PI Zhang H, Cai SX, Drewe JA, Yang W;  
 XX DR WPI; 2000-195079/17.  
 XX PT New fluorescently labeled amino acids or peptides, used as substrates  
 XX PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 XX PT agents, contains a halobenzoyl N-blocking group -  
 XX PS Claim 30; Page 109; 174pp; English.  
 XX CC The invention relates to fluorescently labelled peptides containing  
 XX CC a halobenzoyl group on the fluorophore. They are of the structure  
 XX CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 XX CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 XX CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 XX CC assayed. The labelled peptides are reporters for detecting intracellular  
 XX CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 XX CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 XX CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 XX CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 XX CC identify modulators of these enzymes which may be potentially useful as  
 XX CC agents for treating conditions such as cancer, neurodegeneration,  
 XX CC autoimmune diseases, myocardial infarction and viral infection.  
 XX CC Modulators identified may also be used to prolong the life of cells being  
 XX CC cultured for recombinant protein production, or to monitor the treatment  
 XX CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 XX CC potential anti- angiogenic or anticancer agents. Sequences  
 XX CC AAY80782-Y80910 represent peptides, some of which are specifically  
 XX CC claimed, which may be used in assay methods according to the invention.  
 XX SQ Sequence 5 AA;  
 XX Query Match 100.0%; Score 3; DB 21; Length 5;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 LNF 3  
 XX Db 1 LNF 3  
 XX RESULT 20  
 XX AAY80903  
 XX ID AAY80903 standard; peptide; 5 AA.  
 XX AC AAY80903;  
 XX AC AAY80903;  
 XX DT 22-MAY-2000 (first entry)  
 XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:132.

XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX OS Synthetic.  
 XX PN WO200004914-A1.  
 XX PD 03-FEB-2000.  
 XX PF 21-JUL-1999; 99WO-US16423.  
 XX PR 21-JUL-1998; 98US-0093642.  
 XX PA (CYTO-) CYTOVIA INC.  
 XX PA (ZHAN/) ZHANG H.  
 XX PA (CAIS/) CAI S X.  
 XX PA (DREW/) DREWE J A.  
 XX PA (YANG/) YANG W.  
 XX PI Zhang H, Cai SX, Drewe JA, Yang W;  
 XX DR WPI; 2000-195079/17.  
 XX PT New fluorescently labeled amino acids or peptides, used as substrates  
 XX PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 XX PT agents, contains a halobenzoyl N-blocking group -  
 XX PS Claim 29; Page 109; 174pp; English.  
 XX CC The invention relates to fluorescently labelled peptides containing  
 XX CC a halobenzoyl group on the fluorophore. They are of the structure  
 XX CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 XX CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 XX CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 XX CC assayed. The labelled peptides are reporters for detecting intracellular  
 XX CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 XX CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 XX CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 XX CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 XX CC identify modulators of these enzymes which may be potentially useful as  
 XX CC agents for treating conditions such as cancer, neurodegeneration,  
 XX CC autoimmune diseases, myocardial infarction and viral infection.  
 XX CC Modulators identified may also be used to prolong the life of cells being  
 XX CC cultured for recombinant protein production, or to monitor the treatment  
 XX CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 XX CC potential anti- angiogenic or anticancer agents. Sequences  
 XX CC AAY80782-Y80910 represent peptides, some of which are specifically  
 XX CC claimed, which may be used in assay methods according to the invention.  
 XX SQ Sequence 5 AA;  
 XX Query Match 100.0%; Score 3; DB 21; Length 5;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 LNF 3  
 XX Db 2 LNF 4  
 XX RESULT 21  
 XX AAO15547  
 XX ID AAO15547 standard; protein; 5 AA.  
 XX AC AAO15547;  
 XX AC AAO15547;  
 XX DT 24-OCT-2002 (first entry)  
 XX DE Australian taipan snake venom Beta-taipoxin derived peptide #3.  
 XX KW Australian taipan; snake venom; peptide therapy; Beta-taipoxin; wound;



KW burn; cellular growth medium; beautifying agent; mitogenic peptide;  
 KW oxynor peptide-10.  
 OS Oxyuranus scutellatus scutellatus.  
 XX

XX WO200261044-A2.  
 XX

XX 08-AUG-2002.  
 XX

XX 30-JAN-2002; 2002WO-US02633.  
 XX

XX 30-JAN-2001; 2001US-264984P.  
 XX

XX (LIPP/) LIPPS B V.  
 XX

XX Lippes BV;  
 XX

XX WPI; 2002-627476/67.  
 XX

XX New synthetic peptides with mitogenic properties, useful as a  
 PT medication for treating wounds or burns, as a component of a cellular  
 PT growth medium, or as a beautifying agent -  
 XX

XX Claim 3; Page 8; 12pp; English.  
 XX

XX The invention comprises mitogenic peptides derived from the Australian  
 CC taipan (Oxyuranus scutellatus scutellatus) snake venom Beta-taipoxin  
 CC protein. The Beta-taipoxin derived peptides of the invention are useful  
 CC as a medication for treating wounds (e.g. burns), as a component of a  
 CC cellular growth medium, or as a beautifying agent. The present amino acid  
 CC sequence represents an Australian taipan snake venom Beta-taipoxin  
 CC derived peptide of the invention.  
 XX

XX Sequence 5 AA;  
 SQ

Query Match 100.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3  
 |||  
 Db 3 LNF 5

RESULT 22  
 AAU85424

ID AAU85424 standard; Peptide; 5 AA.

XX AAU85424;  
 XX

XX 21-MAY-2002 (first entry)  
 XX

XX Human colon specific polypeptide antibody binding site #1.  
 DE

XX Human; colon specific gene; CSG; cytostatic; metastasis;  
 KW colon cancer staging; antibody binding site.  
 XX

XX Homo sapiens.  
 OS

XX WO200206515-A2.  
 XX

XX 24-JAN-2002.  
 XX

XX 17-JUL-2001; 2001WO-US22454.  
 XX

XX 17-JUL-2000; 2000US-0618596.  
 XX

XX (DIAD-) DIADEXUS INC.  
 XX

XX Macina RA, Sun Y;  
 XX

XX WPI; 2002-171815/22.  
 XX

PT Diagnosing, staging or monitoring colon cancer involves determining a  
 PT colon specific gene in cells, tissues or body fluids in patient, and  
 PT comparing it with levels of the gene from a normal human control -  
 XX  
 PS Disclosure; Page 20; 52pp; English.  
 XX

XX The invention relates to diagnosing the presence of colon cancer,  
 CC metastases of colon cancer, staging colon cancer, monitoring colon cancer  
 CC for the onset of metastasis or monitoring a change in stage of colon  
 CC cancer in a patient. The method involves determining a colon specific  
 CC gene (CSG) in cells, tissues or bodily fluids and comparing it with  
 CC levels of CSG in cells, tissues or bodily fluids from a normal human  
 CC control. Colon cancer can be treated by administering a molecule which  
 CC down regulates the expression or activity of CSG. An immune response  
 CC against a target cell expressing CSG can be induced by delivering an  
 CC immunologically stimulatory amount of a CSG protein to a patient, so that  
 CC an immune response is mounted. Therapeutic agents are useful for imaging  
 CC colon cancer in a patient by administering an agent labelled with  
 CC paramagnetic ions or a radioisotope to the patient. They are also useful  
 CC for preventing the onset of colon cancer, and in diagnosis and treatment  
 CC of the disease. Sequences AAU85424-AAU85502 represent human colon  
 CC specific protein antibody binding sites used in the method of the  
 CC invention.  
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3  
 |||  
 Db 3 LNF 5

RESULT 23

AAU85673

ID AAR06673 standard; protein; 6 AA.

XX AAR06673;  
 XX

XX 25-MAR-2003 (updated)  
 DT

XX 08-JAN-1991 (first entry)  
 DT

XX Retroviral protease inhibitor.  
 XX

XX AIDS; HIV; ARC; antiviral therapy.  
 XX

XX HIV.  
 XX

XX Key Location/Qualifiers  
 FH Modified-site 3..4

FT /note="CH2-N isostere links these residues"  
 FT

XX EP387231-A.  
 XX

XX 12-SEP-1990.  
 XX

XX 07-MAR-1990; 90EP-0870034.  
 XX

XX 08-MAR-1989; 89US-0320742.  
 XX

XX (UNIV ) UNIV WASHINGTON.  
 XX

XX Marshall GR, Toth MV;  
 XX

XX WPI; 1990-277234/37.  
 XX

XX Novel inhibitors of retroviral protease, partic. HIV protease -  
 PT used in the treatment of AIDS.  
 PT

XX Claim 4; Page 8; 9pp; English.  
 XX

CC Inhibitors are based on substrates for HIV protease derived from  
 CC HIV-1 and HIV-2 known cleavage sites. Inhibitors are potentially  
 CC useful in treatment of AIDS and AIDS related complex.  
 CC The peptides carry an internal CH2-N bond isostere.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 11; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 24  
 AAR28733  
 ID AAR28733 standard; peptide; 6 AA.  
 XX

AC AAR28733;

XX 25-MAR-2003 (updated)  
 DT 02-APR-1993 (first entry)  
 XX

XX Protease chromogenic substrate #4 - to assay retroviral protease.  
 DE AIDS; HIV; acquired immunodeficiency syndrome; protease; peptidase;  
 XX human immunodeficiency virus; proteinase.  
 KW

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 3  
 FT Modified-site 1/note= "p-NO2 Phe"  
 FT Modified-site 1/note= "Acetylated"

XX US5164300-A.

XX 17-NOV-1992.

XX 11-DEC-1990; 90US-0625395.

XX 28-DEC-1989; 89US-0458060.

XX (UNIW ) UNIV WASHINGTON.

XX Marshall GR, Toth MV;

XX WPI; 1992-407144/49.

XX Fluorimetric determ. of activity of retroviral protease - e.g.  
 PT to isolate protease inhibitors for use as anti-AIDS agents

XX Disclosure; Column 6; 8pp; English.

XX This peptide represents a novel fluorimetric substrate for the  
 CC assay of retroviral proteases (esp. that of HIV). It can be used to  
 CC screen for retroviral protease inhibitors which are therapeutic  
 CC possibilities in the search for AIDS drugs.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 25  
 AAW42234  
 ID AAW42234 standard; Peptide; 6 AA.  
 XX

AC AAW42234;

XX 08-APR-1998 (first entry)  
 DT

XX Biotinylated S-protein 6-mer peptide ligand 12.  
 DE

XX Bacteriophage peptide library; peptide epitope; therapeutic target;  
 KW variegated compound library.  
 XX

OS Synthetic.

XX WO9735194-A2.

XX 25-SEP-1997.  
 PD

XX 21-MAR-1997; 97WO-US04176.  
 PF

XX 21-MAR-1996; 96US-0622338.  
 PR

XX (HARD ) HARVARD COLLEGE.  
 PA

XX Forster AC;

XX WPI; 1997-480355/44.  
 DR

XX Identifying compounds which interact with target molecules - using  
 PT enantiomers of the target molecules and testing of enantiomers of  
 PT selected compounds.

XX Disclosure; Fig 3; 89pp; English.

XX 6-mer peptides AAW42223-38 are part of a peptide library. They were  
 CC identified as ligands of the control target, a biotinylated S-protein,  
 CC using the method of the invention. This novel method identifies  
 CC compounds which interact with a target molecule, and comprises contacting  
 CC a screening molecule with a variegated compound library, where the  
 CC the target molecule is chiral. Compounds which have a desired  
 CC interaction with the target molecule are selected, and the ability of  
 CC their enantiomer to interact with the target molecule is tested. Ligands  
 CC for a target protein can be identified by combining a D-enantiomer of a  
 CC target protein (a D-target protein), and a variegated compound library,  
 CC and then selecting one or more compounds from the library which have a  
 CC desired binding interaction with the D-target protein. The methods can  
 CC be used for identifying agonists or antagonists of targets such as  
 CC receptors, enzymes, DNA binding proteins or signal transduction  
 CC proteins. The methods can provide a structurally selective  
 CC approach in addition to scoring for interaction of functional groups.  
 CC They provide a powerful selection method that allows for the production  
 CC of ligands with the same diversity as peptides but with the greatly  
 CC improved pharmacokinetic profiles needed for drug activity.

SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 18; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 26  
 AAW54253  
 ID AAW54253 standard; peptide; 6 AA.  
 XX

AC AAW54253;  
 XX  
 XX DT 30-JUL-1998 (first entry)  
 XX  
 DE Acylated peptide cytolytic peptide inhibitor (b).  
 XX  
 KW Inhibition; melittin; dimeric; melittin-induced haemolysis; lysis;  
 KW CEM T cell lymphoma.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site /note= "N-terminal acetyl"  
 FT Modified-site 6  
 FT Modified-site /note= "C-terminal amide"  
 XX  
 PN WO9806743-A1.  
 XX  
 XX 19-FEB-1998.  
 XX  
 XX 13-AUG-1997; 97WO-AU00511.  
 XX  
 XX 13-AUG-1996; 96AU-0001611.  
 XX  
 XX (BIOM-) BIOMOLECULAR RES INST.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Baell J, Curtain CC, Hewish DR, Matthews BR, Rivett DE;  
 PI Werkmeister J;  
 XX  
 XX WPI; 1998-168791/15.  
 XX  
 XX New acylated peptide compounds - are capable of inhibiting cytolytic  
 PT compounds, and may thus be used in inhibiting melittin-induced  
 PT haemolysis  
 XX  
 PS Claim 16; Page 22; 34pp; English.  
 XX  
 XX Acylated peptides (AAW54242-W54260) inhibit cytolytic peptides such as  
 CC melittin. They may be incorporated into, or conjugated to, larger  
 CC molecules which retain the activity of the above compounds/peptides.  
 CC They may, for example, be in dimeric form and may be used, e.g. to  
 CC inhibit melittin-induced haemolysis and melittin-induced lysis of CEM T  
 CC cell lymphoma cells.  
 XX  
 SQ Sequence 6 AA;  
 XX  
 Query Match 100.0%; Score 3; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LNF 3  
 Db 3 LNF 5  
 XX  
 RESULT 27  
 AAY15740  
 ID AAY15740 standard; Peptide; 6 AA.  
 XX  
 AC AAY15740;  
 XX  
 XX 27-JUL-1999 (first entry)  
 DT  
 XX  
 XX Peptide used to make fluorescent reporter molecules.  
 DE  
 XX  
 XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX  
 OS Synthetic.  
 XX

PN WO9918856-A1.  
 XX  
 XX 22-APR-1999.  
 XX  
 PF 09-OCT-1998; 98WO-US21231.  
 XX  
 XX 03-MAR-1998; 98US-0033661.  
 PR 10-OCT-1997; 97US-0061582.  
 XX  
 XX (CYTO-) CYTOVIA INC.  
 PA  
 XX Cai SX, Drewe JA, Keana JFW, Weber B, Zhang H;  
 PI WPI; 1999-312448/26.  
 XX  
 XX New fluorogenic or fluorescent reporter molecules  
 PT  
 XX Claim 39; Page 193; 202pp; English.  
 PS  
 XX AAY15618-V15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 6 AA;  
 XX  
 Query Match 100.0%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LNF 3  
 Db 2 LNF 4  
 XX  
 RESULT 28  
 AAY15698  
 ID AAY15698 standard; Peptide; 6 AA.  
 XX  
 AC AAY15698;  
 XX  
 XX 27-JUL-1999 (first entry)  
 DT  
 XX  
 XX Peptide used to make fluorescent reporter molecules.  
 DE  
 XX  
 XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9918856-A1.  
 PN  
 XX 22-APR-1999.  
 PD  
 XX 09-OCT-1998; 98WO-US21231.  
 PF  
 XX 03-MAR-1998; 98US-0033661.  
 PR 10-OCT-1997; 97US-0061582.  
 XX

PA (CYTO-) CYTOVIA INC.  
 XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
 XX WPI; 1999-312448/26.  
 DR New fluorogenic or fluorescent reporter molecules  
 XX Disclosure; Page 181; 202pp; English.  
 XX  
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 2 LNF 4  
 RESULT 29  
 AAY15700  
 ID AAY15700 standard; Peptide; 6 AA.  
 XX  
 AC AAY15700;  
 XX  
 DT 27-JUL-1999 (first entry)  
 DE Peptide used to make fluorescent reporter molecules.  
 XX  
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9918856-A1.  
 XX  
 XX 22-APR-1999.  
 XX  
 XX 09-OCT-1998; 98WO-US21231.  
 PF  
 XX 03-MAR-1998; 98US-0033661.  
 PR  
 PR 10-OCT-1997; 97US-0061582.  
 XX  
 XX (CYTO-) CYTOVIA INC.  
 PA  
 PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
 XX WPI; 1999-312448/26.  
 DR  
 XX New fluorogenic or fluorescent reporter molecules  
 XX Disclosure; Page 182; 202pp; English.

XX  
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 1 LNF 3  
 RESULT 30  
 AAY80852  
 ID AAY80852 standard; peptide; 6 AA.  
 XX  
 AC AAY80852;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:81.  
 XX  
 KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200004914-A1.  
 PN  
 PD 03-FEB-2000.  
 XX  
 XX 21-JUL-1999; 99WO-US16423.  
 PF  
 XX 21-JUL-1998; 98US-0093642.  
 PR  
 XX (CYTO-) CYTOVIA INC.  
 PA (ZHAN/) ZHANG H.  
 PA (CAIS/) CAI S X.  
 PA (DREW/) DREW J A.  
 PA (YANG/) YANG W.  
 XX  
 PI Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI; 2000-195079/17.  
 DR  
 XX New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group -  
 XX  
 PS Claim 30; Page 109; 174pp; English.  
 XX  
 CC The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking

CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful as  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and virila infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti- angiogenic or anticancer agents. Sequences  
 CC AAY80782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.

SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db 2 LNF 4

RESULT 31  
 AAY80854  
 ID AAY80854 standard; peptide; 6 AA.  
 XX AC AAY80854;  
 XX DT 22-MAY-2000 (first entry)  
 XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:83.  
 XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX OS Synthetic.  
 XX PN WO200004914-A1.  
 XX PD 03-FEB-2000.  
 XX PF 21-JUL-1999; 99WO-US16423.  
 XX PR 21-JUL-1998; 98US-0093642.  
 XX PA (CYTO-) CYTOVIA INC.  
 XX PA (ZHAN/) ZHANG H.  
 XX PA (CAIS/) CAI S X.  
 XX PA (DREW/) DREWE J A.  
 XX PA (YANG/) YANG W.

XX Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI; 2000-195079/17.  
 XX New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group -  
 XX Claim 30; Page 109; 174pp; English.

XX The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in

CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful as  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and virila infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti- angiogenic or anticancer agents. Sequences  
 CC AAY80782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.

SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db 1 LNF 3

RESULT 32  
 AAY80894  
 ID AAY80894 standard; peptide; 6 AA.  
 XX AC AAY80894;  
 XX DT 22-MAY-2000 (first entry)  
 XX DE Fluorophore-labelled protease substrate peptide, SEQ ID NO:123.  
 XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 KW methionine aminopeptidase type 2; MetAP-2; drug screening.  
 XX OS Synthetic.  
 XX PN WO200004914-A1.  
 XX PD 03-FEB-2000.  
 XX PF 21-JUL-1999; 99WO-US16423.  
 XX PR 21-JUL-1998; 98US-0093642.  
 XX PA (CYTO-) CYTOVIA INC.  
 XX PA (ZHAN/) ZHANG H.  
 XX PA (CAIS/) CAI S X.  
 XX PA (DREW/) DREWE J A.  
 XX PA (YANG/) YANG W.

XX Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI; 2000-195079/17.

XX New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group -  
 XX Claim 29; Page 109; 174pp; English.

XX The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in

CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti-angiogenic or anticancer agents. Sequences  
 CC MAY0782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 Db 2 LNF 4

# RESULT 33

AAR06674  
 ID AAR06674 standard; protein; 7 AA.

XX AAR06674;

XX 25-MAR-2003 (updated)

DT 08-JAN-1991 (first entry)

XX Retroviral protease inhibitor.

XX AIDS; HIV; ARC; antiviral therapy.

XX HIV.

XX Key Location/Qualifiers

FT Modified-site 4..5  
 FT /note="CH2-N isostere links these residues"

XX EP387231-A.

XX 12-SEP-1990.

XX 07-MAR-1990; 90EP-0870034.

XX 08-MAR-1989; 89US-0320742.

XX (UNIW ) UNIV WASHINGTON.

XX Marshall GR, Toth MV;

XX WPI; 1990-277234/37.

XX Novel inhibitors of retroviral protease, partic. HIV protease -  
 PT used in the treatment of AIDS.

XX Claim 4; Page 8; 9pp; English.

XX Inhibitors are based on substrates for HIV protease derived from  
 CC HIV-1 and HIV-2 known cleavage sites. Inhibitors are potentially  
 CC useful in treatment of AIDS and AIDS related complex.  
 CC The peptides carry an internal CH2-N bond isostere.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 Db 2 LNF 4

# RESULT 34

AAR12883  
 ID AAR12883 standard; Protein; 7 AA.

XX AAR12883;

XX 25-MAR-2003 (updated)

DT 17-SEP-1991 (first entry)

XX HIV protease inhibiting variant (2).

XX HIV; protease; inhibition.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1  
 FT /label= N-acetyl-O-benzylSer

FT Modified-site 7  
 FT /label= Val methyl ester

FT Modified-site 4  
 FT /label= amino-2-hydroxy-4-Phe

FT Modified-site 4..5  
 FT /label= Phe(CHOCH2N) Pro

XX WO9108221-A.

XX 13-JUN-1991.

XX 03-DEC-1990; 90NO-US07059.

XX 04-DEC-1989; 89US-0445070.

XX (WISC ) WISCONSIN ALUMNI RES FOUND.

XX Rich DH, Green J, Sun C;

XX WPI; 1991-193150/26.

XX New HIV protease inhibiting variant peptide(s) - are potential  
 PT drugs for human immune deficiency virus infected patient(s)

XX Example 5.2; Page 12; 30 pp; English.

XX The peptide variant preferentially binds to HIV protease so as to  
 CC inhibit its activity. The amino-alcohol variants of the protease's  
 CC pref. binding site are incorporated in the peptide backbone to  
 CC preferentially bind and occupy the protease.  
 CC The peptides are built out from a core which is the ketone precursor  
 CC of the amino-alcohol. The leucine variant or phenyl variant are pref.  
 CC A series of amino acids are linked on one side of the core to build  
 CC half the peptide. Separately the other half of the peptide is  
 CC built up. Then the two halves are coupled together and the alcohol  
 CC formed. See also AAR12882-86.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 Db 2 LNF 4

```
RESULT 35
AAR65689
ID AAR65689 standard; peptide; 7 AA.
XX
AC AAR65689;
XX
XX
DT 25-MAR-2003 (updated)
DT 08-JAN-1995 (first entry)
XX
XX HIV-1 inhibiting pseudopeptide.
DE
XX Aspartic proteinase; reversible inhibitor; pseudopeptide;
KW phosphinate methylene ammonium group; exploding transition analogue;
KW HIV-1.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Acetyl-Ser or hexanoyl-Ser"
FT Misc-difference 2
FT /note= "can also be D-Leu when Ser(1) is acetyl-Ser"
FT Modified-site 4..5
FT /note= "CONH linkage replaced by P(O) (OH)CH2NH"
FT Modified-site 7
FT /note= "Val-OCH3"
XX
XX WO9314114-A1.
PN
XX
XX 22-JUL-1993.
PD
XX
XX 11-JAN-1993; 93WO-US00228.
PF
XX
XX 09-JAN-1992; 92US-0819356.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX Ikeda S, Janda KD, Wirsching P;
PI
XX WPI; 1993-243142/30.
DR
XX
XX New peptide linkage unit - comprising phosphinate methylene
PT ammonium gp., esp. for pseudo-peptide aspartic proteinase
PT inhibitors
XX
XX Claims 31-33; Pages 69,70; 76pp; English.
PS
XX
XX The invention relates to a phosphinic acid methylene amine linkage
CC PO(OH)CH2NH to be used in place of a peptide linkage CONH at the
CC cleavage site in an aspartic proteinase substrate. The linkage is
CC resistant to cleavage and serves as an exploding transition state
CC analogue of the cleavage site. Thus the peptide containing it can
CC bind or interfere with the active site of the aspartic proteinase
CC enzyme and inhibit its activity.
CC The present sequence is a specifically claimed example of a
CC HIV-1 inhibiting peptide containing the linkage.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 3; DB 14; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
2 LNF 4
RESULT 36
AAR60253
ID AAR60253 standard; peptide; 7 AA.
XX
```

```
AC AAW80253;
XX
XX 06-JAN-1999 (first entry)
DT
XX Oxirane compound which is an inhibitor of HIV-1 protease.
DE
XX Oxirane compound; human immunodeficiency virus; HIV protease inhibitor;
KW gag; pol; HIV-1 protease.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Ser is linked to CH3C(O) or C5H11C(O)"
FT Modified-site 4..5
FT /note= "these residues are linked by a pseudo
FT peptide linkage comprising 1-epoxy-ethylene"
FT Modified-site 7
FT /note= "Val is linked to OCH3"
XX
XX US5827827-A.
PN
XX 27-OCT-1998.
PD
XX 20-JUN-1996; 96US-0667001.
PF
XX 20-JUN-1996; 96US-0667001.
PR 16-FEB-1995; 95US-0335039.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX Janda KD, Wirsching P;
PI
XX WPI; 1998-594033/50.
DR
XX Oxirane compounds e.g. oxirane-substituted oligo-peptide(s) - used
PT as human immunodeficiency virus protease inhibitors
PT
XX Disclosure; Column 9; 29pp; English.
PS
XX The present sequence is part of an oxirane compound which acts as a
CC human immunodeficiency virus (HIV) protease inhibitor. The compounds
CC have a terminal epoxide moiety. The compounds inhibit HIV protease
CC and the cleavage of gag and gag pol polyproteins of HIV by HIV-1
CC protease.
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 3; DB 19; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db |||
2 LNF 4
RESULT 37
AAY15697
ID AAY15697 standard; Peptide; 7 AA.
XX
XX AAY15697;
AC
XX 27-JUL-1999 (first entry)
DT
XX Peptide used to make fluorescent reporter molecules.
DE
XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KW apoptosis; protease; peptidase; apoptosis cascade; cancer;
KW chemotherapeutic agent; cell death; viral protease activity.
XX
XX Synthetic.
OS
```

PN WO9918856-A1.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 09-OCT-1998; 98WO-US21231.  
 XX  
 PR 03-MAR-1998; 98US-0033661.  
 PR 10-OCT-1997; 97US-0061582.  
 XX  
 PA (CYTO-) CYTOVIA INC.  
 XX  
 PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
 XX WPI; 1999-312448/26.  
 XX  
 DR New fluorogenic or fluorescent reporter molecules  
 PT  
 PS Disclosure; Page 181; 202pp; English.  
 XX  
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 2 LNF 4  
 RESULT 38  
 AAY15651  
 ID AAY15651 standard; Peptide; 7 AA.  
 XX  
 AC AAY15651;  
 XX  
 DT 27-JUL-1999 (first entry)  
 XX  
 DE Peptide used to make fluorescent reporter molecules.  
 XX  
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9918856-A1.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 09-OCT-1998; 98WO-US21231.  
 XX  
 PR 03-MAR-1998; 98US-0033661.  
 PR 10-OCT-1997; 97US-0061582.  
 XX

PA (CYTO-) CYTOVIA INC.  
 XX  
 PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
 XX WPI; 1999-312448/26.  
 XX  
 DR New fluorogenic or fluorescent reporter molecules  
 PT  
 PS Claim 39; Page 169; 202pp; English.  
 XX  
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequence) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 2 LNF 4  
 RESULT 39  
 AAY85415  
 ID AAY85415 standard; peptide; 7 AA.  
 XX  
 AC AAY85415;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Drosophila Bag protein fragment.  
 XX  
 KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; eag.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200006772-A1.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 20-JUL-1999; 99WO-US16337.  
 XX  
 PR 27-JUL-1998; 98US-0122847.  
 PR 06-JAN-1999; 99US-0226012.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Keating MT, Splawski I;  
 XX WPI; 2000-195319/17.  
 XX  
 PT New isolated mutant HERG nucleic acids, useful for developing products  
 PT for the diagnosis, prevention and treatment of long QT syndrome -  
 XX Disclosure; Fig 12H; 163pp; English.  
 PS  
 XX



CC The invention relates to a HERG protein having a mutation compared to  
 CC wild-type HERG, and is useful for developing products for the diagnosis,  
 CC prevention and treatment of long QT (LQT) syndrome. The products and  
 CC methods can be used for the diagnosis of subjects with LQT syndrome.  
 CC They can also be used to screen for drugs for treating or preventing LQT  
 CC syndrome. The HERG nucleic acids can also be used for gene therapy and  
 CC HERG peptides can be used for peptide therapy. Sequences AAY85407-421  
 CC represents regions of HERG from humans, mouse, rat and drosophila.  
 XX  
 SQ Sequence 7 AA;

Query Match

Best Local Similarity 100.0%; Score 3; DB 21; Length 7;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 4 LNF 6

RESULT 40

AAAY85416

ID AAY85416 standard; peptide; 7 AA.

XX AC AAY85416;

DT 19-JUN-2000 (first entry)

DE Elk protein fragment.

XX KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; elk.

XX OS Unidentified.

XX PN WO200006772-A1.

XX PD 10-FEB-2000.

XX PF 20-JUL-1999; 99WO-US16337.

XX PR 27-JUL-1998; 98US-0122847.

XX PR 06-JAN-1999; 99US-0226012.

XX PA (UTAH ) UNIV UTAH RES FOUND.

XX PI Keating MT, Splawski I;

XX XX WPI; 2000-195319/17.

XX PT New isolated mutant HERG nucleic acids, useful for developing products  
 XX for the diagnosis, prevention and treatment of long QT syndrome -

XX PS Disclosure; Fig 12H; 163pp; English.

XX CC The invention relates to a HERG protein having a mutation compared to  
 CC wild-type HERG, and is useful for developing products for the diagnosis,  
 CC prevention and treatment of long QT (LQT) syndrome. The products and  
 CC methods can be used for the diagnosis of subjects with LQT syndrome.  
 CC They can also be used to screen for drugs for treating or preventing LQT  
 CC syndrome. The HERG nucleic acids can also be used for gene therapy and  
 CC HERG peptides can be used for peptide therapy. Sequences AAY85407-421  
 CC represents regions of HERG from humans, mouse, rat and drosophila.  
 XX

SQ Sequence 7 AA;

Query Match

Best Local Similarity 100.0%; Score 3; DB 21; Length 7;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 4 LNF 6

RESULT 41

AAAY80815

ID AAY80815 standard; peptide; 7 AA.

XX AC AAY80815;

DT 22-MAY-2000 (first entry)

XX DE Fluorophore-labelled HIV protease substrate peptide, SEQ ID NO:34.

XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;

XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;

XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.

XX OS Synthetic.

XX PN WO200004914-A1.

XX PD 03-FEB-2000.

XX PF 21-JUL-1999; 99WO-US16423.

XX PR 21-JUL-1998; 98US-0093642.

XX PA (CYTO-) CYTOVIA INC.

XX PA (ZHAN/) ZHANG H.

XX PA (CAIS/) CAI S X.

XX PA (DREW/) DREWE J A.

XX PA (YANG/) YANG W.

XX PI Zhang H, Cai SX, Drewe JA, Yang W;

XX XX WPI; 2000-195079/17.

XX PT New fluorescently labeled amino acids or peptides, used as substrates  
 XX for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 XX agents, contains a halobenzoyl N-blocking group -

XX PS Claim 29; Page 108; 174pp; English.

XX CC The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-V-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.

XX CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti- angiogenic or anticancer agents. Sequences  
 CC AAY80782-Y80910 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3

Db 2 LNF 4

RESULT 42

AA80851  
ID AAY80851 standard; peptide; 7 AA.

XX AC AAY80851;  
XX DT 22-MAY-2000 (first entry)  
XX DE Core polypeptide fragment T No. 1243.

XX KW Fluorophore-labelled protease substrate peptide, SEQ ID NO:80.  
XX KW Protease substrate; fluorescent label; fluorophore; rhodamine;  
XX KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
XX KW methionine aminopeptidase type 2; MetAP-2; drug screening.

XX OS Synthetic.

XX PN WO200004914-A1.

XX PD 03-FEB-2000.

XX PF 21-JUL-1999; 99WO-US16423.

XX PR 21-JUL-1998; 98US-0093642.

XX PA (CYTO-) CYTOVIA INC.

XX PA (ZHANG/) ZHANG H.

XX PA (CAIS/) CAI S X.

XX PA (DREW/) DREW J A.

XX PA (YANG/) YANG W.

XX ZHANG H, Cai SX, Drewe JA, Yang W;

XX WPI; 2000-195079/17.

XX PT New fluorescently labeled amino acids or peptides, used as substrates  
XX PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
XX PT agents, contains a halobenzoyl N-blocking group -

XX PS Claim 30; Page 109; 174pp; English.

XX CC The invention relates to fluorescently labelled peptides containing  
XX CC a halobenzoyl group on the fluorophore. They are of the structure  
XX CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
XX CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
XX CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
XX CC assayed. The labelled peptides are reporters for detecting intracellular  
XX CC proteolytic enzymes, particularly caspases and other enzymes involved in  
XX CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
XX CC cytomegalovirus and hepatitis C virus proteases); and methionine  
XX CC aminopeptidase type 2 (MetAP-2). The peptides are particularly useful to  
XX CC identify modulators of these enzymes which may be potentially useful as  
XX CC agents for treating conditions such as cancer, neurodegeneration,  
XX CC autoimmune diseases, myocardial infarction and viral infection.  
XX CC Modulators identified may also be used to prolong the life of cells being  
XX CC cultured for recombinant protein production, or to monitor the treatment  
XX CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
XX CC potential anti- angiogenic or anticancer agents. Sequences  
XX CC AAY80782-Y80910 represent peptides, some of which are specifically  
XX CC claimed, which may be used in assay methods according to the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
DB 2 LNF 4

RESULT 43  
AAY89681  
ID AAY89681 standard; peptide; 7 AA.

XX AC AAY89681;

XX DT 23-MAY-2000 (first entry)

XX DE Core polypeptide fragment T No. 1243.

XX KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX KW anti-fusogenic; differentiation factor; interleukin; interferon;  
XX KW colony stimulating factor; hormone; angiogenic factor.

XX OS Unidentified.

XX PN WO9595615-A1.

XX PD 25-NOV-1999.

XX PF 20-MAY-1999; 99WO-US11219.

XX PR 20-MAY-1998; 98US-0082279.

XX PA (TRIM-) TRIMERIS INC.

XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX DR WPI; 2000-136792/12.

XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX PT comprises enhancer sequence -

XX PS Disclosure; Page 42; 124pp; English.

XX CC The invention relates to hybrid polypeptides comprising enhancer peptide  
XX CC sequence linked to core polypeptides. The enhancer polypeptides are  
XX CC derived from various retroviral envelope (gp41) protein sequences,  
XX CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX CC pharmacokinetic properties such as increasing the half-life of any core  
XX CC polypeptide that they are linked to. The core polypeptides are any  
XX CC polypeptide that may be introduced into a living system and that can  
XX CC function as a pharmacologically useful peptide for the treatment or  
XX CC prevention of a disease. The core polypeptides are bioactive peptides  
XX CC selected from a growth factor, cytokine, differentiation factor,  
XX CC interleukin, interferon, colony stimulating factor, hormone or  
XX CC angiogenic factor. The peptides of the invention can be used for  
XX CC inhibiting viral infections and can be used in anti-viral and  
XX CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
XX CC polypeptide fragments that can be used in the invention. Some sequences  
XX CC among those indicated also comprise enhancer fragments at terminal ends  
XX CC and form hybrid polypeptides.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
DB 1 LNF 3

RESULT 44  
ABB01089  
ID ABB01089 standard; Peptide; 7 AA.

XX AC ABB01089;

XX DT 03-JAN-2002 (first entry)

XX DE Viral DP178/107-like region peptide T1243.

XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 XX infection.  
 OS Viridiae.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 7 /note= "N-terminal is substituted by Ac"  
 FT Modified-site 7 /note= "C-terminal amide"  
 XX  
 XX WO200164013-A2.  
 PN  
 XX  
 XX 07-SEP-2001.  
 PD  
 XX  
 XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.  
 XX  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 FT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 XX Disclosure; Page 55; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 XX SQ Sequence 7 AA;  
 PS  
 XX Query Match 100.0%; Score 3; DB 22; Length 7;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 QY 1 LNF 3  
 DB |||  
 DB 1 LNF 3  
 RESULT 45  
 ID ABB02538 standard; Peptide; 7 AA.  
 AC  
 XX ABB02538;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral core polypeptide, SEQ ID NO: 1065.  
 XX  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 XX  
 XX Viridiae.  
 OS  
 XX WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD

XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.  
 XX  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 FT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 XX Disclosure; Page 448; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 XX SQ Sequence 7 AA;  
 PS  
 XX Query Match 100.0%; Score 3; DB 22; Length 7;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 QY 1 LNF 3  
 DB |||  
 DB 1 LNF 3  
 RESULT 46  
 ID AAU13635 standard; Peptide; 7 AA.  
 AC  
 XX AAU13635;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE DP178-like/DP107-like peptide T-1243.  
 XX  
 XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 KW antifeusogenic; antiviral; HIV transmission; mutant; mutein.  
 KW  
 XX Human immunodeficiency virus 1 isolate LAI.  
 OS  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal is substituted by Ac"  
 FT Modified-site 7 /note= "C-terminal amide"  
 FT  
 XX WO200151673-A2.  
 PN  
 XX 19-JUL-2001.  
 PD  
 XX  
 XX 05-JUL-2000; 2000WO-US35727.  
 PF  
 XX 09-JUL-1999; 99US-0350841.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX WPI; 2001-442157/47.  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 XX  
 XX Disclosure; Page 74; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC and absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antifusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents one of the DP178-like/DP107-like peptides  
 CC of the invention.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 Db 1 LNF 3

RESULT 47  
 AAM44074  
 ID AAM44074 standard; Peptide; 7 AA.  
 XX  
 AC AAM44074;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #345.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
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 XX  
 XX Example 4; Page 102; 154pp; English.  
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 CC The present invention describes a composition (I) comprising stress  
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 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 Db 4 LNF 6

RESULT 48  
 AAM44079  
 ID AAM44079 standard; Peptide; 7 AA.  
 XX  
 AC AAM44079;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #350.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
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Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

DB 4 LNF 6

RESULT 49

AAM44124

ID AAM44124 standard; Peptide; 7 AA.

XX AC AAM44124;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #395.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPSC;

XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

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XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3

DB 4 LNF 6

RESULT 50

AAM44129

ID AAM44129 standard; Peptide; 7 AA.

XX AC AAM44129;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #400.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPSC;

XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

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XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3  
 |||  
 Db 4 LNF 6

RESULT 51  
 AAM44134  
 ID AAM44134 standard; Peptide; 7 AA.

XX AC AAM44134;  
 XX DT 25-OCT-2001 (first entry)  
 XX DE H11 binding site consensus conforming peptide (CCP) #405.  
 XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX EN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

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SQ Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3  
 |||  
 Db 4 LNF 6

RESULT 52  
 AAM44139  
 ID AAM44139 standard; Peptide; 7 AA.

XX AC AAM44139;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #410.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX EN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

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XX DR WPI; 2001-425937/46.

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Query Match 100.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
DB 4 LNF 6

RESULT 53  
AAM44144  
ID AAM44144 standard; Peptide; 7 AA.  
XX AC AAM44144;  
XX DT 25-OCT-2001 (first entry)  
XX DE H11 binding site consensus conforming peptide (CCP) #415.  
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN CA2290722-A1.  
XX PD 08-JUN-2001.  
XX PF 08-DEC-1999; 99CA-2290722.  
XX PR 08-DEC-1999; 99CA-2290722.  
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XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
DB 4 LNF 6

RESULT 54  
AAM44194  
ID AAM44194 standard; Peptide; 7 AA.  
XX AC AAM44194;  
XX DT 25-OCT-2001 (first entry)  
XX DE H11 binding site consensus conforming peptide (CCP) #465.  
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
XX KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
XX KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
XX KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
XX KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN CA2290722-A1.  
XX PD 08-JUN-2001.  
XX PF 08-DEC-1999; 99CA-2290722.  
XX PR 08-DEC-1999; 99CA-2290722.  
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db |||  
 4 LNF 6

RESULT 55  
 AAM44560  
 ID AAM44560 standard; Peptide; 7 AA.  
 XX  
 AC  
 XX

25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #831.

Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX  
 PN CH2290722-A1.  
 XX  
 XX  
 PD 08-JUN-2001.  
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 PF 08-DEC-1999; 99CA-2290722.  
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Example 4; Page 104; 154pp; English.

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Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||

Db 4 LNF 6

RESULT 56  
 AAM44565  
 ID AAM44565 standard; Peptide; 7 AA.  
 XX  
 AC  
 XX

25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #836.

Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 ependymoma; medulloblastoma; primitive neural ectodermal tumour.

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 OS Synthetic.  
 XX  
 XX  
 PN CH2290722-A1.  
 XX  
 XX  
 PD 08-JUN-2001.  
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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||

RESULT 57



```
AAW44570
ID AAW44570 standard; Peptide; 7 AA.
AC AAW44570;
XX
XX
DT 25-OCT-2001 (first entry)
DE
XX
XX H11 binding site consensus conforming peptide (CCP) #841.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
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PN CA2290722-A1.
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XX SPPCs specific to target cancer (TC). Also described is an isolated
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XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 4 LNF 6
RESULT 58
AAW44575
ID AAW44575 standard; Peptide; 7 AA.
XX
XX AAW44575;
AC
```

```
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #846.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 104; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
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XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
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XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 4 LNF 6
RESULT 59
AAW44661
ID AAW44661 standard; Peptide; 7 AA.
XX
XX AAW44661;
AC
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #932.
DE
```

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-A1.  
 PN 08-JUN-2001.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 PI WPI; 2001-425937/46.  
 DR Composition useful for treating and diagnosing cancer, comprises stress  
 XX protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 XX Example 4; Page 104; 154pp; English.  
 PS The present invention describes a composition (I) comprising stress  
 XX protein-peptide complexes (SPPC) associated with tumors that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
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 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
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 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 4 LNF 6  
 RESULT 60  
 AAM45665  
 ID AAM45665 standard; Peptide; 7 AA.  
 XX  
 AC AAM45665;  
 XX  
 XX 25-OCT-2001 (first entry)  
 DE H11 binding site consensus conforming peptide (CCP) #1936.  
 XX  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-A1.  
 PN 08-JUN-2001.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 PI WPI; 2001-425937/46.  
 DR Composition useful for treating and diagnosing cancer, comprises stress  
 XX protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 XX Example 4; Page 104; 154pp; English.  
 PS The present invention describes a composition (I) comprising stress  
 XX protein-peptide complexes (SPPC) associated with tumors that is  
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 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendrogloma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 4 LNF 6  
 RESULT 60  
 AAM45665  
 ID AAM45665 standard; Peptide; 7 AA.  
 XX  
 AC AAM45665;  
 XX  
 XX 25-OCT-2001 (first entry)  
 DE H11 binding site consensus conforming peptide (CCP) #1936.  
 XX  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;

XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-A1.  
 PN 08-JUN-2001.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX 08-DEC-1999; 99CA-2290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
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 PI WPI; 2001-425937/46.  
 DR Composition useful for treating and diagnosing cancer, comprises stress  
 XX protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 XX Example 4; Page 107; 154pp; English.  
 PS The present invention describes a composition (I) comprising stress  
 XX protein-peptide complexes (SPPC) associated with tumors that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
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 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 Db |||  
 4 LNF 6  
 RESULT 61  
 AAM45884  
 ID AAM45884 standard; Peptide; 7 AA.  
 XX  
 AC AAM45884;  
 XX  
 XX 25-OCT-2001 (first entry)  
 DE H11 binding site consensus conforming peptide (CCP) #2155.  
 XX  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendrogloma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.

```

OS XX Synthetic.
PN XX CA2290722-A1.
XX
PD XX 08-JUN-2001.
XX
PF XX 08-DEC-1999; 99CA-2290722.
XX
PR XX 08-DEC-1999; 99CA-2290722.
XX
PA XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 108; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
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CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
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CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db |||
4 LNF 6

RESULT 62
AAM45974
ID AAM45974 standard; Peptide; 7 AA.
XX
AC AAM45974;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #2245.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX

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PD XX 08-JUN-2001.
XX
PF XX 08-DEC-1999; 99CA-2290722.
XX
PR XX 08-DEC-1999; 99CA-2290722.
XX
PA XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 109; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
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CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
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CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db |||
4 LNF 6

RESULT 63
AAM46173
ID AAM46173 standard; Peptide; 7 AA.
XX
AC AAM46173;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #2444.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX

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PR 08-DEC-1999; 99CA-2290722.
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
FI Entwistle JM, MacDonald GC;
XX
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumors that is
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CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
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CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 64
AAM46416
ID AAM46416 standard; Peptide; 7 AA.
XX
XX AAM46416;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2687.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.

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PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 110; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumors that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
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CC used in vaccine production and as a tumour-specific immunogenic response
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CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db |||
4 LNF 6

RESULT 65
AAM46609
ID AAM46609 standard; Peptide; 7 AA.
XX
XX AAM46609;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2880.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.

```

XX Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the  
PT complex -  
XX  
PS Example 4; Page 111; 154pp; English.  
XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNER). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LNF 3  
Db |||  
4 LNF 6  
  
RESULT 66  
AAM46895  
ID AAM46895 standard; Peptide; 7 AA.  
XX  
AC AAM46895;  
XX  
DT 25-OCT-2001 (first entry)  
DE  
DE H11 binding site consensus conforming peptide (CCP) #3166.  
XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
EN CR2290722-A1.  
XX  
PD 08-JUN-2001.  
XX  
PF 08-DEC-1999; 99CA-2290722.  
XX  
PR 08-DEC-1999; 99CA-2290722.  
XX  
XX (NOVO-) NOVOPHARM BIOTECH INC.  
PA  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
XX  
XX WPI; 2001-425937/46.  
XX  
XX Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the

PT complex -  
XX Example 4; Page 112; 154pp; English.  
XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNER). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LNF 3  
Db |||  
4 LNF 6  
  
RESULT 67  
AAB78082  
ID AAB78082 standard; Peptide; 7 AA.  
XX  
AC AAB78082;  
XX  
DT 19-APR-2001 (first entry)  
DE  
DE Core polypeptide T1243.  
XX  
KW Core polypeptide; enhancer; antiviral; anti-HIV;  
KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
KW coiled-coil peptide interaction; fusion-related disorder;  
KW bacterial infection; viral infection.  
XX  
OS Unidentified.  
XX  
EN W0200103723-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 10-JUL-2000; 2000WO-US18772.  
XX  
PR 09-JUL-1999; 99US-0350641.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2001-147136/15.  
XX  
XX New hybrid polypeptides, useful for preventing, treating and diagnosing  
PT e.g. viral infections, comprises an enhancer peptide linked to a core  
PT polypeptide -  
XX  
PS Disclosure; Page 55; 151pp; English.  
XX  
XX The present sequence is a core polypeptide which may be linked to  
CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
CC those exhibited by the core polypeptide when introduced into a living

CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC coiled-coil peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.

XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 68  
 ABJ37364  
 ID ABJ37364 standard; Peptide; 7 AA.

XX AC ABJ37364;

XX DT 08-MAY-2003 (first entry)

XX DE G-protein coupled receptor peptide region #76.

XX KM Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB03094.

XX PR 06-JUL-2001; 2001GB-0016570.

XX PA (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX DR WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using  
 PT target sequence information, defining microenvironments interacting  
 PT with ligand and motifs interacting with microenvironment, and  
 PT assembling motifs -

XX PS Disclosure; Fig 3; 39pp; English.

XX CC The invention relates to a novel method for producing a compound library.  
 CC The novel method involves reducing a biological target into a group of  
 CC one or more amino acids required for interaction with a ligand, to  
 CC generate a model of the biological target, using the model to define a  
 CC microenvironment in the biological target capable of interacting with the  
 CC ligand, defining motifs which interact with the microenvironment, and  
 CC assembling the motifs to generate a compound library for screening. The  
 CC novel method is useful to produce a compound libraries for screening  
 CC natural ligands such as peptides and proteins or for producing chemical  
 CC compounds based on drug motifs for screening. This sequence presents a

CC peptide of a G-protein Coupled Receptor (GPCR), which relates to the  
 CC novel compound library production method of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 24; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3

|||

Db 5 LNF 7

RESULT 69  
 ABJ37444  
 ID ABJ37444 standard; Peptide; 7 AA.

XX AC ABJ37444;

XX DT 08-MAY-2003 (first entry)

XX DE G-protein coupled receptor endothelin ET-A receptor peptide #76.

XX KM Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX OS Unidentified.

XX PN WO2003004147-A2.

XX PD 16-JAN-2003.

XX PF 05-JUL-2002; 2002WO-GB03094.

XX PR 06-JUL-2001; 2001GB-0016570.

XX PA (BIOF-) BIOFOCUS PLC.

XX PI Crossley R, Rose VS, Stevens AP;

XX DR WPI; 2003-221549/21.

XX PT Producing compound library, by generating biological target model using  
 PT target sequence information, defining microenvironments interacting  
 PT with ligand and motifs interacting with microenvironment, and  
 PT assembling motifs -

XX PS Disclosure; Fig 7; 39pp; English.

XX CC The invention relates to a novel method for producing a compound library.  
 CC The novel method involves reducing a biological target into a group of  
 CC one or more amino acids required for interaction with a ligand, to  
 CC generate a model of the biological target, using the model to define a  
 CC microenvironment in the biological target capable of interacting with the  
 CC ligand, defining motifs which interact with the microenvironment, and  
 CC assembling the motifs to generate a compound library for screening. The  
 CC novel method is useful to produce compound libraries for screening  
 CC natural ligands such as peptides and proteins or for producing chemical  
 CC compounds based on drug motifs for screening. This sequence represents a  
 CC peptide of a G-protein Coupled Receptor (GPCR) including Endothelin ET-A  
 CC receptor, which relates to the novel compound library production method  
 CC of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 24; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNF 3

|||

Db 5 LNF 7

```

RESULT 70
AAR28732
ID AAR28732 standard; peptide; 8 AA.
XX
AC AAR28732;
XX
DT 25-MAR-2003 (updated)
DT 02-APR-1993 (first entry)
XX
DE Protease chromogenic substrate #3 - to assay retroviral protease.
XX
KW AIDS; HIV; acquired immunodeficiency syndrome; protease; peptidase;
KW human immunodeficiency virus; proteinase.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "p-NO2 Phe"
XX
PN US5164300-A.
XX
PD 17-NOV-1992.
XX
PF 11-DEC-1990; 90US-0625395.
XX
PR 28-DEC-1989; 89US-0458060.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Marshall GR, Toth MV;
XX
DR WPI; 1992-407144/49.
XX
PT Fluorimetric determ. of activity of retroviral protease - e.g.
PT to isolate protease inhibitors for use as anti-AIDS agents
XX
PS Disclosure; Column 6; 8pp; English.
XX
CC This peptide represents a novel fluorimetric substrate for the
CC assay of retroviral proteases (esp. that of HIV). It can be used to
CC screen for retroviral protease inhibitors which are therapeutic
CC possibilities in the search for AIDS drugs.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 3; DB 13; Length 8;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 2 LNF 4
RESULT 71
AAR63662
ID AAR63662 standard; Protein; 8 AA.
XX
AC AAR63662;
XX
DT 28-APR-1995 (first entry)
XX
DE PR/RT HIV protease substrate amino acid sequence.
XX
KW PR/RT HIV protease substrate; HIV protease inhibitors.
XX
OS Synthetic.
XX
PN GB2276621-A.
XX

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```

PD 05-OCT-1994.
XX
PF 24-MAR-1994; 94GB-0005865.
XX
PR 02-APR-1993; 93US-0045264.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Condra JH, Gotlib L, Graham DJ;
XX
DR WPI; 1994-296383/37.
XX
PT New plasmid pPRBG1, vector for mutated HIV protease sequences -
PT used to produce a colour screen vector library to detect drug
PT resistant proteases and new protease inhibitors
XX
PS Disclosure; Page 7; 34pp; English.
XX
CC AAR71462 and AAR63657 to AAR63667 are HIV protease substrate sequences.
CC These sequences were used in the process to isolate and detect new
CC inhibitors of HIV protease, unaffected by HIV drug resistance.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNF 3
Db 2 LNF 4
RESULT 72
AAW38400
ID AAW38400 standard; peptide; 8 AA.
XX
AC AAW38400;
XX
DT 08-APR-1998 (first entry)
XX
DE Synthetic pMEL17 peptide.
XX
KW Melanoma; immunogen; cytotoxic T lymphocyte; CTL;
KW human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3;
KW HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
XX
OS Synthetic.
XX
PN WO9734613-A1.
XX
PD 25-SEP-1997.
XX
PF 17-MAR-1997; 97WO-US04958.
XX
PR 04-OCT-1996; 96US-0027627.
PR 19-MAR-1996; 96US-0013972.
XX
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI Cox AL, Engelhard VH, Hendrikson RC, Hunt DF, Kittlesen D;
PI Shabanowitz J, Skipper J, Slingluff CL;
XX
DR WPI; 1997-479982/44.
XX
PT Melanoma-specific immunogens of pMel-17 and tyrosinase - useful in
PT vaccination for producing melanoma-specific cytotoxic T lymphocytes
XX
PS Example 9; Page 65; 106pp; English.
XX
CC The present peptide was used in the preparation of a novel melanoma
CC specific immunogen, comprising at least 1 melanoma specific
CC cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the

```

CC epitopes is substantially homologous to a human leukocyte  
 CC antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma  
 CC antigen, either pMEU-17 or tyrosinase. The immunogen can be used in  
 CC vaccines for protection against melanoma in mammals.

XX Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

## RESULT 73

AAW57537

ID AAW57537 standard; peptide; 8 AA.

XX AC AAW57537;

XX DT 11-AUG-1998 (first entry)

XX DE Molecular mimetic of unique N. meningitidis epitope, Pep 37.

XX KW Molecular mimetic; epitope; serotype B; MenB; capsular polysaccharide;

XX KM immune disease; non-autoreactive antibody; vaccine; passive immunisation;

XX KW Escherichia coli K1 disease; bacterial meningitis; sepsis;

XX KW oligosaccharide protein conjugate vaccine.

XX OS Synthetic.

XX OS Neisseria meningitidis.

XX PN WO9808874-A1.

XX PD 05-MAR-1998.

XX PF 27-AUG-1997; 97WO-US15167.

XX PR 27-AUG-1996; 96US-0025799.

XX PA (CHIR ) CHIRON CORP.

XX PI Granoff D, Moe GR;

XX PS WPI; 1998-216938/19.

XX PT Antibodies to Neisseria meningitidis serotype B - prepared using

XX PT capsular polysaccharide derivatives, used to develop products for

XX PT treating or preventing infections, e.g. meningitis and sepsis

XX PS Claim 17; Fig 7A; 109pp; English.

XX This sequence represents a molecular mimetic of a unique epitope of  
 CC Neisseria meningitidis serotype B (MenB). This sequence was isolated  
 CC using the antibodies (Ab) of the invention. The Ab are directed against  
 CC a MenB capsular polysaccharide (PS) derivative, and are not autoreactive.  
 CC The Ab either do not cross-react or they are minimally cross-reactive  
 CC with host tissues and therefore pose minimal risk of evoking immune  
 CC disease. The non-autoreactive Ab are particularly useful for identifying  
 CC molecular mimetics of unique MenB PS epitopes that can be used in vaccine  
 CC compositions. Furthermore, the Ab, humanised versions of the Ab,  
 CC fragments and functional equivalents, will also find use in passive  
 CC immunisation against, and/or as an adjunct to therapy for, MenB and  
 CC Escherichia coli K1 disease. Such disease includes bacterial meningitis  
 CC and sepsis in infants, children and adults. The anti-MenB Ab can also be  
 CC used to investigate the bactericidal and/or opsonic function of Ab of  
 CC different specificities, as well as to identify the molecular nature of  
 CC the unique epitopes on the MenB bacterial surface that are not  
 CC cross-reactive with host PS. The anti-MenB Ab can be used to isolated  
 CC fractions of MenB bacteria or MenB PS derivatives. Once isolated, the  
 CC critical epitopes reactive with the anti-MenB Ab can be characterised and

CC employed directly in oligosaccharide protein conjugate vaccines or to  
 CC model synthetic saccharides or mimetics for use in vaccines.

XX Sequence 8 AA;

Query Match 100.0%; Score 3; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

## RESULT 74

AAW75463

ID AAW75463 standard; peptide; 8 AA.

XX AC AAW75463;

XX DT 27-APR-1999 (first entry)

XX DE Mammalian tub protein tyrosine phosphorylation site.

XX KW Human; wild type; tubby; identification; SH2 domain; mammal; obesity;

XX KM body weight disorder; cachexia; anorexia.

XX OS Homo sapiens.

XX OS Mus sp.

XX PN US5861239-A.

XX PD 19-JAN-1999.

XX PF 02-SEP-1997; 97US-0922267.

XX PR 02-SEP-1997; 97US-0922267.

XX PR 12-APR-1996; 96US-0631200.

XX PR 28-MAR-1997; 97US-0829553.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Kapeller R, Kleyn PW, Moore KJ;

XX DR WPI; 1999-130383/11.

XX Identifying compounds which modulate tub protein activity - by  
 CC detecting compounds which alter the interaction of tub protein with  
 CC a SH2 containing peptide, used to develop agents for treating e.g.  
 CC obesity, cachexia or anorexia

XX PS Disclosure; Column 13; 95pp; English.

XX This sequence represents a tyrosine phosphorylation site/SH2 docking  
 CC domain found in the amino acid sequence of the mouse and human "tub"  
 CC proteins (AAW75450 and AAW75451 respectively). The invention relates to  
 CC a method for identifying compounds that modulate tub protein activity.  
 CC especially its interaction with proteins containing an SH2 domain. The  
 CC method can be used for identifying compounds which modulate tub protein  
 CC activity for use in the treatment of mammalian body weight disorders  
 CC including obesity, cachexia and anorexia.

XX Sequence 8 AA;

Query Match 100.0%; Score 3; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 5 LNF 7



```

RESULT 75
AAY70353
ID AAY70353 standard; peptide; 8 AA.
XX
XX
AC AAY70353;
XX
XX 21-JUN-2000 (first entry)
XX
XX Human immunodeficiency virus protease cleavage site-8.
XX
XX Protease cleavage site; PCS; ligand binding domain; DNA binding domain;
XX expression modulator domain; fusion protein; protease; treatment;
XX protease inhibitor; Alzheimer's disease; cystic fibrosis; emphysema;
XX hypertension; tumour; metastasis; viral disease; HIV aspartyl protease;
XX Human immunodeficiency virus; HIV.
XX
XX OS Human immunodeficiency virus.
XX
XX WO200012727-A1.
XX
XX 09-MAR-2000.
XX
XX 31-AUG-1999; 99WO-US19926.
XX
XX 31-AUG-1998; 98US-0144759.
XX
XX (VERT-) VERTEX PHARM INC.
XX
XX PA
XX
XX PI Hermann U, Hock T, Kwong A;
XX
XX WPI; 2000-246756/21.
XX
XX Novel fusion protein comprising a protease cleavage site, a ligand
XX binding domain, and a DNA binding domain useful for characterizing
XX proteases, detecting viral infection, and screening for protease
XX inhibitors -
XX
XX PS Claim 9; Page 62; 80pp; English.
XX
XX The patent discloses fusion proteins comprising a protease cleavage
XX site (PCS), ligand binding domain, DNA binding domain and an expression
XX modulator domain that regulates transcription of a reporter gene.
XX Fusion proteins and the DNA encoding them can be used to detect viral,
XX cellular or microbial proteases, assay protease activity, detect viral
XX infections, determine substrate specificity of proteases, for
XX biochemical characterisation of proteases and to screen for potential
XX protease inhibitors. Protease inhibitors may be useful for treating
XX Alzheimer's disease, cystic fibrosis, emphysema, hypertension, tumour
XX invasion and metastasis and viral-associated diseases. The present
XX peptide sequence is the human immunodeficiency virus (HIV) protease
XX cleavage site, which is recognised by HIV aspartyl protease.
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 100.0%; Score 3; DB 21; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LNF 3
XX |||
XX Db 2 LNF 4

```

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 Job time : 8.63698 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 4.81395 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-33

Perfect score: 3

Sequence: 1 LNF 3

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	100.0	3	15	US-10-281-652-33
2	3	100.0	4	10	US-09-947-387-54
3	3	100.0	4	10	US-09-947-387-85
4	3	100.0	4	12	US-10-138-375-54
5	3	100.0	4	12	US-10-138-375-85
6	3	100.0	5	10	US-09-947-387-82
7	3	100.0	5	10	US-09-947-387-84
8	3	100.0	5	10	US-09-947-387-132
9	3	100.0	5	12	US-10-138-375-82
10	3	100.0	5	12	US-10-138-375-84
11	3	100.0	5	12	US-10-138-375-132
12	3	100.0	6	10	US-09-947-387-81
13	3	100.0	6	10	US-09-947-387-83
14	3	100.0	6	10	US-09-947-387-123
15	3	100.0	6	12	US-10-138-375-81

16	3	100.0	6	12	US-10-138-375-83	Sequence 83, Appl
17	3	100.0	6	12	US-10-138-375-123	Sequence 123, App
18	3	100.0	7	9	US-09-735-995-110	Sequence 110, App
19	3	100.0	7	9	US-09-735-995-111	Sequence 111, App
20	3	100.0	7	10	US-09-947-387-34	Sequence 34, Appl
21	3	100.0	7	10	US-09-947-387-80	Sequence 80, Appl
22	3	100.0	7	12	US-10-351-641-1065	Sequence 1065, Ap
23	3	100.0	7	12	US-10-138-375-34	Sequence 34, Appl
24	3	100.0	7	12	US-10-138-375-80	Sequence 80, Appl
25	3	100.0	7	15	US-10-214-932-70	Sequence 70, Appl
26	3	100.0	8	10	US-09-910-552-37	Sequence 37, Appl
27	3	100.0	8	12	US-10-072-419-4	Sequence 4, Appl
28	3	100.0	8	12	US-10-072-419-9	Sequence 9, Appl
29	3	100.0	8	12	US-10-072-419-10	Sequence 10, Appl
30	3	100.0	8	12	US-10-072-419-11	Sequence 11, Appl
31	3	100.0	8	12	US-10-072-419-15	Sequence 15, Appl
32	3	100.0	8	12	US-10-072-419-20	Sequence 20, Appl
33	3	100.0	8	12	US-10-072-419-21	Sequence 21, Appl
34	3	100.0	8	12	US-10-072-419-25	Sequence 25, Appl
35	3	100.0	8	12	US-10-226-629A-451	Sequence 451, App
36	3	100.0	8	12	US-10-226-629A-464	Sequence 464, App
37	3	100.0	8	12	US-10-226-629A-477	Sequence 477, App
38	3	100.0	8	12	US-10-231-417-346	Sequence 346, App
39	3	100.0	8	14	US-10-079-625-33	Sequence 33, App
40	3	100.0	8	15	US-10-300-757-8	Sequence 8, Appl
41	3	100.0	9	10	US-09-894-018-72	Sequence 72, Appl
42	3	100.0	9	10	US-09-894-018-152	Sequence 152, App
43	3	100.0	9	10	US-09-897-107-2	Sequence 2, Appl
44	3	100.0	9	11	US-09-865-548A-156	Sequence 156, App
45	3	100.0	9	12	US-10-226-629A-452	Sequence 452, App
46	3	100.0	9	12	US-10-226-629A-465	Sequence 465, App
47	3	100.0	9	12	US-10-226-629A-478	Sequence 478, App
48	3	100.0	9	12	US-10-226-629A-491	Sequence 491, App
49	3	100.0	9	12	US-10-371-069-220	Sequence 220, App
50	3	100.0	9	12	US-10-371-069-354	Sequence 354, App
51	3	100.0	9	12	US-10-371-645-220	Sequence 220, App
52	3	100.0	9	12	US-10-371-645-354	Sequence 354, App
53	3	100.0	9	15	US-10-133-210-18	Sequence 18, Appl
54	3	100.0	10	11	US-09-863-054-24	Sequence 24, Appl
55	3	100.0	10	11	US-09-572-404B-781	Sequence 781, App
56	3	100.0	10	11	US-09-572-404B-839	Sequence 839, App
57	3	100.0	10	12	US-10-072-419-1	Sequence 1, Appl
58	3	100.0	10	12	US-10-072-419-35	Sequence 35, Appl
59	3	100.0	10	12	US-10-072-419-36	Sequence 36, Appl
60	3	100.0	10	12	US-10-226-629A-453	Sequence 453, App
61	3	100.0	10	12	US-10-226-629A-466	Sequence 466, App
62	3	100.0	10	12	US-10-226-629A-479	Sequence 479, App
63	3	100.0	10	12	US-10-226-629A-492	Sequence 492, App
64	3	100.0	10	12	US-10-226-629A-505	Sequence 505, App
65	3	100.0	10	12	US-09-573-822C-16	Sequence 16, Appl
66	3	100.0	10	12	US-09-573-822C-18	Sequence 18, Appl
67	3	100.0	10	12	US-09-573-822C-40	Sequence 40, Appl
68	3	100.0	10	12	US-09-573-822C-153	Sequence 153, App
69	3	100.0	10	12	US-10-371-069-343	Sequence 343, App
70	3	100.0	10	12	US-10-371-645-343	Sequence 343, App
71	3	100.0	10	15	US-10-033-662-65	Sequence 65, Appl
72	3	100.0	11	11	US-09-574-879-319	Sequence 319, App
73	3	100.0	11	11	US-09-305-736-319	Sequence 319, App
74	3	100.0	11	12	US-10-226-629A-454	Sequence 454, App
75	3	100.0	11	12	US-10-226-629A-467	Sequence 467, App
76	3	100.0	11	12	US-10-226-629A-480	Sequence 480, App
77	3	100.0	11	12	US-10-226-629A-493	Sequence 493, App
78	3	100.0	11	12	US-10-226-629A-506	Sequence 506, App
79	3	100.0	11	12	US-10-226-629A-518	Sequence 518, App
80	3	100.0	11	12	US-09-818-683-319	Sequence 319, App
81	3	100.0	11	15	US-10-211-088-89	Sequence 89, Appl
82	3	100.0	12	10	US-09-430-221-8	Sequence 8, Appl
83	3	100.0	12	12	US-10-324-023-8	Sequence 8, Appl
84	3	100.0	12	12	US-10-226-629A-455	Sequence 455, App
85	3	100.0	12	12	US-10-226-629A-468	Sequence 468, App
86	3	100.0	12	12	US-10-226-629A-481	Sequence 481, App
87	3	100.0	12	12	US-10-226-629A-494	Sequence 494, App
88	3	100.0	12	12	US-10-226-629A-507	Sequence 507, App

89 Sequence 519, App  
 90 Sequence 530, App  
 91 Sequence 2, Appli  
 92 Sequence 456, App  
 93 Sequence 469, App  
 94 Sequence 482, App  
 95 Sequence 495, App  
 96 Sequence 508, App  
 97 Sequence 520, App  
 98 Sequence 531, App  
 99 Sequence 541, App  
 100 Sequence 89, Appli

US-10-226-629A-519  
 US-10-226-629A-530  
 US-10-204-987-2  
 US-10-226-629A-456  
 US-10-226-629A-469  
 US-10-226-629A-482  
 US-10-226-629A-495  
 US-10-226-629A-508  
 US-10-226-629A-520  
 US-10-226-629A-531  
 US-10-226-629A-541  
 US-10-168-445-89

## ALIGNMENTS

RESULT 1  
 US-10-281-652-33  
 ; Sequence 33, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDGOCH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; PRIOR FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 33  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-33

Query Match 100.0%; Score 3; DB 15; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 2  
 US-09-947-387-54  
 ; Sequence 54, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735.0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10

; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 54  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-947-387-54

Query Match 100.0%; Score 3; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 3  
 US-09-947-387-85  
 ; Sequence 85, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735.0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 85  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-947-387-85

Query Match 100.0%; Score 3; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 4  
 US-10-138-375-54  
 ; Sequence 54, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong

; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; PRIOR FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 54  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-54

Query Match 100.0%; Score 3; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 5  
 US-10-138-375-85  
 ; Sequence 85, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; PRIOR FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 85  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-85

Query Match 100.0%; Score 3; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 6

US-09-947-387-82  
 ; Sequence 82, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735.0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 82  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-947-387-82

Query Match 100.0%; Score 3; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 7  
 US-09-947-387-84  
 ; Sequence 84, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735.0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 84  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic

```
; OTHER INFORMATION: Peptide
US-09-947-387-84
Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 8
US-09-947-387-132
; Sequence 132, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Their Applications for Fluorescent Reporter Molecules
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-132
Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 9
US-10-138-375-82
; Sequence 82, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642

; OTHER INFORMATION: Peptide
US-09-947-387-132
Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 10
US-10-138-375-84
; Sequence 84, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications f
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas
; TITLE OF INVENTION: Other Enzymes and the Use thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-84
Query Match      100.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 11
US-10-138-375-132
; Sequence 132, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications f
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas
; TITLE OF INVENTION: Other Enzymes and the Use thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
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; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 132  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-132

Query Match 100.0%; Score 3; DB 12; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 12  
 US-09-947-387-81  
 ; Sequence 81, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Drewe, John A.  
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735-0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 81  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide

Query Match 100.0%; Score 3; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 13  
 US-09-947-387-83  
 ; Sequence 83, Application US/09947387  
 ; Patent No. US20020150885A1

; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Drewe, John A.  
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735-0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 83  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-947-387-83

Query Match 100.0%; Score 3; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

RESULT 14  
 US-09-947-387-123  
 ; Sequence 123, Application US/09947387  
 ; Patent No. US20020150885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Drewe, John A.  
 ; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735-0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 123  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-09-947-387-123

Query Match 100.0%; Score 3; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 15

US-10-138-375-81  
 ; Sequence 81, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 81  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-81

Query Match 100.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 16

US-10-138-375-83  
 ; Sequence 83, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 83  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence

; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-83

Query Match 100.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 1 LNF 3

## RESULT 17

US-10-138-375-123  
 ; Sequence 123, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 123  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-138-375-123

Query Match 100.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 18

US-09-735-995-110  
 ; Sequence 110, Application US/09735995  
 ; Patent No. US20010034024A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keating, Mark T.  
 ; APPLICANT: Splawski, Igor  
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
 ; FILE REFERENCE: 2323-136  
 ; CURRENT APPLICATION NUMBER: US/09/735,995  
 ; CURRENT FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 09/226,012  
 ; PRIOR FILING DATE: 1999-01-06  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 110  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster

US-09-735-995-110

Query Match 100.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

## RESULT 19

US-09-735-995-111  
; Sequence 111, Application US/09735995  
; Patent No. US20010034024A1  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/735,995  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 09/226,012  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: See Warnke and  
; OTHER INFORMATION: Ganetzky, 1994.

US-09-735-995-111

Query Match 100.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

## RESULT 20

US-09-947-387-34  
; Sequence 34, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

US-09-947-387-34

Query Match 100.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 21

US-09-947-387-80  
; Sequence 80, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

US-09-947-387-80

Query Match 100.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 22

US-10-351-641-1065  
; Sequence 1065, Application US/10351641  
; Publication No. US20030186874A1  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-100  
; CURRENT APPLICATION NUMBER: US/10/351,641  
; CURRENT FILING DATE: 2003-01-24



; PRIOR APPLICATION NUMBER: 09/350,641  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 09/315,304  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: 09/082,279  
 ; PRIOR FILING DATE: 1998-05-20  
 ; NUMBER OF SEQ ID NOS: 1757  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1065  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Core polypeptide  
 ; US-10-351-641-1065

Query Match 100.0%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 1 LNF 3

RESULT 23  
 US-10-138-375-34  
 ; Sequence 34, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 34  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-10-138-375-34

Query Match 100.0%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 24  
 US-10-138-375-80  
 ; Sequence 80, Application US/10138375  
 ; Publication No. US20030208037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu

; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications f  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735.0030001  
 ; CURRENT APPLICATION NUMBER: US/10/138,375  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 80  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-10-138-375-80

Query Match 100.0%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 25  
 US-10-214-932-70  
 ; Sequence 70, Application US/10214932  
 ; Publication No. US20030100707A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HWANG, Inhwan  
 ; APPLICANT: KIM, Dae Heon  
 ; APPLICANT: LEE, Yong Jik  
 ; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE  
 ; FILE REFERENCE: AP02/US  
 ; CURRENT APPLICATION NUMBER: US/10/214,932  
 ; CURRENT FILING DATE: 2002-08-08  
 ; NUMBER OF SEQ ID NOS: 133  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 70  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 ; US-10-214-932-70

Query Match 100.0%; Score 3; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 26  
 US-09-910-552-37  
 ; Sequence 37, Application US/09910552  
 ; Publication No. US20020197260A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Granoff, Dan M.  
 ; APPLICANT: Moe, Gregory R.  
 ; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
 ; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
 ; TITLE OF INVENTION: COMPOSITIONS  
 ; FILE REFERENCE: 1238.002  
 ; CURRENT APPLICATION NUMBER: US/09/910,552

; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/494,822  
; FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence from  
; OTHER INFORMATION: a phage display peptide library  
US-09-910-552-37

Query Match 100.0%; Score 3; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

## RESULT 27

US-10-072-419-4  
; Sequence 4, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Bernice  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Schistocerca gregaria  
US-10-072-419-4

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 28

US-10-072-419-9  
; Sequence 9, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Bernice  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Pyrrhocoris apterus  
US-10-072-419-9

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 29

US-10-072-419-10  
; Sequence 10, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Bernice  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Locusta migratoria  
US-10-072-419-10

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 30

US-10-072-419-11  
; Sequence 11, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Bernice  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Locusta migratoria  
US-10-072-419-11

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 31

US-10-072-419-15  
; Sequence 15, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Bernice  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07

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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Phymateus leprosus
US-10-072-419-15

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 32
US-10-072-419-20
; Sequence 20, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Tenebrio molitor
US-10-072-419-20

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libanasidus vittatus
US-10-072-419-25

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 34
US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libanasidus vittatus
US-10-072-419-25

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      2 LNF 4

RESULT 35
US-10-226-629A-451
; Sequence 451, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 451
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-451

Query Match      100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
Db      4 LNF 6

RESULT 36
US-10-226-629A-464
; Sequence 464, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
```

; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 464  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-464

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 5 LNF 7

## RESULT 37

US-10-226-629A-477  
; Sequence 477, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 477  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-477

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 6 LNF 8

## RESULT 38

US-10-231-417-346  
; Sequence 346, Application US/10231417  
; Publication No. US20030176681A1  
; GENERAL INFORMATION:  
; APPLICANT: Feng et al.  
; TITLE OF INVENTION: 148 Human Secreted Proteins  
; FILE REFERENCE: P2019P1  
; CURRENT APPLICATION NUMBER: US/10/231,417  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/296,622  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 619  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 346  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-231-417-346

Query Match 100.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LNF 3  
|||  
Db 5 LNF 7

## RESULT 39

US-10-079-625-33  
; Sequence 33, Application US/10079625  
; Publication No. US20020182676A1  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/079,625  
; FILING DATE: 2002-FEB-19  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/019002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-079-625-33

Query Match 100.0%; Score 3; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 4 LNF 6

## RESULT 40

US-10-300-757-8  
 ; Sequence 8, Application US/10300757  
 ; Publication No. US20030083467A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hock, Thomas  
 ; APPLICANT: Germann, Ursula  
 ; APPLICANT: Kwong, Ann  
 ; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS  
 ; FILE REFERENCE: VPI/98-08  
 ; CURRENT APPLICATION NUMBER: US/10/300,757  
 ; PRIOR FILING DATE: 2002-11-20  
 ; PRIOR APPLICATION NUMBER: US/09/570,267  
 ; PRIOR FILING DATE: 2000-05-12  
 ; PRIOR APPLICATION NUMBER: 09/144,759  
 ; PRIOR FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-300-757-8

Query Match 100.0%; Score 3; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 41

US-09-894-018-72  
 ; Sequence 72, Application US/09894018  
 ; Patent No. US20020119127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPIMMUNE, Inc.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Chestnut, Robert  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Baker, Denisw  
 ; APPLICANT: Newman, Mark  
 ; APPLICANT: Brown, David  
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
 ; FILE REFERENCE: 39863-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/894,018  
 ; CURRENT FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/173,390  
 ; PRIOR FILING DATE: 1999-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/284,221  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 368  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 72  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligopeptide  
 US-09-894-018-72

Query Match 100.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 42

US-09-894-018-152  
 ; Sequence 152, Application US/09894018  
 ; Patent No. US20020119127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPIMMUNE, Inc.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Chestnut, Robert  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Baker, Denisw  
 ; APPLICANT: Newman, Mark  
 ; APPLICANT: Brown, David  
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
 ; FILE REFERENCE: 39863-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/894,018  
 ; CURRENT FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/173,390  
 ; PRIOR FILING DATE: 1999-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/284,221  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 368  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 152  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Transgenic mouse  
 US-09-894-018-152

Query Match 100.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 43

US-09-897-107-2  
 ; Sequence 2, Application US/09897107  
 ; Patent No. US20020137094A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YAMAGISHI, Akihiko  
 ; TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING  
 ; FILE REFERENCE: 210383USO  
 ; CURRENT APPLICATION NUMBER: US/09/897,107  
 ; CURRENT FILING DATE: 2001-07-03  
 ; PRIOR APPLICATION NUMBER: JP2000-201920  
 ; PRIOR FILING DATE: 2000-07-04  
 ; PRIOR APPLICATION NUMBER: JP2001-164332  
 ; PRIOR FILING DATE: 2001-05-31  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Sulfolobus sp.  
 US-09-897-107-2

Query Match 100.0%; Score 3; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 1 LNF 3  
|||  
Db 6 LNF 8

## RESULT 44

US-09-865-548A-156  
; Sequence 156, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; PRIOR FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 156  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Variola virus  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-156

Query Match 100.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 5 LNF 7

## RESULT 45

US-10-226-629A-452  
; Sequence 452, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; PRIOR FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 452  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-452

Query Match 100.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

## RESULT 46

US-10-226-629A-465  
; Sequence 465, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; PRIOR FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 465  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-465

Query Match 100.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 5 LNF 7

## RESULT 47

US-10-226-629A-478  
; Sequence 478, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
; FILE REFERENCE: 5006.01  
; CURRENT APPLICATION NUMBER: US/10/226,629A  
; PRIOR FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 478  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Variola virus  
US-10-226-629A-478

Query Match 100.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 6 LNF 8

## RESULT 48

US-10-226-629A-491  
; Sequence 491, Application US/10226629A  
; Publication No. US20030166504A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott

```

; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 491
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Variola virus
; US-10-226-629A-491

```

```

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LNF 3
   |||
Db 7 LNF 9

```

```

RESULT 49
US-10-371-069-220
; Sequence 220, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)
US-10-371-069-220

```

```

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LNF 3
   |||
Db 6 LNF 8

```

```

RESULT 50
US-10-371-069-354
; Sequence 354, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.

```

```

; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)
US-10-371-069-354

```

```

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LNF 3
   |||
Db 2 LNF 4

```

```

RESULT 51
US-10-371-645-220
; Sequence 220, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)
US-10-371-645-220

```

```

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LNF 3
   |||
Db 6 LNF 8

```

```

RESULT 52
US-10-371-645-354
; Sequence 354, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)
US-10-371-645-354

Query Match      100.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 53
US-10-133-210-18
; Sequence 18, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-18

Query Match      100.0%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 54
US-09-863-054-24
; Sequence 24, Application US/09863054
; Publication No. US20030021809A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
; Lymphocyte Responses to Hepatitis B Virus
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,054
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,898
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 08/024,120
; FILING DATE: 26-FEB-1993
; APPLICATION NUMBER: US 08/396,283
; FILING DATE: 27-FEB-1995
; APPLICATION NUMBER: US 08/463,486
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lockyer, Jean M.
; REGISTRATION NUMBER: 44,879
; REFERENCE/DOCKET NUMBER: 014740-000421US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-863-054-24

Query Match      100.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 55
US-03-572-404B-781
; Sequence 781, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent

```



; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProtPatent version 1.0  
 ; SEQ ID NO 781  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in APOB at 2799-2808 and may interact with Sequ  
 ; OTHER INFORMATION: in this patent.  
 US-09-572-404B-781

Query Match 100.0%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 6 LNF 8

RESULT 56  
 US-09-572-404B-839  
 ; Sequence 839, Application US/09572404B  
 ; Publication No. US20030078374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProtPatent version 1.0  
 ; SEQ ID NO 839  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in APOB at 2798-2807 and may interact with Sequ  
 ; OTHER INFORMATION: in this patent.  
 US-09-572-404B-839

Query Match 100.0%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 7 LNF 9

RESULT 57  
 US-10-072-419-1  
 ; Sequence 1, Application US/10072419  
 ; Publication No. US2003016217A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schacter, Bernice  
 ; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum  
 ; FILE REFERENCE: 10739-1  
 ; CURRENT APPLICATION NUMBER: US/10/072,419  
 ; CURRENT FILING DATE: 2002-02-07  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Schistoscerca gregaria  
 US-10-072-419-1

Query Match 100.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 58  
 US-10-072-419-35  
 ; Sequence 35, Application US/10072419  
 ; Publication No. US2003016217A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schacter, Bernice  
 ; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum  
 ; FILE REFERENCE: 10739-1  
 ; CURRENT APPLICATION NUMBER: US/10/072,419  
 ; CURRENT FILING DATE: 2002-02-07  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 35  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Schistoscerca gregaria  
 US-10-072-419-35

Query Match 100.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 59  
 US-10-072-419-36  
 ; Sequence 36, Application US/10072419  
 ; Publication No. US2003016217A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schacter, Bernice  
 ; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Hum  
 ; FILE REFERENCE: 10739-1  
 ; CURRENT APPLICATION NUMBER: US/10/072,419  
 ; CURRENT FILING DATE: 2002-02-07  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 36  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Tenthredo arcuata  
 US-10-072-419-36

Query Match 100.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 |||  
 Db 2 LNF 4

RESULT 60  
 US-10-226-629A-453  
 ; Sequence 453, Application US/10226629A  
 ; Publication No. US20030166504A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

```

; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 453
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-453

```

```

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

Qy 1 LNF 3
    |||
Db 4 LNF 6

```

```

RESULT 61
US-10-226-629A-466
; Sequence 466, Application US/10/226,629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-466

```

```

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

Qy 1 LNF 3
    |||
Db 5 LNF 7

```

```

RESULT 62
US-10-226-629A-479
; Sequence 479, Application US/10/226,629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 10

```

```

; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-479

```

```

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

Qy 1 LNF 3
    |||
Db 6 LNF 8

```

```

RESULT 63
US-10-226-629A-492
; Sequence 492, Application US/10/226,629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 492
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-492

```

```

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

Qy 1 LNF 3
    |||
Db 7 LNF 9

```

```

RESULT 64
US-10-226-629A-505
; Sequence 505, Application US/10/226,629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 505
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Variola virus
US-10-226-629A-505

```

```

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

Qy 1 LNF 3

```

```
Db      |||
        8 LNF 10

RESULT 65
US-09-573-822C-16
; Sequence 16, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG241 at 66-75 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-573-822C-16

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
        |||
Db      2 LNF 4

RESULT 66
US-09-573-822C-18
; Sequence 18, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG241 at 65-74 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-573-822C-18

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
        |||
Db      2 LNF 4

RESULT 67
US-09-573-822C-40
; Sequence 40, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C

Db      |||
        3 LNF 5

RESULT 68
US-09-573-822C-153
; Sequence 153, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 153
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG256 at 202-211 and may interact with Sequence
; OTHER INFORMATION: in this patent.
US-09-573-822C-153

Query Match      100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
        |||
Db      3 LNF 5

RESULT 69
US-10-371-069-343
; Sequence 343, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
```

```
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0151)
US-10-371-069-343
```

```
Query Match          100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LNF 3
   |||
Db 3 LNF 5
```

## RESULT 70

```
US-10-371-645-343
; Sequence 343, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0151)
US-10-371-645-343
```

```
Query Match          100.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LNF 3
   |||
Db 3 LNF 5
```

## RESULT 71

```
US-10-033-662-65
; Sequence 65, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-65
```

```
Query Match          100.0%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LNF 3
   |||
Db 6 LNF 8
```

## RESULT 72

```
US-09-974-879-319
; Sequence 319, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-319
```

```
Query Match          100.0%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LNF 3  
Db 6 LNF 8

## RESULT 73

US-09-305-736-319  
; Sequence 319, Application US/09305736  
; Publication No. US20030088078A1  
; GENERAL INFORMATION:  
; APPLICANT: Feng et al.

; TITLE OF INVENTION: 125 Human Secreted Proteins

; CURRENT APPLICATION NUMBER: US/09/305,736  
; CURRENT FILING DATE: 1999-05-05

; EARLIER APPLICATION NUMBER: PCT/US98/23435  
; EARLIER FILING DATE: 1998-11-04

; EARLIER APPLICATION NUMBER: 60/064,911  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,912  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,983  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,900  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,988  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,987  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,908  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,984  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/064,985  
; EARLIER FILING DATE: 1997-11-07

; EARLIER APPLICATION NUMBER: 60/066,094  
; EARLIER FILING DATE: 1997-11-17

; EARLIER APPLICATION NUMBER: 60/066,100  
; EARLIER FILING DATE: 1997-11-17

; EARLIER APPLICATION NUMBER: 60/066,089  
; EARLIER FILING DATE: 1997-11-17

; EARLIER APPLICATION NUMBER: 60/066,095  
; EARLIER FILING DATE: 1997-11-17

; EARLIER APPLICATION NUMBER: 60/066,090  
; EARLIER FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 612  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 319  
; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-305-736-319

Query Match 100.0%; Score 3; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 6 LNF 8

## RESULT 74

US-10-226-629A-454  
; Sequence 454, Application US/10226629A

; Publication No. US20030166504A1  
; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

; FILE REFERENCE: 5006.01

; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22  
; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 454  
; LENGTH: 11

; TYPE: PRT

; ORGANISM: Variola virus

US-10-226-629A-454

Query Match 100.0%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 4 LNF 6

## RESULT 75

US-10-226-629A-467

; Sequence 467, Application US/10226629A

; Publication No. US20030166504A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection

; FILE REFERENCE: 5006.01

; CURRENT APPLICATION NUMBER: US/10/226,629A  
; CURRENT FILING DATE: 2002-08-22

; PRIOR APPLICATION NUMBER: US 60/314,182  
; PRIOR FILING DATE: 2001-08-22

; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 467  
; LENGTH: 11

; TYPE: PRT

; ORGANISM: Variola virus

US-10-226-629A-467

Query Match 100.0%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 5 LNF 7

Search completed: November 25, 2003, 20:37:09  
Job time : 5.81395 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 2.42442 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-33

1-0000. Perfect score: 3

Sequence: 1 LNF 3

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 3
Maximum DB seq length: 20
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Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	3	100.0	4	2	US-08-667-001-1	Sequence 1, Appli
3	3	100.0	4	2	US-08-667-001-2	Sequence 2, Appli
4	3	100.0	4	2	US-08-667-001-4	Sequence 4, Appli
5	3	100.0	4	2	US-08-667-001-5	Sequence 5, Appli
6	3	100.0	4	2	US-08-667-001-9	Sequence 9, Appli
7	3	100.0	4	3	US-09-357-952-54	Sequence 54, Appl
8	3	100.0	4	3	US-09-357-952-85	Sequence 85, Appl
9	3	100.0	4	3	US-09-053-941-24	Sequence 24, Appl
10	3	100.0	4	4	US-09-521-650-54	Sequence 54, Appl
11	3	100.0	4	4	US-09-521-650-85	Sequence 85, Appl
12	3	100.0	4	4	US-09-168-888-54	Sequence 54, Appl
13	3	100.0	4	4	US-09-168-888-85	Sequence 85, Appl
14	3	100.0	4	4	US-09-817-413-24	Sequence 24, Appl
15	3	100.0	4	4	US-09-536-785A-39	Sequence 39, Appl
16	3	100.0	5	3	US-08-485-324-24	Sequence 24, Appl
17	3	100.0	5	3	US-08-447-506-24	Sequence 24, Appl
18	3	100.0	5	3	US-08-235-437-24	Sequence 24, Appl
19	3	100.0	5	3	US-08-981-122-17	Sequence 17, Appl
20	3	100.0	5	3	US-08-447-515-24	Sequence 24, Appl
21	3	100.0	5	3	US-09-357-952-82	Sequence 82, Appl
22	3	100.0	5	3	US-09-357-952-84	Sequence 84, Appl
23	3	100.0	5	3	US-09-521-650-82	Sequence 82, Appl
24	3	100.0	5	4	US-09-521-650-84	Sequence 84, Appl
25	3	100.0	5	4	US-09-521-650-132	Sequence 132, App
26	3	100.0	5	4	US-09-168-888-82	Sequence 82, Appl
27	3	100.0	5	4	US-09-521-650-132	Sequence 132, App

## ALIGNMENTS

RESULT 1  
 US-09-641-803-33  
 ; Sequence 33, Application US/09641803  
 ; Patent No. 6500798  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/09/641,803  
 ; CURRENT FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 33  
 ; LENGTH: 3  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-641-803-33

Query Match 100.0%; Score 3; DB 4; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 1 LNF 3

RESULT 2  
 US-08-667-001-1  
 ; Sequence 1, Application US/08667001  
 ; Patent No. 5827827  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janda, Kim D.  
 ; APPLICANT: Wirsching, Peter  
 ; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
 ; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/667,001  
 ; FILING DATE: 20-JUN-1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/335,039  
 ; FILING DATE: 16-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lewis, Donald G.  
 ; REGISTRATION NUMBER: 28,636  
 ; REFERENCE/DOCKET NUMBER: TSRI 282.1  
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 554-2937  
 ; TELEFAX: (619) 554-6312  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1  
 ; OTHER INFORMATION: /note= "serine is linked to CH3C(O)  
 ; OTHER INFORMATION: - in formula (V A) or (V B)"  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 4  
 ; OTHER INFORMATION: /note= "Pro-Ile-Val-OCH3 is  
 ; OTHER INFORMATION: connected to Phe via Psi[] in formula (V A) or (V B)"  
 ; OTHER INFORMATION: B"  
 US-08-667-001-1

Query Match 100.0%; Score 3; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

RESULT 3  
 US-08-667-001-2  
 ; Sequence 2, Application US/08667001  
 ; Patent No. 5827827  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janda, Kim D.  
 ; APPLICANT: Wirsching, Peter  
 ; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
 ; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/667,001  
 ; FILING DATE: 20-JUN-1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/335,039  
 ; FILING DATE: 16-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lewis, Donald G.  
 ; REGISTRATION NUMBER: 28,636  
 ; REFERENCE/DOCKET NUMBER: TSRI 282.1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 554-2937  
 ; TELEFAX: (619) 554-6312  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal

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; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "serine is linked to
; OTHER INFORMATION: C5H11C(O) in formula (V A) or (V B)"
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; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 4
; OTHER INFORMATION: /note= "Pro-Ile-Val-OCH3 is
; OTHER INFORMATION: connected to Phe via Psi[] in formula (V A) or (V
; OTHER INFORMATION: B)"
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US-08-667-001-2
Query Match 100.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 4
US-08-667-001-4
; Sequence 4, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "serine is linked to CH3C(O)
; OTHER INFORMATION: in formula (V A) or (V B)"
;
US-08-667-001-5
Query Match 100.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4

RESULT 5
US-08-667-001-5
; Sequence 5, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "serine is linked to CH3C(O)
; OTHER INFORMATION: in formula (V A) or (V B)"
;
US-08-667-001-5
Query Match 100.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3
Db 2 LNF 4
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## RESULT 6

US-08-667-001-9  
 ; Sequence 9, Application US/08667001  
 ; Patent No. 5827827  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janda, Kim D.  
 ; APPLICANT: Wirsching, Peter  
 ; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
 ; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/667,001  
 ; FILING DATE: 20-JUN-1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/335,039  
 ; FILING DATE: 16-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lewis, Donald G.  
 ; REGISTRATION NUMBER: 28,636  
 ; REFERENCE/DOCKET NUMBER: TSRI 282.1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 554-2937  
 ; TELEFAX: (619) 554-6312  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1  
 ; OTHER INFORMATION: /note= "sequence = Y1 in formula  
 ; OTHER INFORMATION: (III A) and (III B)"

US-08-667-001-9

Query Match 100.0%; Score 3; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

## RESULT 7

US-09-357-952-54  
 ; Sequence 54, Application US/09357952  
 ; Patent No. 6248904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-  
 ; FILE REFERENCE: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; CURRENT FILING DATE: 1998-04-02  
 ; FILE REFERENCE: 1735.0030001

; CURRENT APPLICATION NUMBER: US/09/357,952  
 ; CURRENT FILING DATE: 1999-07-21  
 ; EARLIER APPLICATION NUMBER: US 60/093,642  
 ; EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 54  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-09-357-952-54

Query Match 100.0%; Score 3; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 2 LNF 4

## RESULT 8

US-09-357-952-85  
 ; Sequence 85, Application US/09357952  
 ; Patent No. 6248904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Yang, Wu  
 ; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
 ; FILE REFERENCE: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; CURRENT FILING DATE: 1999-07-21  
 ; CURRENT APPLICATION NUMBER: US/09/357,952  
 ; EARLIER APPLICATION NUMBER: US 60/093,642  
 ; EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 85  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-09-357-952-85

Query Match 100.0%; Score 3; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
 Db 1 LNF 3

## RESULT 9

US-09-053-941-24  
 ; Sequence 24, Application US/09053941  
 ; Patent No. 6271354  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SRINIVASAN, ALGARSAMY  
 ; APPLICANT: KOPROWSKI, HILARY  
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
 ; FILE REFERENCE: Chimeric Viral Proteins  
 ; CURRENT APPLICATION NUMBER: US/09/053,941  
 ; CURRENT FILING DATE: 1998-04-02  
 ; EARLIER APPLICATION NUMBER: 60/043,380

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; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-053-941-24

Query Match          100.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
DB      2 LNF 4

RESULT 10
US-09-521-650-54
; Sequence 54, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-54

Query Match          100.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
DB      1 LNF 3

RESULT 12
US-09-168-888-54
; Sequence 54, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-54

Query Match          100.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
DB      2 LNF 4

RESULT 13
US-09-168-888-54
; Sequence 54, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
```

## US-09-168-888-85

; Sequence 85, Application US/09168888  
 ; Patent No. 6342611  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735-0290002  
 ; CURRENT APPLICATION NUMBER: US/09/168,888  
 ; CURRENT FILING DATE: 1998-10-09  
 ; EARLIER APPLICATION NUMBER: US 60/061,582  
 ; EARLIER FILING DATE: 1997-10-10  
 ; EARLIER APPLICATION NUMBER: US 09/033,661  
 ; EARLIER FILING DATE: 1998-03-03  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 85  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide

## US-09-168-888-85

Query Match 100.0%; Score 3; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 1 LNF 3

## RESULT 14

US-09-817-413-24  
 ; Sequence 24, Application US/09817413  
 ; Patent No. 6436648  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SRINIVASAN, ALGARSAMY  
 ; APPLICANT: KOPROWSKI, HILARY  
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
 ; FILE REFERENCE: Chimeric Viral Proteins  
 ; CURRENT APPLICATION NUMBER: US/09/817,413  
 ; CURRENT FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 60/043,380  
 ; PRIOR FILING DATE: 1999-04-03  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 24  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; OTHER INFORMATION: Human immunodeficiency virus type 1

Query Match 100.0%; Score 3; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 15

US-09-536-785A-39  
 ; Sequence 39, Application US/09536785A

; Patent No. 6541450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BARBIER, JEAN-RENE  
 ; APPLICANT: MORLEY, PAUL  
 ; APPLICANT: NEUGEBAUER, WITOLD  
 ; APPLICANT: ROSS VIRGINIA J.S.  
 ; APPLICANT: WHITFIELD, JAMES F.  
 ; APPLICANT: WILKICK, GORDON E.  
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF  
 ; TITLE OF INVENTION: OSTEOPOROSIS  
 ; FILE REFERENCE: 1339-9  
 ; CURRENT APPLICATION NUMBER: US/09/536,785A  
 ; CURRENT FILING DATE: 2000-03-28  
 ; PRIOR APPLICATION NUMBER: 08/904,760  
 ; PRIOR FILING DATE: 1997-08-01  
 ; PRIOR APPLICATION NUMBER: 08/691,647  
 ; PRIOR FILING DATE: 1996-08-02  
 ; PRIOR APPLICATION NUMBER: 08/262,495  
 ; PRIOR FILING DATE: 1994-06-20  
 ; PRIOR APPLICATION NUMBER: 60/040,560  
 ; PRIOR FILING DATE: 1997-03-14  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 39  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; OTHER INFORMATION: US-09-536-785A-39

Query Match 100.0%; Score 3; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 16

US-08-485-324-24  
 ; Sequence 24, Application US/08485324  
 ; Patent No. 6043093  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlstatder, Jacob  
 ; TITLE OF INVENTION: SELECTION METHODS  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Curtis, Morris, & Safford  
 ; ADDRESSEE: c/o Barry Evans  
 ; STREET: 530 Fifth Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,324  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,437  
 ; FILING DATE: 29-APR-1994  
 ; APPLICATION NUMBER: US 07/852,412  
 ; FILING DATE: 16-MAR-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Evans, Barry  
 ; REGISTRATION NUMBER: 22,802  
 ; REFERENCE/DOCKET NUMBER: 370132-2000  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-324-24

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 3 LNF 5

RESULT 17  
US-08-447-506-24  
Sequence 24, Application US/08447506  
Patent No. 6066499  
GENERAL INFORMATION:  
APPLICANT: Wohlstatder, Jacob  
TITLE OF INVENTION: SELECTION METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris, & Safford  
ADDRESS: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,506  
FILING DATE: 23-MAY-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,437  
FILING DATE: 29-APR-1994  
APPLICATION NUMBER: US 07/852,412  
FILING DATE: 16-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370132-2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-447-506-24

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 3 LNF 5

RESULT 18  
US-08-235-437-24  
Sequence 24, Application US/08235437  
Patent No. 6087177  
GENERAL INFORMATION:  
APPLICANT: Wohlstatder, Jacob  
TITLE OF INVENTION: SELECTION METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris, & Safford  
ADDRESS: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,437  
FILING DATE: 29-APR-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/852,412  
FILING DATE: 16-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370132-2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-235-437-24

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 3 LNF 5

RESULT 19  
US-08-981-122-17  
Sequence 17, Application US/08981122B  
Patent No. 6127339  
GENERAL INFORMATION:  
APPLICANT: Hatanaka, Yoshihiro  
ADDRESSEE: Arimoto, Masaharu  
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/08/981,122B  
CURRENT FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: JP 7-176904  
PRIOR FILING DATE: 1995-06-21  
PRIOR APPLICATION NUMBER: PCT/JP96/01734  
PRIOR FILING DATE: 1996-06-21  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 5  
TYPE: PPT  
ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form  
; Patent No. 6127339  
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide  
; OTHER INFORMATION: synthesizing system (RAMPs)  
US-08-981-122-17

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

## RESULT 20

US-08-447-515-24  
; Sequence 24, Application US/08447515  
; Patent No. 6162640  
; GENERAL INFORMATION:  
; APPLICANT: Wolsteadter, Jacob  
; TITLE OF INVENTION: SELECTION METHODS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris, & Safford  
; ADDRESSEE: c/o Barry Evans  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,515  
; FILING DATE: 23-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,437  
; FILING DATE: 29-APR-1994  
; APPLICATION NUMBER: US 07/852,412  
; FILING DATE: 16-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Barry  
; REGISTRATION NUMBER: 22,802  
; REFERENCE/DOCKET NUMBER: 370132-2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-447-515-24

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 3 LNF 5

## RESULT 21

US-09-357-952-82  
; Sequence 82, Application US/09357952

; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease:  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-82

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 22

US-09-357-952-84  
; Sequence 84, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.

; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease:  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-84

Query Match 100.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

## RESULT 23

US-09-357-952-132

```
; Sequence 132, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-132

Query Match          100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 2 LNF 4

RESULT 24
US-09-521-650-82
; Sequence 82, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-82

Query Match          100.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 2 LNF 4

RESULT 25
US-09-521-650-84
; Sequence 84, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-84

Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 1 LNF 3

RESULT 26
US-09-521-650-132
; Sequence 132, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-82

Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-132
```

```
Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 LNF 3
    |||
Db 2 LNF 4
```

```
RESULT 27
US-09-168-888-82
; Sequence 82, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-82
```

```
Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LNF 3
    |||
Db 2 LNF 4
```

```
RESULT 28
US-09-168-888-84
; Sequence 84, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
```

```
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-84
```

```
Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LNF 3
    |||
Db 1 LNF 3
```

```
RESULT 29
US-09-168-888-132
; Sequence 132, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-132
```

```
Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LNF 3
    |||
Db 2 LNF 4
```

```
RESULT 30
US-09-357-952-81
; Sequence 81, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
```

; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-81

Query Match 100.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

RESULT 31  
US-09-357-952-83  
; Sequence 83, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-83

Query Match 100.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

RESULT 32  
US-09-357-952-123  
; Sequence 123, Application US/09357952  
; Patent No. 6248904

; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; EARLIER FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 123  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-123

Query Match 100.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

RESULT 33  
US-09-521-650-81  
; Sequence 81, Application US/09521650  
; Patent No. 6335429  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290002  
; CURRENT APPLICATION NUMBER: US/09/521,650  
; EARLIER FILING DATE: 2000-03-08  
; EARLIER APPLICATION NUMBER: 09/168,888  
; EARLIER FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 60/061,582  
; EARLIER FILING DATE: 1997-10-10  
; EARLIER APPLICATION NUMBER: US 09/033,661  
; EARLIER FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-521-650-81

Query Match 100.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||



```
Db          2 LNF 4

RESULT 34
US-09-521-650-83
; Sequence 83, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-83

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          1 LNF 3

RESULT 35
US-09-521-650-123
; Sequence 123, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-123

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          1 LNF 3

RESULT 36
US-09-168-888-81
; Sequence 81, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-81

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LNF 3
           |||
Db          2 LNF 4

RESULT 37
US-09-168-888-83
; Sequence 83, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
```

;/ CURRENT FILING DATE: 1998-10-09  
;/ EARLIER APPLICATION NUMBER: US 60/061,582  
;/ EARLIER FILING DATE: 1997-10-10  
;/ EARLIER APPLICATION NUMBER: US 09/033,661  
;/ EARLIER FILING DATE: 1998-03-03  
;/ NUMBER OF SEQ ID NOS: 142  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 83  
;/ LENGTH: 6  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
;/ OTHER INFORMATION: Peptide  
US-09-168-888-83

Query Match 100.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

## RESULT 38

US-09-168-888-123  
;/ Sequence 123, Application US/0916888  
;/ Patent No. 6342611

;/ GENERAL INFORMATION:  
;/ APPLICANT: Weber, Eckard

;/ APPLICANT: Cai, Sui Xiong

;/ APPLICANT: Keana, John F.W.

;/ APPLICANT: Drewe, John A.

;/ APPLICANT: Zhang, Han-Zhong

;/ TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and  
;/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
;/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
;/ TITLE OF INVENTION: Use Thereof

;/ FILE REFERENCE: 1735.0290002

;/ CURRENT APPLICATION NUMBER: US/09/168,888

;/ CURRENT FILING DATE: 1998-10-09

;/ EARLIER APPLICATION NUMBER: US 60/061,582

;/ EARLIER FILING DATE: 1997-10-10

;/ EARLIER APPLICATION NUMBER: US 09/033,661

;/ EARLIER FILING DATE: 1998-03-03

;/ NUMBER OF SEQ ID NOS: 142

;/ SOFTWARE: PatentIn Ver. 2.0

;/ SEQ ID NO 123

;/ LENGTH: 6

;/ TYPE: PRT

;/ ORGANISM: Artificial Sequence

;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
;/ OTHER INFORMATION: Peptide  
US-09-168-888-123

Query Match 100.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

## RESULT 39

5342922-20

;/ Patent No. 5342922

;/ APPLICANT: MARSHALL, GARLAND R.;TOTH, MIHALY V.

;/ TITLE OF INVENTION: INHIBITORS OF RETROVIRAL PROTEASE

;/ NUMBER OF SEQUENCES: 23

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/07/320,742  
;/ FILING DATE: 08-MAR-1989  
;/ SEQ ID NO:20:  
;/ LENGTH: 6  
5342922-20

Query Match 100.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

## RESULT 40

US-08-401-512-75

;/ Sequence 75, Application US/08401512

;/ Patent No. 5599673

;/ GENERAL INFORMATION:  
;/ APPLICANT: Keating, Mark T.

;/ APPLICANT: Curran, Mark E.

;/ APPLICANT: Wang, Qing

;/ TITLE OF INVENTION: Long QT Syndrome Genes

;/ NUMBER OF SEQUENCES: 81

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti,LLP

;/ STREET: 1201 New York Avenue, Suite 1000

;/ CITY: Washington

;/ STATE: DC

;/ COUNTRY: USA

;/ ZIP: 20005-3917

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible

;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/401,512

;/ FILING DATE: 09-MAR-1995

;/ CLASSIFICATION: 435

;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Saxe, Stephen A.

;/ REGISTRATION NUMBER: 38,609

;/ REFERENCE/DOCKET NUMBER: 19780-113879

;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 202-962-4848

;/ TELEFAX: 202-962-8300

;/ INFORMATION FOR SEQ ID NO: 75:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 7 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ HYPOTHETICAL: NO  
US-08-401-512-75

Query Match 100.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

## RESULT 41

US-08-401-512-76

;/ Sequence 76, Application US/08401512

;/ Patent No. 5599673

;/ GENERAL INFORMATION:  
;/ APPLICANT: Keating, Mark T.

;/ APPLICANT: Curran, Mark E.

; APPLICANT: Wang, Qing  
; TITLE OF INVENTION: Long QT Syndrome Genes  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3917  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/401,512  
; FILING DATE: 09-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Stephen A.  
; REGISTRATION NUMBER: 38,609  
; REFERENCE/DOCKET NUMBER: 19780-113879  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4848  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; US-08-401-512-76

Query Match 100.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
Db 4 LNF 6

RESULT 42  
US-08-598-873-40  
; Sequence 40, Application US/08598873  
; Patent No. 592884  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Huebner, Kay  
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
; METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/598,873  
; FILING DATE: 09-FEB-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Friebe, Thomas E.  
; REGISTRATION NUMBER: 29,258

; REFERENCE/DOCKET NUMBER: 8666-004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-598-873-40

Query Match 100.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
Db 1 LNF 3

RESULT 43  
US-09-226-012-110  
; Sequence 110, Application US/09226012  
; Patent No. 8207383  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/226,012  
; CURRENT FILING DATE: 1999-01-06  
; EARLIER APPLICATION NUMBER: 09/122,847  
; EARLIER FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 110  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; US-09-226-012-110

Query Match 100.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
Db 4 LNF 6

RESULT 44  
US-09-226-012-111  
; Sequence 111, Application US/09226012  
; Patent No. 8207383  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/226,012  
; CURRENT FILING DATE: 1999-01-06  
; EARLIER APPLICATION NUMBER: 09/122,847  
; EARLIER FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown

; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism:See Warmke and  
; OTHER INFORMATION: Ganetzky, 1994.  
US-09-226-012-111

Query Match 100.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

RESULT 45  
US-08-605-430-40  
; Sequence 40, Application US/08605430  
; Patent No. 6242212  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Huebner, Kay  
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
; TITLE OF INVENTION: METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/605,430  
; FILING DATE: 22-FEB-1996

; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Friebe, Thomas E.  
; REGISTRATION NUMBER: 29,258  
; REFERENCE/DOCKET NUMBER: 8666-005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-605-430-40

Query Match 100.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 1 LNF 3

RESULT 46  
US-09-357-952-34  
; Sequence 34, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.

; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-34

Query Match 100.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

RESULT 47  
US-09-357-952-80  
; Sequence 80, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-80

Query Match 100.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

RESULT 48  
US-09-082-279B-1065  
; Sequence 1065, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly

```

; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1065

```

```

Query Match      100.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      1 LNF 3

```

## RESULT 49

```

US-09-521-650-34
; Sequence 34, Application US/09521650
; Patent No. 6335429

```

```

; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong

```

```

; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof

```

```

; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-34

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      2 LNF 4

```

## RESULT 50

```

US-09-521-650-80

```

```

; Sequence 80, Application US/09521650

```

```

; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-80

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 LNF 3
      |||
Db      2 LNF 4

```

## RESULT 51

```

US-09-168-888-34
; Sequence 34, Application US/09168888
; Patent No. 6342611

```

```

; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong

```

```

; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof

```

```

; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-34

```

```

Query Match      100.0%; Score 3; DB 4; Length 7;

```

```
/ OTHER INFORMATION: Core polypeptide
US-09-315-304B-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 52
US-09-168-888-80
; Sequence 80, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-80

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 53
US-09-315-304B-1065
; Sequence 1065, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

/ OTHER INFORMATION: Core polypeptide
US-09-834-784-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 54
US-09-834-784-1065
; Sequence 1065, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1065
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-1065

Query Match      100.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      1 LNF 3

RESULT 55
5342922-21
; Patent No. 5342922
; APPLICANT: MARSHALL, GARLAND R.;TOTH, MIHALY V.
; TITLE OF INVENTION: INHIBITORS OF RETROVIRAL PROTEASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/320,742
; FILING DATE: 08-MAR-1989
; SEQ ID NO:21:
; LENGTH: 7
; 5342922-21

Query Match      100.0%; Score 3; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
      |||
Db      2 LNF 4

RESULT 56
US-08-030-731A-12
; Sequence 12, Application US/08030731A
```

; Patent No. 5426036  
; GENERAL INFORMATION:  
; APPLICANT: Koller, Klaus-Peter  
; APPLICANT: Riess, Guenther Johannes  
; APPLICANT: Uhlmann, Eugen  
; APPLICANT: Wallemier, Holger  
; TITLE OF INVENTION: Processes for the Preparation of Foreign  
; TITLE OF INVENTION: Proteins in Streptomycetes  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSER: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/030,731A  
; FILING DATE: 12-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/189,840  
; FILING DATE: 03-MAY-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/430,622  
; FILING DATE: 01-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/687,610  
; FILING DATE: 19-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,757  
; FILING DATE: 29-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 37 14 866.4  
; FILING DATE: 05-MAY-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 38 37 273.8  
; FILING DATE: 03-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 39 27 449.7  
; FILING DATE: 19-AUG-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 40 12 818.0  
; FILING DATE: 21-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kirschner Michael K.  
; REGISTRATION NUMBER: 34,851  
; REFERENCE/DOCKET NUMBER: 02481-0593-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-030-731A-12

Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
Db 4 LNF 6

RESULT 57  
US-08-264A-20  
; Sequence 20, Application US/08045264A  
; Patent No. 5436131  
; GENERAL INFORMATION:  
; APPLICANT: CONDR, JON H.  
; APPLICANT: GRAHAM, DONALD J.  
; APPLICANT: GOTLIB, LEAH  
; TITLE OF INVENTION: COLOR SCREENING ASSAY FOR IDENTIFYING  
; TITLE OF INVENTION: DRUG-RESISTANT HIV PROTEASE MUTANTS AND INHIBITORS  
; TITLE OF INVENTION: THEREOF.  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc. Lincoln Ave.  
; STREET: PO Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh IIfx  
; OPERATING SYSTEM: System 7  
; SOFTWARE: Microsoft Word 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/045,264A  
; FILING DATE: 02-APR-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MEREDITH, ROY, D.  
; REGISTRATION NUMBER: 30,777  
; REFERENCE/DOCKET NUMBER: 18936  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-4678  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE:  
; DESCRIPTION: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal fragment  
US-08-045-264A-20

Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
Db 2 LNF 4

RESULT 58  
US-08-922-267A-71  
; Sequence 71, Application US/08922267A  
; Patent No. 5861239  
; GENERAL INFORMATION:  
; APPLICANT: Klevn, Patrick W.  
; APPLICANT: Moore, Karen J.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
; NUMBER OF SEQUENCES: 82  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.

```
/
/
/ ZIP: 10036-2711
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/922,267A
/
/ FILING DATE: 2-SEP-1997
/
/ CLASSIFICATION: 530
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 08/829,553
/
/ FILING DATE: 28-MAR-1997
/
/ CLASSIFICATION: 530
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: US 08/631,200
/
/ FILING DATE: 12-APR-1996
/
/ CLASSIFICATION: 530
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Coruzzi, Laura A.
/
/ REGISTRATION NUMBER: 30,742
/
/ REFERENCE/DOCKET NUMBER: 7853-085
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: (212) 790-9090
/
/ TELEFAX: (212) 869-9741/8864
/
/ INFORMATION FOR SEQ ID NO: 71:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 8 amino acids
/
/ TYPE: amino acid
/
/ STRANDEDNESS:
/
/ TOPOLOGY: unknown
/
/ MOLECULE TYPE: peptide
/
/ US-08-922-267A-71

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 5 LNF 7

RESULT 59
US-08-599-455B-33
/ Sequence 33, Application US/08599455B
/ Patent No. 5972621
/ GENERAL INFORMATION:
/ APPLICANT: Tartaglia, Louis A.
/ APPLICANT: Tepper, Robert I.
/ APPLICANT: Culpepper, Janice A.
/ TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
/ TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
/ NUMBER OF SEQUENCES: 44
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Diskette
/
/ COMPUTER: IBM Compatible
/
/ OPERATING SYSTEM: Windows95
/
/ SOFTWARE: FastSeq for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/599,455B
/
/ FILING DATE: 22-JAN-1996
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: 08/583,153
/
/ FILING DATE: 28-DEC-1995
```

```
/
/
/ APPLICATION NUMBER: 08/570,142
/
/ FILING DATE: 11-DEC-1995
/
/ APPLICATION NUMBER: 08/569,485
/
/ FILING DATE: 08-DEC-1995
/
/ APPLICATION NUMBER: 08/566,622
/
/ FILING DATE: 04-DEC-1995
/
/ APPLICATION NUMBER: 08/562,663
/
/ FILING DATE: 27-NOV-1995
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Meiklejohn Ph.D., Anita L.
/
/ REGISTRATION NUMBER: 35,283
/
/ REFERENCE/DOCKET NUMBER: 07334/017001
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: 617-542-5070
/
/ TELEFAX: 617-542-8906
/
/ TELEX: 200154
/
/ INFORMATION FOR SEQ ID NO: 33:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 8 amino acids
/
/ TYPE: amino acid
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: peptide
/
/ US-08-599-455B-33

Query Match 100.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 60
US-08-925-002-37
/ Sequence 37, Application US/08925002
/ Patent No. 6048527
/ GENERAL INFORMATION:
/ APPLICANT: Granoff, Dan M.
/ APPLICANT: Moe, Gregory R.
/ TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
/ TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
/ TITLE OF INVENTION: COMPOSITIONS
/ FILE REFERENCE: 1238.002
/ CURRENT APPLICATION NUMBER: US/08/925,002
/ CURRENT FILING DATE: 1997-08-27
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 37
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: sequence from
/ OTHER INFORMATION: a phage display peptide library
/ US-08-925-002-37

Query Match 100.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 1 LNF 3

RESULT 61
US-09-144-759-8
/ Sequence 8, Application US/09144759
/ Patent No. 6117639
/ GENERAL INFORMATION:
/ APPLICANT: Hooch, Thomas
/ APPLICANT: Germann, Ursula
```



APPLICANT: Kwong, Ann  
TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS  
FILE REFERENCE: VPI/98-08  
CURRENT APPLICATION NUMBER: US/09/144,759  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-09-144-759-8

Query Match 100.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 2 LNF 4

RESULT 62  
US-09-069-781B-33  
Sequence 33, Application US/09069781B  
Patent No. 6287782  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,781B  
FILING DATE: 29-APRIL-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: US 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: US 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: US 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: US 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: US 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: US 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: US 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: US 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/082001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-069-781B-33

Query Match 100.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
|||  
Db 4 LNF 6

RESULT 63  
US-09-137-132-33  
Sequence 33, Application US/09137132  
Patent No. 6380363  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,132  
FILING DATE: 18-AUG-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/864,564  
FILING DATE: 28-MAY-1997  
APPLICATION NUMBER: 08/708,123  
FILING DATE: 03-SEP-1996  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019004

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-09-137-132-33

Query Match          100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
Db 4 LNF 6

RESULT 64
US-08-864-564A-33
/ Sequence 33, Application US/08864564A
/ Patent No. 6395498
/ GENERAL INFORMATION:
/ APPLICANT: Tartaglia, Louis A.
/ APPLICANT: Tepper, Robert I.
/ APPLICANT: Culpepper, Janice A.
/ APPLICANT: White, David W.
/ TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
/ TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
/ TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/864,564A
/ FILING DATE: 28-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/708,123
/ FILING DATE: 03-SEP-1996
/ APPLICATION NUMBER: 08/638,524
/ FILING DATE: 26-APR-1996
/ APPLICATION NUMBER: 08/599,455
/ FILING DATE: 22-JAN-1996
/ APPLICATION NUMBER: 08/583,153
/ FILING DATE: 28-DEC-1995
/ APPLICATION NUMBER: 08/570,142
/ FILING DATE: 11-DEC-1995
/ APPLICATION NUMBER: 08/569,485
/ FILING DATE: 08-DEC-1995
/ APPLICATION NUMBER: 08/566,622
/ FILING DATE: 04-DEC-1995
/ APPLICATION NUMBER: 08/562,663
/ FILING DATE: 27-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meiklejohn, Ph.D., Anita L.
/ REGISTRATION NUMBER: 35,283
/ REFERENCE/DOCKET NUMBER: 07334/019002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: 200154
```

; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-094-410-33

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 4 LNF 6

RESULT 66  
US-08-708-123D-33  
; Sequence 33, Application US/08708123D  
; Patent No. 6482927  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/708,123D  
FILING DATE: 03-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/638,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown

; MOLECULE TYPE: peptide  
US-08-708-123D-33

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 4 LNF 6

RESULT 67  
US-08-583-153A-33  
; Sequence 33, Application US/08583153A  
; Patent No. 6506877  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
; TITLE OF INVENTION: OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-583-153A-33

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3  
Db 4 LNF 6

```
RESULT 68
US-09-570-267-8
; Sequence 8, Application US/09570267
; Patent No. 6528276
; GENERAL INFORMATION:
; APPLICANT: Hock, Thomas
; APPLICANT: Hermann, Ursula
; APPLICANT: Kwong, Ann
; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
; TITLE OF INVENTION: USEFUL FOR MEASURING PROTEASE ACTIVITY
; FILE REFERENCE: VPI/98-08
; CURRENT APPLICATION NUMBER: US/09/570,267
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 09/144,759
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-570-267-8

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 2 LNF 4

RESULT 69
US-08-638-524B-33
; Sequence 33, Application US/08638524B
; Patent No. 6548269
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 26-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-638-524B-33

Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 4 LNF 6

RESULT 70
US-08-435-241A-5
; Sequence 5, Application US/08435241A
; Patent No. 5674833
; GENERAL INFORMATION:
; APPLICANT: Mikkelsen et al.
; TITLE OF INVENTION: Detergent Compositions Containing Protease And
; TITLE OF INVENTION: No. 5674833el Inhibitors For Use Therein
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5674833o No. 5674833disk of No. 5674833th America, Inc.
; STREET: 405 Lexington Ave., Suite 6200
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,241A
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Elias J. Lambiris, Esq.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3486.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 867-0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-241A-5

Query Match 100.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNF 3
DB 6 LNF 8
```

## RESULT 71

US-09-053-941-25  
 ; Sequence 25, Application US/09053941  
 ; Patent No. 6271354  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SRINIVISAN, ALGARSAMY  
 ; APPLICANT: KOPROWSKI, HILARY  
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
 ; FILE REFERENCE: Chimeric Viral Proteins  
 ; CURRENT APPLICATION NUMBER: US/09/053,941  
 ; CURRENT FILING DATE: 1998-04-02  
 ; EARLIER APPLICATION NUMBER: 60/043,380  
 ; EARLIER FILING DATE: 1999-04-03  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 25  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Flag  
 ; OTHER INFORMATION: protein--HIV-1 protease chimera  
 US-09-053-941-25

Query Match 100.0%; Score 3; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 7 LNF 9

## RESULT 72

US-09-817-413-25  
 ; Sequence 25, Application US/09817413  
 ; Patent No. 6436648  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SRINIVISAN, ALGARSAMY  
 ; APPLICANT: KOPROWSKI, HILARY  
 ; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS  
 ; FILE REFERENCE: Chimeric Viral Proteins  
 ; CURRENT APPLICATION NUMBER: US/09/817,413  
 ; CURRENT FILING DATE: 2001-03-25  
 ; PRIOR APPLICATION NUMBER: 60/043,380  
 ; PRIOR FILING DATE: 1999-04-03  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 25  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Flag  
 ; OTHER INFORMATION: protein--HIV-1 protease chimera  
 US-09-817-413-25

Query Match 100.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 7 LNF 9

## RESULT 73

US-09-311-784A-220  
 ; Sequence 220, Application US/09311784A  
 ; Patent No. 6534482  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FIKES, JOHN D.

; APPLICANT: Hermanson, Gary G.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Ishioka, Glenn Y.  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Chesnut, Robert W.  
 ; APPLICANT: Epiimmune Inc.  
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an  
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
 ; FILE REFERENCE: 39963-20022.01  
 ; CURRENT APPLICATION NUMBER: US/09/311,784A  
 ; CURRENT FILING DATE: 1999-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/085,751  
 ; PRIOR FILING DATE: 1998-05-15  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 220  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)  
 ; OTHER INFORMATION: HBV ENV 197 (peptide 20.0137)  
 US-09-311-784A-220

Query Match 100.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 6 LNF 8

## RESULT 74

US-09-311-784A-354  
 ; Sequence 354, Application US/09311784A  
 ; Patent No. 6534482  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FIKES, JOHN D.  
 ; APPLICANT: Hermanson, Gary G.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Ishioka, Glenn Y.  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Chesnut, Robert W.  
 ; APPLICANT: Epiimmune Inc.  
 ; TITLE OF INVENTION: Expression Vectors for Stimulating an  
 ; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
 ; FILE REFERENCE: 39963-20022.01  
 ; CURRENT APPLICATION NUMBER: US/09/311,784A  
 ; CURRENT FILING DATE: 1999-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/085,751  
 ; PRIOR FILING DATE: 1998-05-15  
 ; NUMBER OF SEQ ID NOS: 463  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 354  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)  
 ; OTHER INFORMATION: HIV1 POL 96 (peptide 25.0041)  
 US-09-311-784A-354

Query Match 100.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNF 3  
 |||  
 Db 2 LNF 4

## RESULT 75

US-08-185-448-10  
 ; Sequence 10, Application US/08185448

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; Patent No. 5580747
; GENERAL INFORMATION:
; APPLICANT: SHULTZ, JOHN W.
; APPLICANT: WHITE, DOUGLAS H.
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDRUS, SCARLES, STARKE & SAWALL
; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,448
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,928
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SARA, CHARLES S
; REGISTRATION NUMBER: 30492
; REFERENCE/DOCKET NUMBER: F.3347-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 255-2022
; TELEFAX: (608) 255-2182
; TELEX: 26832 ANDSTARK
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1
; OTHER INFORMATION: /label= LABEL
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
; OTHER INFORMATION: DETECTION TAG"
US-08-185-448-10

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Query Match      100.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LNF 3
        |||
Db       3 LNF 5

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Search completed: November 25, 2003, 20:30:09  
Job time : 3.42442 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 10.2907 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPPQLPPTWMP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4	26.7	8	SI0783	enamelin f - bovin
2	4	26.7	12	PN0863	dystrophin-associ
3	4	26.7	13	I84603	deoxynucleotidyltr
4	4	26.7	19	PH1352	Ig heavy chain DJ
5	4	26.7	20	PC2030	tumor-derived adhe
6	3	20.0	7	S71299	ICL2 protein - Par
7	3	20.0	7	PT0283	Ig heavy chain CRD
8	3	20.0	8	SI6324	hypothetical prote
9	3	20.0	9	B38740	Ig kappa chain C r
10	3	20.0	10	PC2171	triacylglycerol li
11	3	20.0	10	SI8396	probable glucose-6
12	3	20.0	10	C39745	sphingomyelinase -
13	3	20.0	11	XASNEA	bradykinin-potent
14	3	20.0	11	YHRT	morphogenetic neur
15	3	20.0	11	YHUU	morphogenetic neur
16	3	20.0	11	YHBO	morphogenetic neur
17	3	20.0	11	YHXAE	morphogenetic neur
18	3	20.0	11	YHJFY	seed protein ws-18
19	3	20.0	11	C61497	173K exoantigen -
20	3	20.0	11	I33098	hypothetical 1.2K
21	3	20.0	12	C39109	ATP synthase D cha
22	3	20.0	12	PN0046	inhibin alpha chai
23	3	20.0	13	A60856	actin 7 - soybean
24	3	20.0	13	SI5755	neural cell adhesi
25	3	20.0	13	D39690	cell surface glyco
26	3	20.0	13	A40207	Ig lambda chain V-
27	3	20.0	13	G61458	18K iron-sulfur pr
28	3	20.0	14	PQ0152	223K exoantigen -
29	3	20.0	14	C33098	

30	3	20.0	14	2	PH1566	cerebrin 30 - huma
31	3	20.0	14	2	PH1348	Ig heavy chain DJ
32	3	20.0	14	2	H83778	hypothetical prote
33	3	20.0	15	2	PQ0545	capsid protein VPI
34	3	20.0	15	2	B39109	hypothetical 1.5K
35	3	20.0	15	2	S29386	nigerythrin - Desu
36	3	20.0	15	2	PA0014	seed storage prote
37	3	20.0	15	2	PN0173	protein QF200037 -
38	3	20.0	15	2	PA0060	alpha-glucosidase
39	3	20.0	15	2	B61457	apolipoprotein A-I
40	3	20.0	15	2	A60221	chitinase (EC 3.2.
41	3	20.0	16	2	F44908	alpha-conotoxin Pn
42	3	20.0	16	2	A54877	alpha-conotoxin Pn
43	3	20.0	16	2	B54877	superoxide dismuta
44	3	20.0	16	2	E58503	hypothetical prote
45	3	20.0	16	2	S01104	T-cell receptor be
46	3	20.0	16	2	PH0763	T-cell receptor be
47	3	20.0	16	2	PH0759	actin 6 - soybean
48	3	20.0	17	2	SI5754	L-ascorbate peroxi
49	3	20.0	17	2	S32587	hydroxyproline-ric
50	3	20.0	17	2	S59481	thyroid hormone re
51	3	20.0	17	2	I55612	enamelin, 26K - bo
52	3	20.0	17	2	SI0786	N4-(beta-N-acetylgl
53	3	20.0	18	2	S04229	prolylendopeptidas
54	3	20.0	18	2	PC2280	2-aminobenzoate-Co
55	3	20.0	18	2	S39845	arsenite oxidase I
56	3	20.0	18	2	B45138	hypothetical prote
57	3	20.0	18	2	SI0452	Na+/K+-exchanging
58	3	20.0	18	2	A54195	endopeptidase Clp
59	3	20.0	19	2	PC1323	H+-transporting tw
60	3	20.0	19	2	S60633	thyroglobulin - pi
61	3	20.0	19	2	C32735	thyroglobulin - sh
62	3	20.0	19	2	B32735	genome polyprotein
63	3	20.0	19	2	B61409	cell wall protein,
64	3	20.0	19	2	S59486	neural surface pro
65	3	20.0	19	2	A37968	36K microfibril-as
66	3	20.0	19	2	A34467	coumarin 7-monooxy
67	3	20.0	20	2	S21737	cytochrome P450 2C
68	3	20.0	20	2	S29817	notechis II-5b non
69	3	20.0	20	2	A33878	ribulose-bisphosph
70	3	20.0	20	2	A39328	tubulin alpha chai
71	3	20.0	20	2	A37111	apolipoprotein A-I
72	3	20.0	20	2	A54519	acetyl-CoA synthet
73	3	20.0	20	2	A05313	alpha-amylase (EC
74	3	20.0	20	2	T44453	dimeric protein (B
75	3	20.0	20	2	PH1380	glue protein - Cal
76	3	20.0	20	2	S65605	octopamine recepto
77	3	20.0	20	2	A61093	interphotoreceptor
78	3	20.0	20	2	S28779	acidic fibroblast
79	3	20.0	20	2	F24417	somatotropin - syn
80	3	20.0	20	2	S03954	tyrosine-melanocyt
81	3	20.0	20	2	I53672	starvation-induced
82	3	20.0	20	4	I78890	proctolin - Americ
83	2	13.3	4	2	A32039	peptidyl-dipectida
84	2	13.3	4	2	S53508	flagellar protein
85	2	13.3	5	1	H0R0HA	ribulose-bisphosph
86	2	13.3	5	2	JN0860	acid proteinase li
87	2	13.3	5	2	E42364	proctolin - Atlant
88	2	13.3	5	2	PS0324	27.5 kDa structura
89	2	13.3	5	2	B37988	27.5K structural p
90	2	13.3	5	2	A60411	27.5K structural p
91	2	13.3	5	2	I44817	28.5K structural p
92	2	13.3	5	2	E44817	28.5K structural p
93	2	13.3	5	2	C44817	28K structural pro
94	2	13.3	5	2	A44817	halo-toxin - Pseud
95	2	13.3	5	2	A61049	hypothetical prote
96	2	13.3	6	2	A37765	contraction-inhibi
97	2	13.3	6	2	A27696	transferrin - bovi
98	2	13.3	6	2	B27696	
99	2	13.3	6	2	A19780	
100	2	13.3	6	2		

## ALIGNMENTS

```

RESULT 1
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A>Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match      26.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      2 PLPP 5

RESULT 2
PN0663
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A>Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the plasma membrane of skeletal muscle
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0663
A:Molecule type: protein
A:Residues: 1-12 <YCS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match      26.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      3 PLPP 6

RESULT 3
I84603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I84603
R:Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A>Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A:Reference number: I45884; MUID:87213162; PMID:3579900
A:Accession: I84603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M26144; NID:g951194; PID:n951195
C:Genetics:
A:Gene: GDB:DNTT
A:Cross-references: GDB:l19100; OMIM:187410
A:Map position: 10q23-10q24

Query Match      26.7%; Score 4; DB 2; Length 13;

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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QPLP 9
      |||||
Db      8 QPLP 11

RESULT 4
PH1352
Ig heavy chain DJ region (clone C100-115) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1352
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A>Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1352
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A>Note: the authors translated the stop codon for residue 2 as X
C:Keywords: heterotetramer; immunoglobulin

```

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Query Match      26.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
      |||||
Db      8 PPTV 11

RESULT 5
PC2030
tumor-derived adhesion factor - human (fragment)
N:Alternate names: 30K protein
C:Species: Homo sapiens (man)
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
C:Accession: PC2030
R:Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.; Umehara, K.
Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
A>Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder cancer cells
A:Reference number: PC2030; MUID:94161713; PMID:8117260
A:Accession: PC2030
A:Molecule type: protein
A:Residues: 1-20 <AKA>
A:Experimental source: cell line EJ-1
C:Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match      26.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
      |||||
Db      16 PLPP 19

RESULT 6
S71299
ICL2 protein - Paramesidium tetraurelia (fragment)
C:Species: Paramesidium tetraurelia
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beissson, J.
Eur. J. Biochem. 238, 121-128, 1996
A>Title: Characterization of centrin genes in Paramesidium
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2

```



```
C;Genetics:
A;Genetic code: SCCS

Query Match      20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
   |||
Db 2 QPP 4

RESULT 7
PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0283
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0283
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match      20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
   |||
Db 5 QPP 7

RESULT 8
S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PTDN:CAA41624.1; PID:g579259

Query Match      20.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
   |||
Db 6 LPP 8

RESULT 9
B38740
Ig kappa chain C region (PY20) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: B38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: B38740

C;Genetics:
A;Molecule type: mRNA
A;Residues: 1-9 <RUF>

Query Match      20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12
   |||
Db 5 PTV 7

RESULT 10
PC2171
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fra
C;Species: Rhizopus niveus
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2171
R;Kobno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
A;Title: Purification, characterization, and crystallization of two types of lipase fr
A;Reference number: PC2171; MUID:94319059; PMID:7765029
A;Accession: PC2171
A;Molecule type: protein
A;Residues: 1-10 <KOH>
A;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
C;Keywords: carboxylic ester hydrolase

Query Match      20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
   |||
Db 5 LPP 7

RESULT 11
S18396
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fra
C;Species: Acetobacter hansenii
C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C;Accession: S18396
R;Levy, H.R.; Cook, C.
Arch. Biochem. Biophys. 291, 161-167, 1991
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase
A;Reference number: S18396; MUID:92027789; PMID:1929428
A;Accession: S18396
A;Molecule type: protein
A;Residues: 1-10 <LEV>
A;Experimental source: ATCC 23769
C;Function:
A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosphat
A;Pathway: pentose phosphate pathway
C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match      20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
   |||
Db 3 LPP 5

RESULT 12
C39745
spingomyelinase - Rhodococcus sp. (fragment)
C;Species: Rhodococcus sp.
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C;Accession: C39745
R;Ito, M.; Ikegami, Y.; Yamagata, T.
```

J. Biol. Chem. 266, 7919-7926, 1991  
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosceramidases. E  
ble using these activator proteins.  
A:Reference number: A39745; MUID:91210321; PMID:1850427  
A:Accession: C39745  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <ITO>

Query Match 20.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
|||  
Db 3 PLP 5

RESULT 13  
XASNEA  
bradykinin-potentiating peptide B - mamushi  
C:Species: Agkistrodon blomhoffi (mamushi)  
C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995  
C:Accession: A01254  
R:Kato, H.; Suzuki, T.  
Proc. Jpn. Acad. 46, 176-181, 1970  
A:Reference number: A01254  
A:Accession: A01254  
A:Molecule type: protein  
A:Residues: 1-11 <KAT>  
A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; v  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
|||  
Db 3 LPP 5

RESULT 14  
YHBT  
morphogenetic neuropeptide - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A01427  
R:Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele  
A:Reference number: A93266; MUID:82035850; PMID:7290191  
A:Accession: A01427  
A:Molecule type: protein  
A:Residues: 1-11 <BOD>  
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A:Reference number: A91296; MUID:82050803; PMID:7297679  
A:Contents: annotation; synthesis  
A:Note: the synthetic peptide was identical with the natural peptide in chemical structu  
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head  
C:Superfamily: unassigned animal peptides  
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 1 QPP 3

## RESULT 15

YHHU

morphogenetic neuropeptide - human

C:Species: Homo sapiens (man)

C&gt;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C:Accession: B01427; A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coe

A:Reference number: A93266; MUID:82035850; PMID:7290191

A:Accession: B01427

A:Molecule type: protein

A:Residues: 1-11 &lt;BOD&gt;

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical struct

C:Comment: this peptide was first isolated from nerve cells of hydra and was called hea

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neurope

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #stat

Query Match 20.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5

|||

Db 1 QPP 3

## RESULT 16

YHBO

morphogenetic neuropeptide - bovine

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C:Accession: C01427; A01427

R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coe

A:Reference number: A93266; MUID:82035850; PMID:7290191

A:Accession: C01427

A:Molecule type: protein

A:Residues: 1-11 &lt;BOD&gt;

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical struct

C:Comment: this peptide was first isolated from nerve cells of hydra and was called hea

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neurope

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #stat

Query Match 20.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5

|||

Db 1 QPP 3

## RESULT 17

YHXA  
morphogenetic neuroepitide - sea anemone (Anthopleura elegantissima)  
N/Alternate names: head activator  
C/Species: Anthopleura elegantissima  
C/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C/Accession: A93900; A01427  
R/Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A/Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A/Reference number: A93900  
A/Accession: A93900  
A/Molecule type: protein  
A/Residues: 1-11 <SCH>  
R/Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A/Title: Synthesis of a new neuroepitide, the head activator from hydra.  
A/Contents: annotation; synthesis  
A/Note: This synthetic peptide was identical with the natural peptide in chemical structure  
C/Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
n mammalian intestine and hypothalamus.  
C/Superfamily: unassigned animal peptides  
C/Keywords: growth factor; hormone; neuroepitide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
|||  
Db 1 QPP 3

## RESULT 18

YHJFY  
morphogenetic neuroepitide - Hydra attenuata  
N/Alternate names: head activator  
C/Species: Hydra attenuata  
C/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C/Accession: B93900; A01427  
R/Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A/Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A/Reference number: A93900  
A/Accession: B93900  
A/Molecule type: protein  
A/Residues: 1-11 <SCH>  
R/Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A/Title: Synthesis of a new neuroepitide, the head activator from hydra.  
A/Contents: annotation; synthesis  
A/Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C/Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
n mammalian intestine and hypothalamus.  
C/Superfamily: unassigned animal peptides  
C/Keywords: growth factor; hormone; neuroepitide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
|||  
Db 1 QPP 3

## RESULT 19

C61497  
seed protein ws-18 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C/Accession: C61497  
R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989  
A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis  
A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: C61497  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <HIR>  
C/Keywords: glycoprotein; seed

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12  
|||  
Db 3 PTV 5

## RESULT 20

I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C/Species: Plasmodium falciparum  
C/Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C/Accession: I33098  
R/Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990  
A/Reference number: A33098  
A/Accession: I33098  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
|||  
Db 2 LPP 4

## RESULT 21

C39109  
hypothetical 1.2K protein - hepatitis C virus  
N/Alternate names: hypothetical protein 3  
C/Species: hepatitis C virus  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
A/Reference number: A39109; MUID:91156678; PMID:1705704  
A/Accession: C39109  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-12 <HAN>  
R/Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992

A/Title: Cloning and sequencing of the structural region and expression of putative core  
A/Reference number: JQ1584; MUID:92300349; PMID:1318944  
A/Accession: JQ1586  
A/Molecule type: genomic RNA  
A/Residues: 1-12 <KUM>  
A/Experimental source: strain U.K.

Query Match 20.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      4 PPQ 6
      |||
Db      8 PPQ 10

RESULT 22
PN0046
A:Title: ATP synthase D chain, mitochondrial - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0046
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0046
A:Molecule type: protein
A:Residues: 1-12 <KAT>
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blocked
C:Keywords: brain; mitochondrion

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 HOP 4
      |||
Db      6 HOP 8

RESULT 23
A60856
inhibin alpha chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60856
R:Levensha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenthal
J. Endocrinol. 113, 213-221, 1997
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; MUID:87224684; PMID:3585232
A:Accession: A60856
A:Molecule type: protein
A:Residues: 1-13 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLP 9
      |||
Db      4 PLP 6

RESULT 24
S15755
actin 7 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C:Accession: S15755
R:Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A:Reference number: S15754; MUID:91346640; PMID:2102831
A:Accession: S15755
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <PEA>
A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528

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C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 QPL 8
      |||
Db      8 QPL 10

RESULT 25
D39690
neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: D39690
R:Reyes, A.A.; Small, S.J.; Akeson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: D39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 1-13 <REV>
A:Cross-references: GB:M63970
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPQ 6
      |||
Db      7 PPQ 9

RESULT 26
A40207
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 31-Dec-1993
C:Accession: A40207
R:Gao, E.N.; Shier, P.; Siu, C.H.
J. Biol. Chem. 267, 9409-9415, 1992
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150)
A:Reference number: A40207; MUID:92250549; PMID:1577768
A:Accession: A40207
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <GAO>
C:Keywords: glycoprotein

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PPT 11
      |||
Db      3 PPT 5

RESULT 27
G61458
IG lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; PI0159
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass

```

J. Neurochem. 61, 533-540, 1993  
 A;Title: Micropurification of two human cerebrosplinal fluid proteins by high performanc  
 A;Reference number: PH1566; MUID:93329419; PMID:8336140  
 A;Accession: PH1566  
 A;Molecule type: protein  
 A;Residues: 1-13 <BRO>  
 C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycop  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
 |||  
 Db 6 QPP 8

## RESULT 28

PQ0152  
 18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)

N;Alternate names: frxB homolog

C;Species: Chloroplast Chlamydomonas reinhardtii

C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-Sep-1993

C;Accession: PQ0152

R;Wu, M.; Nie, Z.Q.; Yang, J.

Plant Cell 1, 551-557, 1989

A;Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is an i

A;Reference number: PQ0152; MUID:92404720; PMID:2562513

A;Accession: PQ0152

A;Molecule type: protein

A;Residues: 1-14 <WUM>

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 MFP 15  
 |||  
 Db 1 MFP 3

## RESULT 29

C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: C33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: C33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
 |||  
 Db 2 LPP 4

## RESULT 30

PH1566

cerebrin 30 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C;Accession: PH1566

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; MO, M.; Silvestrini, B.; Cheng, C.Y.

J. Neurochem. 61, 533-540, 1993  
 A;Title: Micropurification of two human cerebrosplinal fluid proteins by high performanc  
 A;Reference number: PH1566; MUID:93329419; PMID:8336140  
 A;Accession: PH1566  
 A;Molecule type: protein  
 A;Residues: 1-14 <LEO>

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8  
 |||  
 Db 9 QPL 11

## RESULT 31

PH1348

IG heavy chain DJ region (clone C100-106) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PH1348

R;Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1348

A;Molecule type: DNA

A;Residues: 1-14 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPT 11  
 |||  
 Db 4 PPT 6

## RESULT 32

H83778

hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C;Accession: H83778

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: H83778

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-14 <STO>

A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04751.1; GSPDB:GNO

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1032

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13  
 |||  
 Db 8 TVM 10

## RESULT 33

PQ0545

capsid protein VP19C - human herpesvirus 1 (fragment)

C;Species: human herpesvirus 1

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

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C;Accession: PQ0545
R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
A;Reference number: PQ0544; MUID:93019027; PMID:1328483
A;Accession: PQ0545
A;Molecule type: protein
A;Residues: 1-15 <DAV>
A;Experimental source: strain 17
A;Genetics:
C;Gene: UL38
C;Keywords: capsid protein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9
Db 5 PLP 7

RESULT 34
B39109
hypothetical 1.5K protein - hepatitis C virus
N;Alternate names: hypothetical protein 2
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C;Accession: B39109; JQ1585
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: B39109
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <HAN>
A;Cross-references: GB:M58406
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
J. Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Accession: JQ1585
A;Molecule type: genomic RNA
A;Residues: 1-15 <KOM>
A;Experimental source: strain U.K.

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
Db 5 QPP 7

RESULT 35
S29386
nigerythrin - Desulfovibrio vulgaris
C;Species: Desulfovibrio vulgaris
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S29386
R;Pierik, A.J.; Wolbert, R.B.G.; Portier, G.L.; Verhagen, M.F.J.M.; Hagen, W.R.
Eur. J. Biochem. 212, 237-245, 1993
A;Title: Nigerythrin and rubrerythrin from Desulfovibrio vulgaris each contain two mononit
A;Reference number: S29385; MUID:93185629; PMID:8383040
A;Accession: S29386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <PTE>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Accession: PQ0014
seed storage protein 12S3 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PA0014
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimension.
A;Reference number: PA0001
A;Accession: PA0014
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: seed
C;Keywords: seed; storage protein

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6
Db 7 PPQ 9

RESULT 37
PN0173
seed storage protein 12S4 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
C;Accession: PN0173
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PN0173
A;Accession: PN0173
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: seeds

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6
Db 7 PPQ 9

RESULT 38
PA0060
protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0060
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PA0051
A;Accession: PA0060
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MFP 15  
|||  
Db 6 MFP 8

## RESULT 42

A54877  
alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)  
N;Alternate names: alpha-Crx-PnIA  
C;Species: Conus pennaceus  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C;Accession: A54877

R;Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot  
Biochemistry 33, 9523-9529, 1994

A;Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rec  
A;Reference number: A54877; MUID:94347719; PMID:8068627

A;Accession: A54877

A;Molecule type: protein

A;Residues: 1-16 <FAI>

R;Hu, S.H.; Gehrman, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.  
submitted to the Brookhaven Protein Data Bank, January 1996

A;Reference number: A66355; PDB:1PEN

C;Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F;2-8,3-16/Disulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
|||  
Db 5 LPP 7

## RESULT 43

B54877

alpha-conotoxin PnIB - cone shell (Conus pennaceus)

C;Species: Conus pennaceus

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997

C;Accession: B54877

R;Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot  
Biochemistry 33, 9523-9529, 1994

A;Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rec  
A;Reference number: A54877; MUID:94347719; PMID:8068627

A;Accession: B54877

A;Molecule type: protein

A;Residues: 1-16 <FAI>

C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
C;Superfamily: alpha-conotoxin

C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F;2-8,3-16/Disulfide bonds: #status experimental

F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
|||  
Db 5 LPP 7

QY .7 PLP 9  
|||

Db 4 PLP 6

## RESULT 39

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SCS

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 20.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
|||

Db 2 LPP 4

## RESULT 40

A60221

apolipoprotein A-I - common carp (fragment)

C;Species: Cyprinus carpio (common carp)

C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993

C;Accession: A60221

R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.

J. Neurochem. 55, 1237-1243, 1990

A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg  
A;Reference number: A60221; MUID:90376100; PMID:2118944

A;Accession: A60221

A;Molecule type: protein

A;Residues: 1-15 <HAR>

A;Note: protein from plasma and from optic nerve yielded the same sequence

C;Keywords: lipid binding; lipoprotein

Query Match 20.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||

Db 2 QPP 4

## RESULT 41

F44908

chitinase (EC 3.2.1.14), 23.4K - Streptomyces olivaceoviridis (fragment)

C;Species: Streptomyces olivaceoviridis

C;Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-May-2000

C;Accession: F44908

R;Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.  
J. Bacteriol. 174, 3450-3454, 1992

A;Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for m  
A;Reference number: A44908; MUID:92276319; PMID:1592803

A;Accession: F44908

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <ROM>

A;Experimental source: ATCC 11238

A;Note: sequence extracted from NCBI backbone (NCBIP:104594)

## RESULT 44

E58503  
superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)  
N;Alternate names: 21.3K bladder and kidney stone protein  
C;Species: unidentified bacterium  
C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 05-Mar-1999  
C;Accession: E58503  
R;Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A;Description: The proteins of kidney and gallbladder stones.  
A;Reference number: A58501  
A;Accession: E58503  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BIN>  
A;Experimental source: human bladder and kidney stones  
C;Function:  
C;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C;Keywords: metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
|||  
Db 5 LPP 7

## RESULT 45

S01104  
hypothetical protein 3 - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 21-Jul-2000  
C;Accession: S01104  
R;Evelleth, D.D.; Marsh, J.L.  
Mol. Gen. Genet. 209, 290-298, 1987  
A;Title: Overlapping transcription units in Drosophila: sequence and structure of the C5  
A;Reference number: S01102; MUID:88038375; PMID:3478553  
A;Accession: S01104  
A;Molecule type: DNA  
A;Residues: 1-16 <EVE>  
A;Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762  
C;Genetics:  
A;Gene: Cs  
A;Cross-references: FlyBase:FBgn0002036

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12  
|||  
Db 13 PTV 15

## RESULT 46

PH0763  
T-cell receptor beta chain (F15) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0763  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0763  
A;Molecule type: mRNA  
A;Residues: 1-16 <CAS>  
A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

## Query Match

20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 5 PPQ 7

## RESULT 47

PH0759  
T-cell receptor beta chain (QB7.3.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0759  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0759  
A;Molecule type: mRNA  
A;Residues: 1-16 <CAS>  
A;Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 5 PPQ 7

## RESULT 48

S15754  
actin 6 - soybean (fragment)  
C;Species: Glycine max (soybean)  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 13-Aug-1999  
C;Accession: S15754; S08049  
R;Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
A;Reference number: S15754; MUID:91346640; PMID:2102831  
A;Accession: S15754  
A;Molecule type: DNA  
A;Residues: 1-17 <PEA>  
A;Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526  
C;Superfamily: actin  
C;Keywords: cytoskeleton

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8  
|||  
Db 8 QPL 10

## RESULT 49

S32587  
L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Sep-1993  
C;Accession: S32587; S15878  
R;Kubo, A.; Saji, H.; Tanaka, K.; Tanaka, K.; Kondo, N.  
Plant Mol. Biol. 18, 691-701, 1992  
A;Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidopsi  
A;Reference number: S20866; MUID:92216045; PMID:1558944



A;Accession: S32587  
 A;Molecule type: protein  
 A;Residues: 1-17 <KUB>  
 A;Note: this is a revision to the sequence from reference S15878  
 R;Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.  
 Arch. Biochem. Biophys. 286, 371-375, 1991  
 A;Title: Two immunologically different isozymes of ascorbate peroxidase from spinach leaves  
 A;Reference number: S15878; MUID:91378325; PMID:1897962  
 A;Accession: S15878  
 A;Molecule type: protein  
 A;Residues: 1,3-17 <TAN>  
 A;Note: this sequence has been revised in reference S20866  
 C;Keywords: chloroplast; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12  
 ||||  
 Db 5 PTV 7

## RESULT 50

S59481  
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
 C;Species: Phaseolus vulgaris (kidney bean)  
 C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
 A;Accession: S59481  
 R;Wojtaszek, P.; Iretchowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
 A;Reference number: S59481; MUID:96011753; PMID:7548825  
 A;Accession: S59481  
 A;Molecule type: protein  
 A;Residues: 1-17 <WOU>  
 C;Keywords: Glycoprotein; hydroxyproline  
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
 ||||  
 Db 4 LPP 6

## RESULT 51

I55612  
 thyroid hormone receptor beta - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C;Accession: I55612  
 R;Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.  
 J. Clin. Invest. 94, 506-515, 1994  
 A;Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th  
 A;Reference number: I55612; MUID:94314950; PMID:8040303  
 A;Accession: I55612  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-17 <RES>  
 A;Cross-references: GB:S72623; NID:G633779; PIDN:AA81420.1; PID:G633780  
 C;Genetics:  
 A;Gene: TRbeta

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
 ||||  
 Db 5 LPP 7

## RESULT 52

S10786  
 enamelin, 26K - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C;Accession: S10786  
 R;Strawich, E.; Glincher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990  
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is alt  
 A;Reference number: S10780; MUID:90336641; PMID:2379503  
 A;Accession: S10786  
 A;Molecule type: protein  
 A;Residues: 1-17 <STB>  
 C;Keywords: enamel; phosphoprotein

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
 ||||  
 Db 3 QPP 5

## RESULT 53

S04229  
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)  
 N;Alternate names: Glycosylasparaginase  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
 C;Accession: S04229  
 R;Tollersrud, O.K.; Aronson Jr., N.N.  
 Biochem. J. 260, 101-108, 1989  
 A;Title: Purification and characterization of rat liver glycosylasparaginase.  
 A;Reference number: S04228; MUID:89374025; PMID:2775174  
 A;Accession: S04229  
 A;Molecule type: protein  
 A;Residues: 1-18 <TOL>  
 C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase  
 C;Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9  
 ||||  
 Db 3 PLP 5

## RESULT 54

PC2280  
 prolylendopeptidase-inhibiting peptide - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997  
 C;Accession: PC2280  
 R;Omori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.  
 Biochem. Biophys. Res. Commun. 202, 809-815, 1994  
 A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.  
 A;Reference number: PC2280; MUID:94324971; PMID:8048952  
 A;Accession: PC2280  
 A;Molecule type: protein  
 A;Residues: 1-18 <OHM>  
 A;Experimental source: brain  
 C;Superfamily: cytoskeletal keratin

Query Match 20.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9

```

Db          |||
            4 PLP 6

RESULT 55
S39845
2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)
C;Species: Pseudomonas sp.
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Accession: S39845
R;Altenschmidt, U.; Fuchs, G.
Eur. J. Biochem. 205, 721-727, 1992
A;Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization of
a from a denitrifying Pseudomonas sp.
A;Reference number: S22402; MUID:92241310; PMID:1315272
A;Accession: S39845
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10, 'X', 12-14, 'X', 16-18 <ALT>

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPP 10
        |||
Db      12 LPP 14

RESULT 56
B45138
arsenite oxidase I - Alcaligenes faecalis (fragment)
C;Species: Alcaligenes faecalis
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C;Accession: B45138
R;Anderson, G.L.; Williams, J.; Hille, R.
J. Biol. Chem. 267, 23674-23682, 1992
A;Title: The purification and characterization of arsenite oxidase from Alcaligenes faecalis
A;Reference number: A45138; MUID:93054722; PMID:1331097
A;Accession: B45138
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <AND>
A;Note: sequence extracted from NCBI backbone (NCBIP:118543)

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPP 10
        |||
Db      9 LPP 11

RESULT 57
S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C;Species: Aspergillus niger
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C;Accession: S10452
R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A;Reference number: S10452
A;Accession: S10452
A;Molecule type: DNA
A;Residues: 1-18 <VAN>
A;Cross-references: EMBL:X52521; NID:g23336; PID:g2337

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QPL 8

Db          |||
            4 QPL 6

RESULT 58
A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C;Accession: A54195
R;Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase
A;Reference number: A54195; MUID:94297020; PMID:8025109
A;Accession: A54195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <ESM>
A;Experimental source: rectal gland
A;Note: sequence extracted from NCBI backbone (NCBIP:149363)
C;Keywords: Hydrolase

Query Match      20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPT 11
        |||
Db      9 PPT 11

RESULT 59
PC1323
endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroplast
C;Species: chloroplast Nicotiana glauca (curled-leaved tobacco)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-2000
C;Accession: PC1323
R;Rejes, E.; Engler, D.; Maliga, P.
Theor. Appl. Genet. 79, 28-32, 1990
A;Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana glauca
A;Reference number: PC1323
A;Accession: PC1323
A;Molecule type: DNA
A;Residues: 1-19 <FEJ>
C;Genetics:
C;Genome: chloroplast
C;Function:
A;Description: ATP-driven cleavage of proteins to small peptides
A;Note: magnesium required
C;Superfamily: endopeptidase Clp chain P
C;Keywords: ATP; chloroplast; hydrolase; serine proteinase
F;3/Active site: His #status predicted

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HQP 4
        |||
Db      3 HQP 5

RESULT 60
S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion
C;Species: mitochondrion Artemia sp. (brine shrimp)
A;Variety: strain La Mata
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002
C;Accession: S60633
R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
J. Mol. Evol. 38, 156-168, 1994
A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par
A;Reference number: S60624; MUID:94223692; PMID:8169960

```

A;Accession: S60633  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-19 <PER>  
A;Cross-references: EMBL:X67263; NID:g11210; PID:CAA47685.1; PID:g11211  
A;Experimental source: Strain La Mata  
A;Note: the source is designated as Artemia parthenogenetica  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C;Genetics:  
A;Gene: ATP8  
A;Genome: mitochondrion  
A;Genetic code: SGC4  
C;Superfamily: H+-transporting ATP synthase protein 8  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9  
|||  
Db 6 PLP 8  
|||

RESULT 61  
C32735  
thyroglobulin - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 11-Apr-1997  
C;Accession: C32735  
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.  
Biochem. Biophys. Res. Commun. 118, 423-429, 1984  
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin  
A;Reference number: A32735; MUID:84153804; PMID:6704086  
A;Accession: C32735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <RAW>  
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol  
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis  
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8  
|||  
Db 10 QPL 12  
|||

RESULT 62  
B32735  
thyroglobulin - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 11-Apr-1997  
C;Accession: B32735  
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.  
Biochem. Biophys. Res. Commun. 118, 423-429, 1984  
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin  
A;Reference number: A32735; MUID:84153804; PMID:6704086  
A;Accession: B32735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <RAW>  
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol  
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis  
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8  
|||  
Db 10 QPL 12  
|||

RESULT 63  
B61409  
genome polyprotein (clone L3/S2) - Skalica virus (fragment)  
C;Species: Skalica virus  
C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Nov-2000  
C;Accession: B61409  
R;Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.  
J. Gen. Virol. 72, 333-338, 1991  
A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by nucleotide sequencing  
A;Reference number: A61409; MUID:91132129; PMID:1847173  
A;Accession: B61409  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: genomic RNA  
A;Residues: 1-19 <GUI>  
C;Superfamily: yellow fever virus genome polyprotein

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
|||  
Db 1 LPP 3  
|||

RESULT 64  
S59486  
cell wall protein, 22K - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S59486  
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to different lectins  
A;Reference number: S59481; MUID:96011753; PMID:7548825  
A;Accession: S59486  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <WOJ>

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
|||  
Db 3 QPP 5  
|||

RESULT 65  
A37968  
neural surface protein Bravo - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 15-Aug-1997  
C;Accession: A37968; A36345  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 112, 1049, 1991  
A;Reference number: A37968; MUID:91154309; PMID:1999455  
A;Contents: erratum  
A;Accession: A37968  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <DEL>  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 111, 3087-3096, 1990  
A;Title: Topologically restricted appearance in the developing chick retinotectal system  
A;Reference number: A36345; MUID:91100421; PMID:2269667  
A;Accession: A36345

A:Molecule type: protein  
A;Residues: 1-7,9-19 <DE2>

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 15 QPP 17

## RESULT 66

A34467

36K microfilament-associated protein - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 08-Jun-1990 #sequence\_revision 08-Jun-1990 #text\_change 18-Jun-1993

C;Accession: A34467

R;Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa

J. Biol. Chem. 264, 17437-17444, 1989

A;Title: Isolation and characterization of a new 36-kDa microfilament-associated glycoprotein

A;Reference number: A34467; MUID:90008913; PMID:2793866

A;Accession: A34467

A;Status: preliminary

A:Molecule type: protein

A;Residues: 1-19 &lt;KOB&gt;

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8  
Db 16 QPL 18

## RESULT 67

S21737

coulmarin 7-monoxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragment)

N;Alternate names: coumarin 7-hydroxylase

C;Species: Papio papio (western baboon)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Mar-1999

C;Accession: S21737

R;Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Maurel, P.; Bonfils, C.

Eur. J. Biochem. 204, 641-648, 1992

A;Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene families

A;Reference number: S21737; MUID:92174920; PMID:1541278

A;Accession: S21737

A;Status: preliminary

A:Molecule type: protein

A;Residues: 1-20 &lt;DAL&gt;

C;Genetics:

A;Gene: CYP2A7

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13  
Db 16 TVM 18

## RESULT 68

S29817

cytochrome P450 2C23 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Mar-1999

C;Accession: S29817

R;Marie, S.; Roussel, F.; Cresteil, T.

Biochim. Biophys. Acta 1172, 124-130, 1993

A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.  
A;Reference number: S29817; MUID:93176794; PMID:7679925

A;Accession: S29817

A:Molecule type: mRNA

A;Residues: 1-20 &lt;MAR&gt;

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C;Keywords: heme; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9  
Db 4 PLP 6

## RESULT 69

A33878

myosin light chain kinase, smooth muscle - turkey (fragment)

C;Species: Meleagris gallopavo (common turkey)

C;Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 07-Nov-1997

C;Accession: A33878

R;Ikabe, M.; Maruta, S.; Reardon, S.

J. Biol. Chem. 264, 6967-6971, 1989

A;Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.

A;Reference number: A33878; MUID:89214114; PMID:2708351

A;Accession: A33878

A;Status: preliminary

A:Molecule type: protein

A;Residues: 1-20 &lt;IKE&gt;

C;Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homology  
C;Keywords: smooth muscle

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPO 6  
Db 14 PPO 16

## RESULT 70

A39328

notechis II-Sb nontoxic venom protein - common tiger snake (fragment)

C;Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)

C;Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 30-Sep-1993

C;Accession: A39328

R;Yang, C.C.; Chang, L.S.; Wu, F.S.

Toxicol. 29, 1337-1344, 1991

A;Title: Venom constituents of Notechis scutatus scutatus (Australian tiger snake) from

A;Reference number: A39328; MUID:92263371; PMID:1814009

A;Accession: A39328

A;Status: preliminary

A:Molecule type: protein

A;Residues: 1-20 &lt;YAN&gt;

C;Superfamily: phospholipase A2

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8  
Db 17 QPL 19

## RESULT 71

A37111

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)

C;Species: Spinacia oleracea (spinach)

C;Date: 15-Feb-1991 #sequence\_revision 15-Feb-1991 #text\_change 12-Apr-1995

C;Accession: A37111  
R;Sato, M.H.; Hisabori, T.; Yoshida, M.  
J. Biol. Chem. 265, 13419-13422, 1990  
A;Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M LiCl  
A;Reference number: A37111; MUID:90337936; PMID:2143183  
A;Accession: A37111  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <SAT>  
A;Superfamily: ribulose-bisphosphate carboxylase small chain  
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10  
Db 18 LPP 20

RESULT 72  
A54519  
tubulin alpha chain - Leishmania enriettii (fragment)  
C;Species: Leishmania enriettii  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 13-Aug-1999  
C;Accession: A54519  
R;Wirth, D.F.; Slater, C.  
Mol. Biochem. Parasitol. 9, 83-92, 1983  
A;Title: Isolation and characterization of an alpha-tubulin gene from Leishmania enriettii  
A;Reference number: A54519; MUID:8412075; PMID:6321982  
A;Accession: A54519  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-20 <WIR>  
A;Cross-references: GE:M28001; NID:g159409; PIDN:AAA29273.1; PID:g159410  
C;Superfamily: tubulin

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PTV 12  
Db 2 PTV 4

RESULT 73  
A05313  
apolipoprotein A-I - red guenon (fragment)  
N;Alternate names: apo-A-I  
C;Species: Erythrocebus patas (red guenon, hussar)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-May-2000  
C;Accession: A05313  
R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.  
Biochemistry 15, 1928-1933, 1976  
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus  
A;Reference number: A90395; MUID:76184721; PMID:178359  
A;Accession: A05313  
A;Molecule type: protein  
A;Residues: 1-20 <MAH>  
C;Superfamily: apolipoprotein A-I  
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQ 6  
Db 3 PPQ 5

RESULT 74  
T44453  
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T44453  
R;Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.  
J. Bacteriol. 180, 5559-5566, 1998  
A;Title: Molecular characterization and regulation of an operon encoding a system for tRNA<sup>Met</sup> charging in Pseudomonas aeruginosa  
A;Reference number: Z22777; MUID:99008987; PMID:9791103  
A;Accession: T44453  
A;Status: preliminary; translated from GE/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-20 <NTS>  
A;Cross-references: EMBL:AF012537; NID:g2668593; PIDN:AAC71069.1; PID:g2668594  
A;Experimental source: strain PAOI

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9  
Db 11 PLP 13

RESULT 75  
PH1380  
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)  
C;Species: Bacillus sp.  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 07-May-1999  
C;Accession: PH1380  
R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.  
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992  
A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly isolated Bacillus sp.  
A;Reference number: PH1380; MUID:93113087; PMID:11369074  
A;Accession: PH1380  
A;Molecule type: protein  
A;Residues: 1-20 <KAW>  
A;Experimental source: strain N0.195  
C;Comment: This enzyme has an optimum pH of 7.0.  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 VMP 14  
Db 11 VMP 13

Search completed: November 25, 2003, 19:36:14  
Job time : 10.2907 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 5.31977 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-34  
Perfect score: 15  
Sequence: 1 MHQPPQLPPTVMFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	12	1 FIF1_SARBU	P83349 sarcophaga
2	3	20.0	8	1 CPD1_ENTFA	P13269 enterococcus
3	3	20.0	9	1 AL10_CARMA	P81813 carcinus ma
4	3	20.0	9	1 RT33_BOVIN	P82926 bos taurus
5	3	20.0	10	1 PAR6_PANAE	P82660 panagrellus
6	3	20.0	11	1 BFPB_AGRFA	P01021 agkistrodon
7	3	20.0	11	1 MORN_HUMAN	P01163 homo sapien
8	3	20.0	11	1 TIN4_HOPTI	P82654 hoplobatr
9	3	20.0	12	1 TIN2_HOPTI	P82652 hoplobatr
10	3	20.0	12	1 TIN3_HOPTI	P82653 hoplobatr
11	3	20.0	13	1 ACT7_SOYEN	P15987 glycine max
12	3	20.0	14	1 EDCD_LYMDI	P80940 lymantria d
13	3	20.0	15	1 PRP_MYCBO	P80149 mycobacteri
14	3	20.0	16	1 AF25_MALPA	P83142 malva parvi
15	3	20.0	16	1 CXXA_CONPE	P50984 conus penna
16	3	20.0	16	1 CXAB_CONPE	P50985 conus penna
17	3	20.0	17	1 ACT6_SOYEN	P15986 glycine max
18	3	20.0	18	1 UC21_MALZE	P80627 zea mays (m
19	3	20.0	20	1 AIBG_EQUAS	P33090 equus asinu
20	3	20.0	20	1 APAL_ERYPA	P18647 erythrocebu
21	3	20.0	20	1 BULB_NARPS	P80554 narcissus p
22	3	20.0	20	1 CPA7_PAPSP	P80055 papio sp. (
23	3	20.0	20	1 OAR_PHOXY	P14803 photinus py
24	2	13.3	5	1 E104_LITRU	P81100 litoria rub
25	2	13.3	5	1 PAP2_PARMA	P81864 pardachirus
26	2	13.3	5	1 PRCT_PERAM	P01373 periplaneta
27	2	13.3	6	1 CIP1_MYTED	P13736 mytilus edu
28	2	13.3	6	1 CIP2_MYTED	P13737 mytilus edu
29	2	13.3	6	1 TMOF_SARBU	P41495 sarcophaga
30	2	13.3	6	1 TRPI_PSEPU	P36414 pseudomonas
31	2	13.3	6	1 VP19_HSVIK	P23210 herpes simp
32	2	13.3	7	1 LANC_CARUI	P36960 carnobacter
33	2	13.3	7	1 MNP1_LEPDE	P42984 leptinotars

34	2	13.3	7	1 TPFY_PACDA	P83455 pachymedusa
35	2	13.3	7	1 UP04_MOUSE	P38642 mus musculus
36	2	13.3	7	1 UN06_PINPS	P81675 pinus pinas
37	2	13.3	8	1 ACI_THUAL	P18691 thunnus alb
38	2	13.3	8	1 ALL5_CALVO	P41841 calliphora
39	2	13.3	8	1 ALL6_CYDPO	P82157 cydia pomon
40	2	13.3	8	1 COW2_CONPU	P58785 conus purpu
41	2	13.3	8	1 NPB_BOVIN	P15507 bos taurus
42	2	13.3	8	1 PPK2_PERAM	P82692 periplaneta
43	2	13.3	9	1 COXE_THUOB	P80975 thunnus obe
44	2	13.3	9	1 FAR1_CALVO	P41856 calliphora
45	2	13.3	9	1 FAR3_PENMO	P83318 penaeus mon
46	2	13.3	9	1 FAR4_PENMO	P83319 penaeus mon
47	2	13.3	9	1 FAR5_ASCSU	P43170 ascaris suu
48	2	13.3	9	1 FAR9_ASCSU	P43172 ascaris suu
49	2	13.3	9	1 FLA2_TREHY	P80159 treponema h
50	2	13.3	9	1 FRF1_SARBU	P83350 sarcophaga
51	2	13.3	9	1 KNL3_BOMVA	P83058 bombina var
52	2	13.3	9	1 LMT3_LOQMI	P41489 locusta mig
53	2	13.3	9	1 OXYA_SQUAC	P42999 squalus aca
54	2	13.3	9	1 OXYT_EISFO	P42998 eisenia foe
55	2	13.3	9	1 OXYT_RABIT	P32878 oryctolagus
56	2	13.3	9	1 OXYT_RAJCL	P42994 raja clavav
57	2	13.3	9	1 SAMP_MUSCA	P19095 mustelus ca
58	2	13.3	9	1 TKC1_CALVO	P41517 calliphora
59	2	13.3	9	1 UP3A_HUMAN	P30089 homo sapien
60	2	13.3	9	1 YBFR_AZOVI	P25825 azotobacter
61	2	13.3	10	1 AH3_FRUSE	P29261 prunus sero
62	2	13.3	10	1 AL19_CARMA	P81822 carcinus ma
63	2	13.3	10	1 BPP2_BOTIN	P30422 bothrops in
64	2	13.3	10	1 BPP2_BOTJA	P01022 bothrops ja
65	2	13.3	10	1 BPP8_BOTIN	P30426 bothrops in
66	2	13.3	10	1 BPP_VIPAS	P31351 viperas aspi
67	2	13.3	10	1 BRK_ONCMY	Q9prz1 oncorhynch
68	2	13.3	10	1 CATB_SHEEP	P83205 ovis aries
69	2	13.3	10	1 COXM_RAT	P80431 rattus norv
70	2	13.3	10	1 COXQ_RABIT	P80336 oryctolagus
71	2	13.3	10	1 COXQ_SHEEP	P80337 ovis aries
72	2	13.3	10	1 GONI_ALLEMI	P37041 alligator m
73	2	13.3	10	1 GON3_ONCKE	P20367 oncorhynch
74	2	13.3	10	1 GONL_SQUAC	P27429 squalus aca
75	2	13.3	10	1 LABA_JATMU	P13270 jatrophu mu
76	2	13.3	10	1 LPK2_LOQMI	P41488 locusta mig
77	2	13.3	10	1 NS1_MYCTU	P81185 mycobacteri
78	2	13.3	10	1 ODP2_BOVIN	P11180 bos taurus
79	2	13.3	10	1 PVK_LOQMI	P83382 locusta mig
80	2	13.3	10	1 Q2OB_COMTE	P80465 comamonas t
81	2	13.3	10	1 SLAP_BACTG	P49325 bacillus th
82	2	13.3	10	1 TEMK_RANTE	P56923 rana tempor
83	2	13.3	10	1 TKL2_LOQMI	P16224 locusta mig
84	2	13.3	10	1 TKL3_LOQMI	P30249 locusta mig
85	2	13.3	10	1 TNKX_PIG	P01292 sus scrofa
86	2	13.3	10	1 TMOF_AEDAE	P19425 aedes aegyp
87	2	13.3	10	1 UHA3_HUMAN	P40930 homo sapien
88	2	13.3	10	1 UP2A_HUMAN	P30088 homo sapien
89	2	13.3	10	1 UP2A_HUMAN	P30091 homo sapien
90	2	13.3	10	1 UP2A_HUMAN	P30095 homo sapien
91	2	13.3	10	1 URE3_MORMO	P17339 morganella
92	2	13.3	11	1 ASL1_BACSE	P83146 bacteroides
93	2	13.3	11	1 BPP3_BOTIN	P30423 bothrops in
94	2	13.3	11	1 BPP4_BOTIN	P30424 bothrops in
95	2	13.3	11	1 BPP_AGKUP	P04562 agkistrodon
96	2	13.3	11	1 BRK_MEGFL	P12797 megascollia
97	2	13.3	11	1 CEPI_ACHFU	P22790 achatina fu
98	2	13.3	11	1 EFG_CLOPA	P81350 clostridium
99	2	13.3	11	1 LADD_ONCMY	P81018 oncorhynch
100	2	13.3	11	1 LPW_THETH	P05624 thermus the

ALIGNMENTS

RESULT 1

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FIF1_SARBU
ID FIF1_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen I., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQP 7
DB 2 PPQP 5

RESULT 2
CPDI_ENTFA
ID CPDI_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOGIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 VMF 14
DB 3 VMF 5

RESULT 3
AL10_CARMA

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ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoida; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQP 7
DB 2 PQP 4

RESULT 4
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MPPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8
DB 5 QPL 7

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## RESULT 5

FAR6\_PANRE  
ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
AC P82660;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRamide-like neuropeptide F6 (NGAPQFVR-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of RMRamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -1- FUNCTION: MYOACTIVE.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7  
DB 4 POP 6

## RESULT 6

BPBP\_ACKHA  
ID BPBP\_ACKHA STANDARD; PRT; 11 AA.  
AC P01021;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide B (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys blunhoffi (Mamushi) (Gloydius blunhoffi).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Agkistrodon.  
OX NCBI\_TaxID=61300;  
RN [1]  
SEQUENCE.  
RC TISSUE=Venom;  
RA Kato H., Suzuki T.;  
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
RT the venom of Agkistrodon halys blunhoffi.";  
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181 (1970).  
CC -1- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01254; XASNBA.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
DB 3 LPP 5

## RESULT 7

MORN\_HUMAN  
ID MORN\_HUMAN STANDARD; PRT; 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human).  
OS Rattus norvegicus (Rat).  
OS Bos taurus (Bovine).  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]  
SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RC MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
RT from coelenterates to humans.";  
RL Nature 293:579-580 (1981).  
RN [2]  
SEQUENCE.  
RC SPECIES=A.elegantissima, and H.attenuata;  
RA Schaller H.C., Bodenmuller H.;  
RT "Isolation and amino acid sequence of a morphogenetic peptide from  
RT hydra.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004 (1981).  
RN [3]  
SYNTHESIS.  
RX MEDLINE=82050803; PubMed=7297679;  
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
RT "Synthesis of a new neuropeptide, the head activator from hydra.";  
RL FEBS Lett. 131:317-321 (1981).  
RN [4]  
FUNCTION.  
RX MEDLINE=90059923; PubMed=2583101;  
RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
RT in the G2/mitosis transition.";  
RL EMBO J. 8:3311-3318 (1989).  
CC -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS  
CC IN THE G2/MITOSIS TRANSITION.  
CC -1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.  
DR PIR; A01427; YHRT.  
DR PIR; A93900; YHXAE.  
DR PIR; B01427; YHHU.  
DR PIR; B93900; YHUPHY.  
DR PIR; C01427; YHBO.  
DR GK; P01163; -.  
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 1 QPP 3

## RESULT 8

TIN4\_HOPTI



ID TIN4 HOPTI STANDARD; PRT; 11 AA.  
 AC P82654;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tigerin-4.  
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;  
 OC Hoplobatrachus.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,  
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 20.0%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PLP 9  
 DB 7 PLP 9  
 RESULT 9  
 TIN2 HOPTI STANDARD; PRT; 12 AA.  
 AC P82652;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tigerin-2.  
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;  
 OC Hoplobatrachus.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,  
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT DISULFID 3 11  
 FT MOD RES 12 12  
 SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PLP 9  
 DB 7 PLP 9  
 RESULT 10  
 TIN3 HOPTI STANDARD; PRT; 12 AA.  
 AC P82653;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tigerin-3.  
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;  
 OC Hoplobatrachus.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,  
 CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT DISULFID 3 11  
 FT MOD RES 12 12  
 SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PLP 9  
 DB 7 PLP 9  
 RESULT 11  
 ACT7 SOYBN STANDARD; PRT; 13 AA.  
 AC P15987;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin 7 (Fragment).  
 GN SACT.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Wayne;  
 RX MEDLINE=91346640; PubMed=2102831;  
 RA Pearson L., Meagher R.B.;  
 RT "Diverse soybean actin transcripts contain a large intron in the 5',  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes.";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.

CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
 CC -!- SIMILARITY: Belongs to the actin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X17120; CAA34980.1; -.  
 CC PIR; S15755; S15755.  
 CC InterPro; IPR004001; Actin.  
 CC InterPro; IPR004000; Actin like.  
 CC PROSITE; PS00406; ACTINS\_1; PARTIAL.  
 CC PROSITE; PS00432; ACTINS\_2; PARTIAL.  
 CC PROSITE; PS01132; ACTINS\_ACT-LIKE; PARTIAL.  
 CC Structural protein; Multigene family.  
 FT NON TER 13  
 FT 13  
 SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QPL 8  
 Db 8 QPL 10

RESULT 12  
 ECDC LYMDI STANDARD; PRT; 14 AA.  
 AC P80940;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE Testis ecdysiotropin peptide C (TE).  
 OS Lymantria dispar (Gypsy moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
 OC Lymantriidae; Lymantria.  
 OX NCBI\_TaxID=13123;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=97387807; PubMed=9243792;  
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
 RA Bell R.A.;  
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
 RT gonadotropin isolated from brains of Lymantria dispar pupae."  
 RL Arch. Insect Biochem. Physiol. 36:37-50 (1997).  
 CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES  
 CC OF LARVAE AND PUPAE.  
 CC SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PLP 9  
 Db 9 PLP 11  
 RESULT 13  
 PRP\_MYCBO STANDARD; PRT; 15 AA.  
 ID PRP\_MYCBO

AC P80149;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS Mycobacterium bovis.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=BCG / Paris 1173 P2;  
 RX MEDLINE=93281750; PubMed=8506381;  
 RA Romain F., Augier J., Pescher P., Marchal G.A.;  
 RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-  
 RT type hypersensitivity reactions only in guinea pigs immunized with  
 RT living mycobacteria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326 (1993).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY  
 CC REACTIONS IN GUINEA PIGS.  
 FT NON TER 15  
 FT 15  
 SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPQ 6  
 Db 9 PPQ 11

RESULT 14  
 AF2S MALPA STANDARD; PRT; 16 AA.  
 ID AF2S MALPA  
 AC P83142;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
 OS Malva parviflora (Little mallow) (Cheeseweed).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosid II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RT parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673 (2000).  
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 CC GO; GO:0003799; F:antifungal peptide activity; IDA.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON TER 16  
 FT 16  
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7BE65 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPQ 6  
 Db 9 PPQ 11

```

RESULT 15
CXAB_CONPE
ID_CXAA_CONPE STANDARD; PRT; 16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1A.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors."
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry."
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RL Structure 4:417-423(1996).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A54877; A54877.
DR PDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY , 8 LPP 10
Db |||
5 LPP 7

RESULT 16
CXAB_CONPE
ID_CXAA_CONPE STANDARD; PRT; 16 AA.
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1A.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors."
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry."
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RL Structure 4:417-423(1996).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A54877; A54877.
DR PDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY , 8 LPP 10
Db |||
5 LPP 7

RESULT 17
ACT6_SOYBN
ID_ACT6_SOYBN STANDARD; PRT; 17 AA.

```

AC P15986;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin 6 (Fragment).  
 GN SACC6.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. Wayne;  
 RC MEDLINE=91346640; PubMed=2102831;  
 RX Pearson L., Meagher R.B.;  
 RA "Diverse soybean actin transcripts contain a large intron in the 5'  
 RT untranslated leader: structural similarity to vertebrate muscle actin  
 RT genes";  
 RL Plant Mol. Biol. 14:513-526(1990).  
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.  
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
 CC -!- SIMILARITY: Belongs to the actin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X17119; CRA34979.1; -;  
 DR PIR; S15754; S15754.  
 DR InterPro; IPR004001; Actin.  
 DR InterPro; IPR004000; Actin\_like.  
 DR Pfam; PF00022; actin; 1.  
 DR PROSITE; PS00406; ACTINS 1; PARTIAL.  
 DR PROSITE; PS00432; ACTINS 2; PARTIAL.  
 DR PROSITE; PS01132; ACTINS ACT LIKE; PARTIAL.  
 KW Structural protein; Multigene family.  
 FT NON TER 17 17  
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QPL 8  
 DB 8 QPL 10  
 RESULT 18  
 UC21\_MAIZE  
 ID UC21\_MAIZE STANDARD; PRT; 18 AA.  
 AC P80627;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;

RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.  
 CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.  
 DR Maize-2DPAGE; P80627; COLEOPTILE.  
 DR MaizeDB; 123953; -. 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PTV 12  
 DB 5 PTV 7  
 RESULT 19  
 A1BG\_EQUAS  
 ID A1BG\_EQUAS STANDARD; PRT; 20 AA.  
 AC P39090;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Alpha-1B-glycoprotein (Alpha-1-B glycoprotein) (Postalbumin)  
 DE (Fragment).  
 GN A1BG.  
 OS Equus asinus (Donkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9793;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=9130579; PubMed=1868686;  
 RA Patterson S.D., Bell K., Shaw D.C.;  
 RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization  
 RT and new alleles";  
 RL Comp. Biochem. Physiol. 98B:523-528(1991).  
 CC -!- FUNCTION: Unknown.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma.  
 KW Immunoglobulin domain; Glycoprotein; Plasma.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 POP 7  
 DB 6 POP 8  
 RESULT 20  
 APAL\_ERYPA  
 ID APAL\_ERYPA STANDARD; PRT; 20 AA.  
 AC P18647;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Apolipoprotein A-I (Apo-AI) (Fragment).  
 GN APOA1.

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OS Erythrocebus patas (Red guenon) (Ruszar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=76184721; PubMed=178359;
RA Mabey R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RL Erythrocebus patas monkey."
CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR PIR; A05313; A05313
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQ 6
Db 3 PPQ 5

RESULT 21
BULB NARPS
ID BULB NARPS STANDARD; PRT; 20 AA.
AC P80554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Bulb protein (Fragment).
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 13 LPP 15

RESULT 22
CPA7 PAPSP
ID CPA7 PAPSP STANDARD; PRT; 20 AA.
AC P80055;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1994 (Rel. 38, Last annotation update)
DE Cytochrome P450 2A7 (EC 1.14.14.1) (CYPIA7) (P450 FT) (Coumarin 7-
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DE hydroxylase) (Fragment).
GN CYP2A7.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RT "Purification of two cytochrome P450 isozymes related to CYP2A and
RT CYP3A gene families from monkey (baboon, Papio papio) liver
RT microsomes. Cross reactivity with human forms."
RL Bur. J. Biochem. 204:641-648(1992).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; CYTOCHROME_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT UNSURE 14 14
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TVM 13
Db 16 TVM 18

RESULT 23
OAR PHOPY
ID OAR PHOPY STANDARD; PRT; 20 AA.
AC P14503;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Octopamine receptor (Octopamine binding protein) (Fragment).
DE Photinus pyralis (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia;
OC Cantharoides; Lampyridae; Photinus.
OX NCBI_TaxID=7054;
RN [1]
RP SEQUENCE.
RC TISSUE=Light organ;
RX MEDLINE=9092510; PubMed=2513233;
RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
RT binding protein."
RL FEBS Lett. 259:117-120(1989).
CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
CC NEUROTRANSMITTER. NEUROHORMONE, AND NEUROMODULATOR IN
CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S28779; S28779.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
KW G-protein coupled receptor.
FT UNSURE 2 2
FT UNSURE 9 9
FT UNSURE 19 19
```

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FT NON TER 20 20
SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11B8D4AB CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQ 3
Db 18 MHQ 20

RESULT 24
EI04_LITRU
ID -EI04_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 4.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSU=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella";
RL Aust. J. Chem. 52:639-645 (1999).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TV 12
Db 3 TV 4

RESULT 25
PAP2_PAPMA
ID -PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSU=Skin secretion;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -I- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
```

```
CC in membranes. At high concentration causes cell membrane lysis.
CC -I- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FP 15
Db 4 FP 5

RESULT 26
PRCT_PPRAM
ID -PRCT_PPRAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569 (1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas; PubMed=2872661;
RX MEDLINE=96232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -I- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -I- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
```

Query Match 13.3%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 ||  
 Db 3 LP 4

RESULT 27  
 CIP1 MYTED  
 ID CIP1 MYTED STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.  
 CC -!- SIMILARITY: TO MIP II.  
 DR PIR; A27696; A27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6  
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MF 14  
 ||  
 Db 4 MF 5

RESULT 28  
 CIP2 MYTED  
 ID CIP2 MYTED STANDARD; PRT; 6 AA.  
 AC P13737;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide II (MIP II).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN MUSCLES.  
 CC -!- SIMILARITY: TO MIP I.  
 DR PIR; B27696; B27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6  
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MF 14  
 ||  
 Db 4 MF 5

RESULT 29  
 TMOF SARB  
 ID TMOF SARB STANDARD; PRT; 6 AA.  
 AC P41495;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOF).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ovary;  
 RX MEDLINE=94211930; PubMed=8159807;  
 RA Eylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
 RA de Loof A.;  
 RT "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";  
 RL Regul. Pept. 50:61-72(1994).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN OF OOCYTE CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11  
 ||  
 Db 2 PT 3

RESULT 30  
 TRPI\_PSEPU  
 ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TrpBA operon transcriptional activator (fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPG1 C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.

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DR EMBL; X13299; CAA31660.1; -;  
DR InterPro: IPR000847; HTH\_LysR.  
DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
KW Tryptophan biosynthesis; Transcription regulation; Activator;  
KW DNA-binding.  
FT NON TER 6  
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
||  
Db 5 LP 6

RESULT 31  
VP19 HSV1K STANDARD; PRT; 6 AA.  
AC P23210;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Capsid assembly and DNA maturation protein (Virion protein UL38)  
DE (Capsid protein VP19C) (Fragment).  
GN UL38.

OS Herpes simplex virus (type 1 / strain KOS).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_taxID=10306;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91101287; PubMed=1846198;  
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
RA Silverstein S., Wagner E.K.;  
RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
RT expression of UL38, a true late gene involved in capsid assembly.";  
RL J. Virol. 65:769-786(1991).  
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE  
CC EMBEDDED. BINDS DNA.  
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.

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DR EMBL; M57646; AAA45830.1; -;  
KW Capsid assembly; Coat protein; DNA-binding.  
FT NON TER 6  
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8  
||  
Db 5 PL 6

RESULT 32  
LANC CARUI STANDARD; PRT; 7 AA.  
ID \_LANC\_CARUI  
AC P36960; 1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
[1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
RT a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db 5 QP 6

RESULT 33  
MNPI LEPDE STANDARD; PRT; 7 AA.  
AC P42984;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myotropic neuropeptide 1 (Lep-MNP-I).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxID=7539;  
[1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=95380343; PubMed=7651886;  
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,  
RA Grauwels L., van Leuven F., de Loof A.;  
RT "Identification, characterization, and immunological localization of  
RT a novel myotropic neuropeptide in the Colorado potato beetle,  
RT Leptinotarsa decemlineata.";  
RL Peptides 16:365-374(1995).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 7 PL 8  
||  
5 PL 6

## RESULT 34

TPFY\_PACDA STANDARD; PRT; 7 AA.  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-1 (Pdt-1).  
OS Pachymedusa dactinolor (Giant Mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.  
RP TISSUE=Skin secretion;  
RC Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA.";  
RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0045986; P:negative regulation of smooth muscle contractility; NAS.  
KW Amphibian defense peptide; Amidation; Hydroxylation.  
FT MOD\_RES 3 3 HYDROXYLATION.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
2 PP 3

## RESULT 35

UF04\_MOUSE STANDARD; PRT; 7 AA.  
AC P38642;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=9500907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 46 kDa.  
FT NON\_TER 7 7  
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
3 PP 4

## RESULT 36

UN06\_PINPS STANDARD; PRT; 7 AA.  
AC P81675;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of needles (N141) (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RT Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
FT NON\_TER 1 1  
FT NON\_TER 7 7  
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
||  
5 LP 6

## RESULT 37

ACI\_THUAL STANDARD; PRT; 8 AA.  
AC P18691;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Angiotensin-converting enzyme inhibitor.  
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8236;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=88326322; PubMed=3415688;  
RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.";  
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
DR PIR: A31570; A31570.  
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11  
Db 1 PT 2

RESULT 38  
ALL5 CALVO  
ID -ALL5\_CALVO STANDARD; PRT; 8 AA.  
AC P41841;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RN SEQUENCE  
RP MEDLINE=93211980; PubMed=8460157;  
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
RA Thorpe A.;  
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
RT with sequence homology to cockroach allatostatins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RN CHARACTERIZATION, AND HYDROXYLATION.  
RP TISSUE=Head;  
RC MEDLINE=94342269; PubMed=8063725;  
RX Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
RA "[Hyp3]Met-callatostatin. Identification and biological properties of  
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";  
RL J. Biol. Chem. 269:21059-21066(1994).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
DR PIR; E47393; E47393  
KW Neuropeptide; Amidation; Hydroxylation.  
FT MOD RES 3 3 HYDROXYLATION (20%).  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No.1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
Db 2 PP 3

RESULT 39  
ALL6 CYDPO  
ID -ALL6\_CYDPO STANDARD; PRT; 8 AA.  
AC P82157;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydastatin 6.  
OS Cydia pomonella (Coddling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RN SEQUENCE

RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No.1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
Db 1 LP 2

RESULT 40  
CONW2 CONPU  
ID -CONW2\_CONPU STANDARD; PRT; 8 AA.  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leu-contryphan-F.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=41690;  
RN [1]  
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RP STRAIN=Clipperton Island; TISSUE=Venom;  
RC MEDLINE=9338839; PubMed=10461743;  
RX Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
RA Olivera B.M.;  
RT "A novel D-leucine-containing Conus peptide: diverse conformational  
RT dynamics in the contryphan family.";  
RL J. Pept. Res. 54:93-99(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
KW Toxin; Hydroxylation; D-amino acid.  
FT DISULFID 2 8  
FT MOD RES 4 4 D-LEUCINE.  
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No.1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
Db 5 LP 6

RESULT 41  
NPB BOVIN  
ID -NPB\_BOVIN STANDARD; PRT; 8 AA.  
AC P15507;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropeptide B.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;

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[1]
RP TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
characterization of two brain neuropeptides that modulate the action
of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 4 QP 5

RESULT 42
FPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

[1]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 43

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COXE_THUOB STANDARD; PRT; 9 AA.
ID COXE_THUOB
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 44
FAR1_CALVO STANDARD; PRT; 9 AA.
ID FAR1_CALVO
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.

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RT	of the giant tiger prawn Penaeus monodon.";			
RL	Comp. Biochem. Physiol. 131B:325-337(2002).			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- MASS SPECTROMETRY: MW=1119.8; METHOD=WALDI.			
CC	-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.			
KW	Neuropeptide; Amidation.			
FT	MOD RES	9	9	AMIDATION.
SQ	SEQUENCE	9 AA; 1121 MW;	DA0B07340685A776 CRC64;	
Query Match 13.3%; Score 2; DB 1; Length 9;				
Best Local Similarity 100.0%; Pred. No. 1.3e+05;				
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	3 QP 4			
	2 QP 3			
Db				
RESULT 47				
FAR5_ASCSU STANDARD; PRT; 9 AA.				
ID	FAR5_ASCSU STANDARD; PRT; 9 AA.			
AC	P43170;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	FMRFamide-like neuropeptide AF5.			
OS	Ascaris suum (Pig roundworm) (Ascaris lumbricoides).			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;			
OC	Ascarididae; Ascaris.			
OX	NCBI_TaxID=6253;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=95380362; PubMed=7651904;			
RA	Cowden C., Stretton A.O.W.;			
RT	"Eight novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum.";			
RL	Peptides 16:491-500(1995)..			
CC	-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.			
KW	Neuropeptide; Amidation.			
FT	MOD RES	9	9	AMIDATION.
SQ	SEQUENCE	9 AA; 1052 MW;	340B0059D1B76338 CRC64;	
Query Match 13.3%; Score 2; DB 1; Length 9;				
Best Local Similarity 100.0%; Pred. No. 1.3e+05;				
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

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Qy      10 PT 11
      ||
Db      4 PT 5

RESULT 48
FAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P41172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 01-FEB-1996 (Rel. 33, last annotation update)
DE FWRamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_taxid=6253;
RN [1]
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Right novel FWRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
RC -1- SIMILARITY: BELONGS TO THE FARP (FWRamide RELATED PEPTIDE)

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CC  FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD RES 9 9  AMIDATION.
SQ  SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 PL 8
DB  6 PL 7

RESULT 49
FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- SUBUNIT: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- FUNCTION: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND
CC FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 8 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C58B4772D1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TV 12
DB 2 TV 3

RESULT 50
PRF1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FWRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;

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RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 51
KNL3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RT Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 52
LMT3 LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.

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OX NCBI_TaxID=7004;
RN [1] --
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE172C9D776C6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db |||
3 QP 4

RESULT 53
OXYA SQUAC
ID -OXYA SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1] --
RP SEQUENCE.
RC MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2] --
RP SEQUENCE.
RC MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW Hormone; Amidation.
FT MOD RES 1 6
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PL 8
Db |||
7 PL 8

RESULT 54
OXYT_EISFO
ID -OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1] --
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; PC2021; PC2021.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PT 11
Db |||
7 PT 8

RESULT 55
OXYT_RABIT
ID -OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus),
OS Balenoptera physalus (Finback whale) (Common rorqual),
OS Tachylophus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus colliie (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1] --
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophysial hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2] --
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;

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RA Ferguson D.R., Pickering B.T.;  
 RT "Arginine and lysine vasopressins in the hippopotamus  
 RL neurohypophysis.";  
 RL Gen. Comp. Endocrinol. 13:425-429 (1969).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=B.physalus;  
 RA Acher R., Chauvet J., Chauvet M.-T.;  
 RT "Isolation of finback whale oxytocin and vasopressin.";  
 RL Nature 201:191-192 (1964).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=A. aculeatus;  
 RX MEDLINE=73223515; PubMed=4515919;  
 RA Acher R., Chauvet J., Chauvet M.-T.;  
 RT "Neurohypophysial hormones and evolution of tetrapods.";  
 RL Nature New Biol. 244:124-126 (1973).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.colliel;  
 RX MEDLINE=7008110; PubMed=5366118;  
 RA Pickering B.T., Heller H.;  
 RT "Oxytocin as a neurohypophysial hormone in the holoccephalian  
 RL elasmobranch fish, *Hydrolagus collei*.";  
 CC J. Endocrinol. 45:597-606 (1969).  
 CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE  
 CC UTERUS AND OF THE MAMMARY GLAND.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; A91466; A91466.  
 DR PIR; A92774; A92774.  
 DR PIR; A93147; A93147.  
 DR PIR; A93408; A93408.  
 DR PIR; B90667; B90667.  
 DR PDB; 1XY1; 15-OCT-90.  
 DR PDB; 1XY2; 15-OCT-90.  
 DR InterPro; IPR000981; Neurhyp horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Hypothalamus; Amidation; 3D-structure.  
 FT DISULFID 1 6  
 FT MOD RES 9 9  
 FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;  
 QY Query Match 13.3%; Score 2; DB 1; Length 9;  
 DB Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PL 8  
 DB 7 PL 8  
 RESULT 56  
 OXYT\_RAJCL  
 ID OXYT\_RAJCL STANDARD; PRT; 9 AA.  
 AC P42994;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Glumitocin.  
 OS Raja clavata (Thornback ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalia; Hyposqualea; Pristioraja; Batoidae;  
 OC Rajiformes; Rajidae; Raja.  
 OX NCBI\_TaxID=7781;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=66123415; PubMed=5880565;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,  
 RL glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,  
 RT the ray (*Raja clavata*).";  
 RL Biochim. Biophys. Acta 107:393-396 (1965).

CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurhyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9  
 FT SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;  
 QY Query Match 13.3%; Score 2; DB 1; Length 9;  
 DB Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PQ 6  
 DB 7 PQ 8  
 RESULT 57  
 SAMP\_MUSCA  
 ID SAMP\_MUSCA STANDARD; PRT; 9 AA.  
 AC P19095;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P-component (SAP) (Fragment).  
 OS *Mustelus canis* (Smooth dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
 OC *Mustelus*.  
 OX NCBI\_TaxID=7812;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83160932; PubMed=6403520;  
 RA Robey F.A., Tanaka T., Liu T.-Y.;  
 RT "Isolation and characterization of two major serum proteins from the  
 RT dogfish, *Mustelus canis*, C-reactive protein and amyloid P  
 RT component.";  
 RL J. Biol. Chem. 258:3889-3894 (1983).  
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 DR PIR; B20569; B20569.  
 DR InterPro; IPR001759; Pentaxin.  
 DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
 FT DOMAIN 1 >9  
 FT NON\_TER 9 9  
 FT SEQUENCE 9 AA; 965 MW; D05B5735B386769 CRC64;  
 QY Query Match 13.3%; Score 2; DB 1; Length 9;  
 DB Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 FP 15  
 DB 2 FP 3  
 RESULT 58  
 TKC1\_CALVO  
 ID TKC1\_CALVO STANDARD; PRT; 9 AA.  
 AC P41517;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin I.  
 OS *Calliphora vomitoria* (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PT 11
DB 2 PT 3

RESULT 59
UPA3 HUMAN
ID UPA3 HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459057;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PL 8
DB 2 PL 3

RESULT 60
YBFR AZOVI
ID YBFR AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).

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OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M83692; AAA22122.1; -
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 61
AH3 PRUSE
ID AH3 PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC Glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

3 PP 4

Db

RESULT 62

AL19\_CARMA

ID \_AL19\_CARMA STANDARD; PRT; 10 AA.

AC P81822;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 19.

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Portunoidae; Portunidae; Carcinus.

OX NCBI\_TaxID=6759;

RN [1]

SEQUENCE

PC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=9461295;

RA Duve H., Johansen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;

RA "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";

RL Eur. J. Biochem. 250:727-734 (1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

CC Neuropeptide; Amidation; Multigene family.

FW MOD\_RES 10 10 AMIDATION (POTENTIAL);

FT SEQUENCE 10 AA; 1101 MW; 96687CD5NB569AB1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 PP 5

Db

10 PT 11

2 PT 3

Db

RESULT 63

BPP2\_BOTIN

ID \_BPP2\_BOTIN STANDARD; PRT; 10 AA.

AC P30422;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

SEQUENCE

PC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RA "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227 (1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.

CC PIR; B37196; B37196.

DR KW

FW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 PP 5

Db

9 PP 10

Db

RESULT 64

BPP2\_BOTIN

ID \_BPP2\_BOTIN STANDARD; PRT; 10 AA.

AC P01022;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).

OS Bothrops jararaca (Jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8724;

RN [1]

SEQUENCE

PC TISSUE=Venom;

RX MEDLINE=72118526; PubMed=4334402;

RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocys O.;

RA "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";

RL Biochemistry 10:4033-4039 (1971).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.

CC PIR; A01255; XAVI6B.

DR KW

FW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 PP 5

Db

9 PP 10

Db

RESULT 65

BPP8\_BOTIN

ID \_BPP8\_BOTIN STANDARD; PRT; 10 AA.

AC P30426;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

SEQUENCE

PC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RA "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227 (1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.

CC PIR; B37196; B37196.

DR KW

FW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 PP 5

Db

9 PP 10

Db

CC It acts as an indirect hypotensive agent.  
 DR PIR; M37196; H37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1173 MW; 2F835545761F6D8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
 Db 9 PP 10

RESULT 66  
 BPP VIPAS  
 ID BPP VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Venom;  
 RC MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327696773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
 Db 9 PP 10

RESULT 67  
 BRK ONCMY  
 ID BRK ONCMY STANDARD; PRT; 10 AA.  
 AC Q9PZL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94039817; PubMed=8224232;  
 RA Conlon J.M., Olson K.R.;  
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from

RT trout plasma.";  
 RL FEBS Lett. 334:75-78(1993).  
 CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma.  
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 DR PIR; S39030; S39030.  
 KW Bradykinin; Vasodilator.  
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
 Db 3 PP 4

RESULT 68  
 CA1B SHEEP  
 ID CA1B SHEEP STANDARD; PRT; 10 AA.  
 AC P83205;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
 GN CTSB.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Placenta;  
 RC MEDLINE=22394055; PubMed=12506352;  
 RA El Amri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z., Mboko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated glycoproteins from the ewe placenta.";  
 RL Mol. Reprod. Dev. 64:199-206(2003).  
 CC -!- FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Has also been implicated in tumor invasion and metastasis.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in small molecule substrates (thus differing from cathepsin L). In addition to being an endopeptidase, shows peptidyl-dipeptidase activity, liberating C-terminal dipeptides.  
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked by a disulfide bond (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro: IPR000169; Shprot.acsite.  
 DR PROSITE; PS00640; THIOI\_PROTEASE\_ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 Db 1 LP 2

RESULT 69

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Qy      10 PT 11
Db      9 PT 10

RESULT 71
COXQ SHEEP
ID_COXQ_SHEEP STANDARD; PRT; 10 AA.
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 PT 11
Db      9 PT 10

RESULT 72
GONI ALLMI
ID_GONI_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-1991 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OC NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RT Regul. Pept. 33:105-116(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
CC PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.

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KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 8 QP 9

RESULT 73
GON3_ONCKE
ID GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberein III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-
RH III) (Luliberin III).
GN GNRH3.
OS Oncorhynchus keta (Chum salmon), and
Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 30724;
RN [1]
RP SPECIES=O.keta;
RC MEDLINE=83195140; PubMed=6341999;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
CC PIR; A21114; A21114.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9
Db 8 LP 9

RESULT 74
GONL_SQUAC
ID GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;

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DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberein (Gonadotropin-releasing hormone) (GNRH) (LH-RH)
(Luliberin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamwongchon S., Craig A.G.,
Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A46030; A46030.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9
Db 8 LP 9

RESULT 75
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids I; Malpighiales; Euphorbiales; Euphorbiaceae; Jatropha.
RN NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AAB6362D1B362 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TV 12

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Db           ||  
              5 TV 6

Search completed: November 25, 2003, 19:28:28  
Job time : 5.3912 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 28.1686 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPPQPLPPTVMFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	26.7	9	10	P82429
2	4	26.7	12	2	Q8KZ86
3	4	26.7	12	4	Q9BZ49
4	4	26.7	13	2	Q9L8K1
5	4	26.7	13	4	Q14182
6	4	26.7	15	10	Q9S8N8
7	4	26.7	15	10	Q40562
8	4	26.7	15	10	Q40563
9	4	26.7	16	13	Q9PRU6
10	4	26.7	17	13	Q9PRU7
11	4	26.7	18	12	Q84129
12	4	26.7	19	2	Q9RBV1
13	4	26.7	20	2	Q46499
14	4	26.7	20	4	Q9UCAR
15	4	26.7	20	10	Q9S8A8
16	4	26.7	20	13	Q9PRN3

17	3	20.0	9	2	P83157
18	3	20.0	9	4	Q9UCS8
19	3	20.0	9	5	Q9TWV0
20	3	20.0	9	10	Q9S8J8
21	3	20.0	9	16	Q935G1
22	3	20.0	10	2	Q9R5T2
23	3	20.0	10	4	Q14096
24	3	20.0	10	11	Q9QVF7
25	3	20.0	10	11	Q8VHM9
26	3	20.0	10	12	Q8JV78
27	3	20.0	10	13	Q90ZV8
28	3	20.0	11	2	Q47569
29	3	20.0	11	4	Q60761
30	3	20.0	11	4	Q9UCR1
31	3	20.0	11	6	Q9GL48
32	3	20.0	11	10	Q9S8Z9
33	3	20.0	11	13	Q8UUP1
34	3	20.0	12	4	Q9P116
35	3	20.0	12	4	Q9NTQ2
36	3	20.0	12	6	Q9TRU1
37	3	20.0	12	10	P82329
38	3	20.0	13	4	Q9UEE2
39	3	20.0	13	4	Q14890
40	3	20.0	13	4	Q9UNV6
41	3	20.0	13	6	Q9TRW6
42	3	20.0	13	10	Q42373
43	3	20.0	13	11	Q88176
44	3	20.0	13	12	Q67604
45	3	20.0	14	8	Q9T2K7
46	3	20.0	14	10	P82326
47	3	20.0	14	11	Q70599
48	3	20.0	14	16	Q9K326
49	3	20.0	15	2	Q9R5D5
50	3	20.0	15	6	Q9TR62
51	3	20.0	15	11	Q9QV25
52	3	20.0	15	12	Q69353
53	3	20.0	16	2	Q9R5K7
54	3	20.0	16	4	Q9NNZ2
55	3	20.0	16	4	Q9UCH1
56	3	20.0	16	5	Q18378
57	3	20.0	16	6	Q9TRR1
58	3	20.0	16	8	P92732
59	3	20.0	16	11	Q9JHB6
60	3	20.0	17	2	Q8VMB2
61	3	20.0	17	2	P97135
62	3	20.0	17	3	Q06800
63	3	20.0	17	4	Q15276
64	3	20.0	17	4	Q96P96
65	3	20.0	17	4	Q14001
66	3	20.0	17	6	Q9TRU8
67	3	20.0	17	10	P83061
68	3	20.0	17	12	Q8B4C4
69	3	20.0	18	2	Q9RSU2
70	3	20.0	18	2	Q9R5F9
71	3	20.0	18	2	Q9R4V9
72	3	20.0	18	2	Q9EYW5
73	3	20.0	18	2	Q9R4C6
74	3	20.0	18	4	Q9UCG7
75	3	20.0	18	4	Q96F98
76	3	20.0	18	4	Q16244
77	3	20.0	18	4	Q9UCT9
78	3	20.0	18	4	Q8NFB4
79	3	20.0	18	4	Q9S915
80	3	20.0	18	11	Q9JIE9
81	3	20.0	19	2	Q9K4X0
82	3	20.0	19	4	Q9UC80
83	3	20.0	19	4	Q9NFK2
84	3	20.0	19	4	Q9UC6
85	3	20.0	19	8	Q31687
86	3	20.0	19	8	Q9GI97
87	3	20.0	19	10	Q9S8F5
88	3	20.0	19	12	Q69099
89	3	20.0	19	13	Q9PRT0

P83157 anabaena sp  
Q9UCS8 homo sapien  
Q9TWV0 anthopleura  
Q9S8J8 oryza sativ  
Q935G1 salmoneilla  
Q9R5T2 acetobacter  
Q14096 homo sapien  
Q9QVF7 rattus sp.  
Q8VHM9 mus musculu  
Q8JV78 polyomaviru  
Q90ZV8 psittacus e  
Q47569 escherichia  
Q60761 homo sapien  
Q9UCR1 homo sapien  
Q9GL48 sus scrofa  
Q9S8Z9 psophocarpu  
Q8UUP1 xenopus lae  
Q9P116 homo sapien  
Q9NTQ2 homo sapien  
Q9TRU1 bos taurus  
P82329 pisum sativ  
Q9UEE2 homo sapien  
Q14890 homo sapien  
Q9UNV6 homo sapien  
Q9TRW6 bos taurus  
Q42373 solanum tub  
Q88176 mus musculu  
Q67604 squash leaf  
Q9T2K7 chlamydomon  
P82326 pisum sativ  
Q70599 rattus norv  
Q9K326 bacillus ha  
Q9R5D5 chromatium  
Q9TR62 oryctolagus  
Q9QV25 rattus sp.  
Q69353 herpes simp  
Q9R5K7 streptomyce  
Q9NNZ2 homo sapien  
Q9UCH1 homo sapien  
Q18378 drosophila  
Q9TRR1 oryctolagus  
P92732 fejevarya  
Q9JHB6 mus musculu  
Q8VMB2 pseudomonas  
P87135 mycobacteri  
Q06800 saccharomyc  
Q15276 homo sapien  
Q96P96 homo sapien  
Q14001 homo sapien  
Q9TRU8 bos taurus  
P83061 spinacia ol  
Q8B4C4 hepatitis b  
Q9RSU2 pseudomonas  
Q9R5F9 alcaligenes  
Q9R4V9 campylobact  
Q9EYW5 erwinia ste  
Q9R4C6 agrobacteri  
Q9UCG7 homo sapien  
Q96F98 homo sapien  
Q16244 homo sapien  
Q9UCT9 homo sapien  
Q8NFB4 homo sapien  
Q9S915 triticum tu  
Q9JIE9 mus musculu  
Q9K4X0 planktothri  
Q9UC80 homo sapien  
Q9NFK2 homo sapien  
Q9UC6 homo sapien  
Q31687 artemia par  
Q9GI97 sargassum p  
Q9S8F5 beta vulgar  
Q69099 herpes simp  
Q9PRT0 gallus gall

90 Q9prn4 petromyzon  
 91 Q90f8 human immun  
 92 Q905e8 human immun  
 93 Q905k8 human immun  
 94 Q90rg5 human immun  
 95 Q9r4m9 pseudomonas  
 96 Q93il1 vibrio harv  
 97 Q53370 escherichia  
 98 Q50180 pseudomonas  
 99 Q9r5e8 bacillus sp  
 100 Q96t45 homo sapien

## ALIGNMENTS

```

RESULT 1
P82429 PRELIMINARY; PRT; 9 AA.
AC Q9BZ49;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DE 44 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -|- SUBCELLULAR LOCATION: CELL WALL.
CW -|- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON TER
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPO 6
Db 2 QPPO 5

RESULT 2
Q8KZ86 PRELIMINARY; PRT; 12 AA.
ID Q8KZ86
AC Q8KZ86;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Class I integron DNA integrase (fragment).
GN INT11.
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=204A;
RA Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,
RA Tonin E., Monti-Bragadin C.;
RT "Carriage of class I and II integrons in Italian clinical isolates of
RT Acinetobacter baumannii.";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ133334; CAC85941.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 7 PLPP 10

RESULT 3
Q9BZ49 PRELIMINARY; PRT; 12 AA.
ID Q9BZ49
AC Q9BZ49;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Glycophorin C (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RT "The association of the glycoprotein C exon 3 deletion with
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
RT Guinea.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -.
FT NON TER
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 7 PLPP 10

RESULT 4
Q9L8K1 PRELIMINARY; PRT; 13 AA.
ID Q9L8K1
AC Q9L8K1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Vans (Fragment).
GN VANSB.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BM4281.
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
RT resistant enterococci and characterization of two novel insertion
RT sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF201896; AAF73374.1; -.
FT NON TER
SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 26.7%; Score 4; DB 2; Length 13;

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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPT 11
Db 7 LPPT 10

RESULT 5
ID Q14182 PRELIMINARY; PRT; 13 AA.
AC Q14182;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
GN DNTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87213162; PubMed=3579900;
RA Koitai O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
RT expressible in mammalian cells."
RL Biochem. Biophys. Res. Commun. 144:185-190 (1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transferase.
FT NON TER 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
Db 8 QPLP 11

RESULT 6
ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flengrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis."
RL Electrophoresis 14:1060-1066 (1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937B908B9E CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQ 6
Db 4 QPPQ 7

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RESULT 7
Q40562 PRELIMINARY; PRT; 15 AA.
ID Q40562;
AC Q40562;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RC MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565 (1994).
DR EMBL; L16786; AAA73564.1; -.
KW GTP-binding.
FT NON TER 1
SQ SEQUENCE 15 AA; 1707 MW; 8A889F924EA30CAF CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
Db 3 QPLP 6

RESULT 8
Q40563 PRELIMINARY; PRT; 15 AA.
ID Q40563;
AC Q40563;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RC MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565 (1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON TER 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
Db 4 QPLP 7

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RESULT 9
Q9PRU6 PRELIMINARY; PRT; 16 AA.
AC Q9PRU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO
DE (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
RA Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of
RT p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1480 MW; CAB880A931F8873F CRC64;

Query Match 26.7%; Score 4; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQP 7
DB 13 PPQP 16

RESULT 10
Q9PRU7 PRELIMINARY; PRT; 17 AA.
AC Q9PRU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-Crk in VIVO
DE (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
RA Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of
RT p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 26.7%; Score 4; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQP 7
DB 13 PPQP 16

RESULT 11
Q84129 PRELIMINARY; PRT; 18 AA.
AC Q84129;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
DE 8), COOH terminus of NS1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FEBEF CRC64;

Query Match 26.7%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
DB 12 PLPP 15

RESULT 12
Q9REVI PRELIMINARY; PRT; 19 AA.
AC Q9REVI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Integrase (Fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phyloplane bacteria in Michigan apple orchards.";
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL; AF157798; AAD47998.1; -.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
DB 7 PLPP 10

RESULT 13
Q46499 PRELIMINARY; PRT; 20 AA.
AC Q46499;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)

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DE Periplasmic (Fragment).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49192; AAA91808.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D36C22999B CRC64;

Query Match 26.7%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLP 8
DB 10 PQLP 13

RESULT 14
Q9UCA8 PRELIMINARY; PRT; 20 AA.
ID Q9UCA8
AC Q9UCA8
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94161713; PubMed=8117260;
RA Akcogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-kDa major secreted protein from human
RT bladder carcinoma cells."
RL Biochem. Biophys. Res. Commun. 198;1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0A8E8 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
DB 16 PLPP 19

RESULT 15
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8
AC Q9S8A8
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RA Rocher A., Calero M., Soriano F., Mendez E.;

RT "Identification of major rye secalins as coeliac immunoreactive
RT proteins";
RL Biochim. Biophys. Acta 1295:13-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098BB5C80 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
DB 16 QPLP 19

RESULT 16
Q9PRN3 PRELIMINARY; PRT; 20 AA.
ID Q9PRN3
AC Q9PRN3
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Melanotropin MSH-B.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Anemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands."
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 20 AA; 2403 MW; AC4DAD67CC69AB0D CRC64;

Query Match 26.7%; Score 4; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLP 9
DB 17 QPLP 20

RESULT 17
P83157 PRELIMINARY; PRT; 9 AA.
ID P83157
AC P83157
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=23412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD MN; PARTIAL.
DR Oxidoreductase; Iron; Metal-binding.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;
```

Query Match 20.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 ||||  
 DB 6 PLP 8

## RESULT 18

Q9UCS8 PRELIMINARY; PRT; 9 AA.  
 AC Q9UCS8;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE Apolipoprotein A-I (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92075698; PubMed=1742316;  
 RA Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metsä J.,  
 RA Murphy B., Walker I.D.;  
 RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40  
 RT protein of human blood are different proteins which both bind to  
 RT apolipoprotein A-I";  
 RL Biochim. Biophys. Acta 1086:255-260(1991).  
 FT NON\_TER 1  
 FT NON\_TER 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 981 MW; 7FE3775A6C7776B CRC64;

Query Match 20.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
 ||||  
 DB 3 PPQ 5

## RESULT 19

Q9TWV0 PRELIMINARY; PRT; 9 AA.  
 AC Q9TWV0;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE Antho-RPAMIDE-NEUROPEPTIDE.  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nyantharia; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93126143; PubMed=1480510;  
 RA Carstensen K., Rinshart K.L., McFarlane I.D., Gimmelikhuijzen C.J.;  
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPAMIDE),  
 RT an N-terminally protected, biologically active neuropeptide from sea  
 RT anemones.";  
 RL Peptides 13:851-857(1992).  
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
 ||||  
 DB 1 LPP 3

## RESULT 20

Q9S8J8 PRELIMINARY; PRT; 9 AA.  
 AC Q9S8J8;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE OryzATENSIN=BIODACTIVE peptide.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriocaulaceae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95102521; PubMed=7804141;  
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;  
 RT "Isolation and characterization of oryzatensin: a novel bioactive  
 RT peptide with ileum-contracting and immunomodulating activities derived  
 RT from rice albumin.";  
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).  
 DR Gramene; Q9S8J8;  
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 20.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 ||||  
 DB 6 PLP 8

## RESULT 21

Q935G1 PRELIMINARY; PRT; 9 AA.  
 AC Q935G1;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DE Putative membrane protein (Fragment).  
 GN HCM1.01C.  
 OS Salmonella typhi.  
 OC Plasmid pHCM1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatnia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL513383; CAD09867.1; -  
 KW Plasmid; Complete proteome.  
 FT NON\_TER 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 904 MW; 5FCDCT7776D86767 CRC64;

Query Match 20.0%; Score 3; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5

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Db          ||||
           5 QPP 7

RESULT 22
Q9R5T2      PRELIMINARY;      PRT;      10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]_TaxID=436;
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match          20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 LPP 10
           ||||
Db          3 LPP 5

RESULT 23
Q14096      PRELIMINARY;      PRT;      10 AA.
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308828;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
RT cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1;
SQ SEQUENCE 10 AA; 885 MW; 4181BD9D87DC77767 CRC64;

Query Match          20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 LPP 10
           ||||
Db          3 LPP 5

RESULT 24
Q9QVF7      PRELIMINARY;      PRT;      10 AA.
AC Q9QVF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]_TaxID=10118;
RP SEQUENCE.
RX MEDLINE=92135065; PubMed=1777418;
RA Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Yasuda T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1100 MW; 94E681B767376E1 CRC64;

Query Match          20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 LPP 9
           ||||
Db          5 LPP 7

RESULT 25
Q8VHM9      PRELIMINARY;      PRT;      10 AA.
AC Q8VHM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interferon receptor 2a' (Fragment).
GN IFNAR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The organization, transcriptional regulation and chromosomal
RT localization of the locus encoding the gene for the murine type I
RT interferon receptor, Ifnar2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440786; AAL40944.1;
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match          20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 LPP 10
           ||||
Db          1 LPP 3

RESULT 26
Q8JV78      PRELIMINARY;      PRT;      10 AA.
ID Q8JV78

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AC Q8JV78;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USAL;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Garones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303946; AAM97796.1; -;  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;  
 Query Match 20.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPP 10  
 Db ||||  
 7 LPP 9  
 RESULT 27  
 Q90ZV8 PRELIMINARY; PRT; 10 AA.  
 ID Q90ZV8  
 AC Q90ZV8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Adenylate kinase (Fragment).  
 OS Psittacus erithacus (grey parrot).  
 OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.  
 OX NCBI\_TaxID=57247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shapiro L.H., Dumbacher J.P.;  
 RT "Adenylate kinase intron 5: a new nuclear locus for avian  
 RT systematics.";  
 RL Auk 118:248-255(2001).  
 DR EMBL; AF307895; AAK43534.1; -;  
 KW Kinase.  
 FT NON TER 1 1  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;  
 Query Match 20.0%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PPT 11  
 Db ||||  
 3 PPT 5  
 RESULT 28  
 Q47569 PRELIMINARY; PRT; 11 AA.  
 ID Q47569  
 AC Q47569;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE Hypothetical 1.3 kDa protein (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=94162733; PubMed=7764507;  
 RA Yanada M., Yanai S., Talkuder A.;  
 RT "Analysis of products of the Escherichia coli genomic genes and  
 RT regulation of their expressions: an applicable procedure for genomic  
 RT analysis of other microorganisms.";  
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).  
 DR EMBL; D21156; BAA04692.1; -;  
 KW Hypothetical protein.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1322 MW; C0B8E40E37672732 CRC64;  
 Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHQ 3  
 Db ||||  
 1 MHQ 3  
 RESULT 29  
 O60761 PRELIMINARY; PRT; 11 AA.  
 ID O60761  
 AC O60761;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NPT-1 protease (Fragment).  
 GN NPT-1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98207719; PubMed=9545579;  
 RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,  
 RA Tatsumi S., Morita K., Takeda E.;  
 RT "Characterization of the 5' flanking region of the human NPT-1  
 RT Na+/phosphate cotransporter gene.";  
 RL Biochim. Biophys. Acta 1396:267-272(1998).  
 DR EMBL; D83236; BAA25645.1; -;  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;  
 Query Match 20.0%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPP 10  
 Db ||||  
 7 LPP 9  
 RESULT 30  
 Q9UCR1 PRELIMINARY; PRT; 11 AA.  
 ID Q9UCR1  
 AC Q9UCR1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE AUTOTAXIN (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

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RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1171 MW; 273615AA0437737 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8
Db 3 QPL 5

RESULT 31
Q9GL48
ID Q9GL48 PRELIMINARY; PRT; 11 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Souillou J.-P., Chazreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAG33870.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match      20.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPT 11
Db 2 PPT 4

RESULT 32
Q9S8Z9
ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eursoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1

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FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABC77772D1 CRC64;

Query Match      20.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
Db 3 PTV 5

RESULT 33
Q8UUP1
ID Q8UUP1 PRELIMINARY; PRT; 11 AA.
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus
RT laevis.";
RL Thesis (2001), Department of Genetica e Biologia Molecolare,
RL University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
Db 9 QPP 11

RESULT 34
Q9P116
ID Q9P116 PRELIMINARY; PRT; 12 AA.
AC Q9P116;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Apolipoprotein E receptor 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Korschneck I., Gharehbaghi-Schnell E., Lang I., Binder R.B.;
RT "Expression of Apolipoprotein E Receptor 2 in atherosclerosis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129170; AAF66440.1; -.
KW Lipoprotein; Receptor.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1467 MW; 4E8935410404877 CRC64;

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Query Match 20.0%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPT 11  
 |||  
 Db 1 PPT 3

RESULT 35  
 Q9NTQ2 PRELIMINARY; PRT; 12 AA.  
 AC Q9NTQ2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE D40219.1 (Mu opiate receptor (MOR1)) (Fragment).  
 GN D40219.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Phillimore B.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL132774; CAB76846.1; -.  
 KW Receptor.  
 FT NON TER 1 1  
 SQ SEQUENCE 12 AA; 1296 MW; 68479422BDABLDDB CRC64;

Query Match 20.0%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 |||  
 Db 10 PLP 12

RESULT 36  
 Q9TRU1 PRELIMINARY; PRT; 12 AA.  
 AC Q9TRU1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OX Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92132498; PubMed=1734497;  
 RA Vaiboy O.P., Sletten K., Husby G., Nordstoga K.;  
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils  
 of bovine kidney.";  
 RL Scand. J. Immunol. 35:63-69(1992).  
 FT NON TER 1 1  
 SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AA4 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY \* 10 PTV 12  
 |||  
 Db 7 PTV 9

RESULT 37  
 P82329 PRELIMINARY; PRT; 12 AA.  
 AC P82329;  
 DT 01-JUN-2000 (TREMBLrel. 14, Created)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT111) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 RA Adamska I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 targeting analysis of luminal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000)  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.  
 KW Chloroplast; Thylakoid membrane.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
 |||  
 Db 9 LPP 11

RESULT 38  
 Q9UEE2 PRELIMINARY; PRT; 13 AA.  
 AC Q9UEE2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ERGB transcription factor (Fragment).  
 GN FL11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;  
 RT "Molecular analysis on the breakpoint region of a t(11;22)  
 translocation in Ewing's sarcoma.";  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB012625; BAA32806.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7  
 |||  
 Db 4 POP 6

RESULT 39

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Q14890
ID Q14890 PRELIMINARY; PRT; 13 AA.
AC Q14890;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mucin (Fragment).
GN MUC5AC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=tracheobronchial mucosa;
RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,
RA Zouitina-Gallegue S., Pigny P., Degand P., Aubert J., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for l1p15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10
DB 6 LPP 8

RESULT 40
Q9UNV6 PRELIMINARY; PRT; 13 AA.
AC Q9UNV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN INPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF085628; AAD22141.1; -.
DR EMBL; AF085627; AAD22141.1; JOINED.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 PTV 12
DB 9 PTV 11

RESULT 41
Q9TRW6 PRELIMINARY; PRT; 13 AA.
ID Q9TRW6;
AC Q9TRW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide P3 (Fragment).
OS Bos taurus (Sovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 6 PTV 8

RESULT 42
Q42373 PRELIMINARY; PRT; 13 AA.
ID Q42373;
AC Q42373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin class I (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226014; PubMed=3371564;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON TER 13
FT NON TER 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 11 TVM 13

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RESULT 43
O88176 01-MAY-2000 (TrEMBLrel. 13, Created)
ID O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9882442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RL of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLP 9
Db 3 PLP 5

RESULT 44
O67604 01-NOV-1996 (TrEMBLrel. 01, Created)
ID O67604 PRELIMINARY; PRT; 13 AA.
AC O67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BCI.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
RT del Fuerte, Sinaloa, Mexico.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 OPP 5
Db 7 QPP 9

RESULT 45
O972K7 01-AUG-1998 (TrEMBLrel. 07, Created)
ID O972K7 PRELIMINARY; PRT; 14 AA.
AC O972K7;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 18-kDa chloroplast DNA-binding iron-sulfur protein (Fragment).
OS Chlamydomonas reinhardtii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RC MEDLINE=92404720; PubMed=2562513;
RA Wu M., Nie Z.Q., Yang J.;
RT "The 18-kD protein that binds to the chloroplast DNA replicative
RT origin is an iron-sulfur protein related to a subunit of NADH
RT dehydrogenase.";
RL Plant Cell 1:551-557(1989).
SQ SEQUENCE 14 AA; 1698 MW; 7799E02B12C200CB CRC64;

Query Match 20.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 MFP 15
Db 1 MFP 3

RESULT 46
P82326 PRELIMINARY; PRT; 14 AA.
ID P82326
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 5 LPP 7

RESULT 47
O70599 PRELIMINARY; PRT; 14 AA.
ID O70599
AC O70599;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.
DR EMBL; AF006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12
DB 7 PTV 9

RESULT 48
Q9KE26 PRELIMINARY; PRT; 14 AA.
AC Q9KE26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BH1032.
GN BH1032.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AP001510; BAB04751.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 14 AA; 1697 MW; A9A302145A7AE8A6 CRC64;

Query Match 20.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 8 TVM 10

RESULT 49
Q9R5D5 PRELIMINARY; PRT; 15 AA.
AC Q9R5D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE POLY (3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein
DE (Fragment).
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochrochromatium.
OX NCBI_TaxID=1049;

[1]
RN SEQUENCE.
RX MEDLINE=93146381; PubMed=1490603;
RA Liebergessel M., Schmidt B., Steinbuechel A.;
RT "Isolation and identification of granule-associated proteins relevant
RT for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT D.";
RL FEMS Microbiol. Lett. 78:227-232 (1992).
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65BB8E CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MFP 15
DB 1 MFP 3

RESULT 50
Q9TR62 PRELIMINARY; PRT; 15 AA.
AC Q9TR62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Cryotolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=95329112; PubMed=7605356;
RA Mezdoor H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178 (1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115BB7351F0ABC CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TVM 13
DB 9 TVM 11

RESULT 51
Q9QV25 PRELIMINARY; PRT; 15 AA.
AC Q9QV25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sigma receptor cyclophilin-like component (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=94322640; PubMed=8046989;
RA Schuster D.I., Ehrlich G.K., Murphy R.B.;
RT "Purification and partial amino acid sequence of a 28 kDa cyclophilin-
RT like component of the rat liver sigma receptor.";
RL Life Sci. 55:151-151 (1994).
SQ SEQUENCE 15 AA; 1622 MW; 95E384B4EC8D14D4 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 PTV 12  
 Db |||  
 3 PTV 5

RESULT 52  
 Q69353  
 ID Q69353 PRELIMINARY; PRT; 15 AA.  
 AC Q69353;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HSV-2 (333) N terminus of 17.8 kda protein gene (0.642 mu)  
 DE (Fragment).  
 OS Herpes simplex virus (type 2).  
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10310;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=85033906; PubMed=6092683;  
 RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,  
 RA Wagner E.K.;  
 RT "Herpes simplex virus types 1 and 2 homology in the region between  
 RT 0.58 and 0.68 map units";  
 RT J. Virol. 52:615-623(1984).  
 RL EMBL; K03360; AAA45840.1; -.  
 DR NON TER 15  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match 20.0%; Score 3; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPL 8  
 Db |||  
 11 QPL 13

RESULT 53  
 Q9R5K7  
 ID Q9R5K7 PRELIMINARY; PRT; 16 AA.  
 AC Q9R5K7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE 23.4-kda chitinase (Fragment).  
 OS Streptomyces olivaceoviridis (Streptomyces corchorusii).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1921;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=92276319; PubMed=1592803;  
 RX Romaguera A., Menge U., Breves R., Diekmann H.;  
 RA "Chitinases of Streptomyces olivaceoviridis and significance of  
 RT processing for multiplicity";  
 RL J. Bacteriol. 174:3450-3454(1992).  
 FT NON TER 1  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 2014 MW; 0F732A24DC14CE01 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MFP 15  
 Db |||  
 6 MFP 8

RESULT 54

Q9NNZ2  
 ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.  
 AC Q9NNZ2;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Integrin alpha-2 subunit (Fragment).  
 GN ITGA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98421383; PubMed=9746778;  
 RA Kitzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,  
 RA Kunicki T.J.;  
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles  
 RT that are associated with differences in platelet alpha2 beta1  
 RT density";  
 RL Blood 92:2382-2388(1998).  
 DR EMBL; AF062039; AAF77577.1; -.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 Db |||  
 10 PLP 12

RESULT 55  
 Q9UCH1  
 ID Q9UCH1 PRELIMINARY; PRT; 16 AA.  
 AC Q9UCH1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE LIPOAMIDASE (EC 3.1.1.13) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=93228634; PubMed=8471055;  
 RX Hui D.Y., Hayakawa K., Oizumi J.;  
 RA "Lipoamidase activity in normal and mutagenized pancreatic cholesterol  
 RT esterase (bile salt-stimulated lipase).";  
 RL Biochem. J. 291:65-69(1993).  
 SQ SEQUENCE 16 AA; 1844 MW; 147321FA60374B3C CRC64;

Query Match 20.0%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POP 7  
 Db |||  
 6 POP 8

RESULT 56  
 O18378  
 ID O18378 PRELIMINARY; PRT; 16 AA.  
 AC O18378;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Hypothetical 1.5 kda protein in ANON-37CS 5'REGION (ORF3).  
 GN ANON-37CC.

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88038375; PubMed=3478553;  
 RA Eveleth D.D., Marsh J.L.;  
 RT "Overlapping transcription units in Drosophila: sequence and structure  
 of the Cs gene.";  
 RL Mol. Gen. Genet. 209:290-298(1987).  
 DR EMBL; X05991; CAA29407.1; -.  
 DR FlyBase; FBgn0026744; anon-37Cc.  
 KW Hydrothermal protein.  
 SQ SEQUENCE 16 AA; 1543 MW; F5F881ED5A799277 CRC64;  
 Query Match 20.0%; Score 3; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PTV 12  
 Db 13 PTV 15  
 RESULT 57  
 QSTR1 PRELIMINARY; PRT; 16 AA.  
 ID Q9TRR1  
 AC Q9TRR1  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Fibronectin 47 kDa fragment (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92283375; PubMed=1597256;  
 RA Lesot H., Fausser J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,  
 RA Ruch J.V.;  
 RT "The carboxy-terminal extension of the collagen binding domain of  
 fibronectin mediates interaction with a 165 kDa membrane protein  
 involved in odontoblast differentiation.";  
 RT Differentiation 49:109-118(1992).  
 RL NON\_TER 1  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1764 MW; B196CAAC53F5739 CRC64;  
 Query Match 20.0%; Score 3; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 POP 7  
 Db 2 POP 4  
 RESULT 58  
 P92732 PRELIMINARY; PRT; 16 AA.  
 ID P92732  
 AC P92732  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NADH dehydrogenase subunit II (Fragment).  
 GN ND2.  
 OS Fejervarya limnocharis (Boie's wart frog).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;

OC Fejervarya.  
 OX NCBI\_TaxID=110108;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153826; PubMed=9000757;  
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;  
 RT "Two novel gene orders and the role of light-strand replication in  
 rearrangement of the vertebrate mitochondrial genome.";  
 RL Mol. Biol. Evol. 14:91-104(1997).  
 DR EMBL; U71324; AAB48287.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1860 MW; DD1C1017F8B19DEE CRC64;  
 Query Match 20.0%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 MFP 15  
 Db 5 MFP 7  
 RESULT 59  
 Q9JHB6 PRELIMINARY; PRT; 16 AA.  
 ID Q9JHB6  
 AC Q9JHB6  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Meprin 1 beta (Fragment).  
 GN MEPIB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96147211; PubMed=8567689;  
 RA Dietrich J.M., Jiang W., Bond J.S.;  
 RT "A novel meprin beta mRNA in mouse embryonal and human colon  
 carcinoma cells.";  
 RL J. Biol. Chem. 271:2271-2278(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Jiang W., Kumar J.M., Bond J.S.;  
 RT "Structure of the mouse metalloprotease meprin beta gene (Mep1b):  
 alternative splicing in cancer cells.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF160982; AAF80401.1; -.  
 DR MGD; MGI:96964; Mep1b.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1979 MW; EB9785A3F6189622 CRC64;  
 Query Match 20.0%; Score 3; DB 11; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 HQP 4  
 Db 5 HQP 7  
 RESULT 60  
 Q8VME2 PRELIMINARY; PRT; 17 AA.  
 ID Q8VME2  
 AC Q8VME2  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE PaC protein (Fragment).  
 GN PARC.  
 OS Pseudomonas putida.

01-DEC-2001 (EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (EMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)  
DE NHP2-like protein (Fragment) .  
DE Homo sapiens (Human) .  
OS Homo sapiens (Human) .  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N. A.  
RP Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;  
RA "Characterization of TPA-responsive genes in U937 cells using ordered  
RT differential display PCR."  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF401217; AL02173.1; -.  
DR NON TBR 1 1  
SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEFCRC64;  
FO

Query Match 20.0%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 Db 14 PLP 16

## RESULT 65

Q14001 PRELIMINARY; PRT; 17 AA.  
 ID Q14001  
 AC Q14001;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Cyclic nucleotide phosphodiesterase (Fragment).  
 GN CGIPDEL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9709687; PubMed=8921398;  
 RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;  
 RT "Molecular cloning and chromosomal assignment of the human homologue  
 of the rat cAMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved  
 in fat metabolism located at 11p15.1.";  
 RL Genomics 37:211-218(1996).  
 DR EMBL; X95522; CAA64776.1; .  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
 Db 15 QPP 17

## RESULT 66

Q9TRU8 PRELIMINARY; PRT; 17 AA.  
 ID Q9TRU8  
 AC Q9TRU8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell  
 growth (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92115728; PubMed=1370585;  
 RA Ferrara N., Winer J., Hensel W.J.;  
 RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial  
 cell growth: identification as leukemia inhibitory factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLP 9  
 Db 2 PLP 4

## RESULT 67

P83061 PRELIMINARY; PRT; 17 AA.  
 ID P83061  
 AC P83061;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans  
 isomerase) (PPIase) (EC 5.2.1.8) (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE, AND SUBCELLULAR LOCATION.  
 RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,  
 R Kieselbach T.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY  
 SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.  
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 DR InterPro; IPR001179; FKBP\_PPIase.  
 KW Isomerase; Rotamase; Chloroplast.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPP 10  
 Db 3 LPP 5

## RESULT 68

Q8B4C4 PRELIMINARY; PRT; 17 AA.  
 ID Q8B4C4  
 AC Q8B4C4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Precore.  
 OS Hepatitis B virus.  
 OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vaishali C., Acharya S.K., Panda S.K.;  
 RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic  
 sequence of HBV from nine patients with seronegative viral  
 hepatitis.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY161158; AAO12630.1; .  
 SQ SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802588 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PTV 12  
 Db 15 PTV 17

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RESULT 69
Q9R5U2 ID Q9R5U2 PRELIMINARY; PRT; 18 AA.
DE 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA ligase-E3 (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=91358327; PubMed=1885526;
RA Altschmidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp.";
RL J. Bacteriol. 173:5494-5501 (1991).
RN [1]
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 12 LPP 14

RESULT 70
Q9R5F9 ID Q9R5F9 PRELIMINARY; PRT; 18 AA.
DE 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Arsenite oxidase, AOI (Fragment).
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054722; PubMed=1331097;
RA Anderson G.L., Williams J., Hille R.;
RT "The purification and characterization of arsenite oxidase from
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase.";
RL J. Biol. Chem. 267:23674-23682 (1992).
RN [1]
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPP 10
Db 9 LPP 11

RESULT 71
Q9R4V9 ID Q9R4V9 PRELIMINARY; PRT; 18 AA.
DE 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 14, Last annotation update)

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DE 10 kDa heat shock- and alkaline pH-induced protein (Fragment).
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE.
RX MEDLINE=95012609; PubMed=7927682;
RA Wu Y.L., Lee L.H., Rollins D.M., Ching W.M.;
RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni:
RT characterization and immunological properties.";
RL Infect. Immun. 62:4256-4260 (1994).
SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7BB4DA76C4 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 4 QPL 6

RESULT 72
Q9EYW5 ID Q9EYW5 PRELIMINARY; PRT; 18 AA.
DE 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE RepB.
GN REPB.
OS Erwinia stewartii.
OG Plasmid pSW800.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=66271;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu C.-Y., Liu S.-T.;
RT "Erwinia stewartii plasmid pSW800 basic replicon, repA and repB
RT genes.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF310258; AAG47776.1; -.
KW Plasmid.
SQ SEQUENCE 18 AA; 1952 MW; C8FD2873F9CAC66C CRC64;

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPL 8
Db 6 QPL 8

RESULT 73
Q9R4C6 ID Q9R4C6 PRELIMINARY; PRT; 18 AA.
DE 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Protocatechuate 3,4-dioxygenase type I alpha subunit (EC 1.13.11.3)
DE (Fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE.
RX MEDLINE=96337865; PubMed=8772173;
RA Hammer A., Stolz A., Knackmuss H.;

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RT "Purification and characterization of a novel type of protocatechuate  
RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";  
RL Arch. Microbiol. 166:92-100(1996).  
SQ SEQUENCE 18 AA; 2152 MW; BFC56CA8D4376D84 CRC64;  
Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 QPL 8  
Db 2 QPL 4  
RESULT 74  
Q9UCG7 PRELIMINARY; PRT; 18 AA.  
AC Q9UCG7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Urinary gonadotrophin peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93229246; PubMed=8471426;  
RA Kardana A., Bagshaw K.D., Coles B., Read D., Taylor M.;  
RT "Characterisation of UGP and its relationship with beta-core  
fragment.";  
RL Br. J. Cancer 67:686-692(1993).  
DR HSP; P10153; IHI2.  
SQ SEQUENCE 18 AA; 2214 MW; BB0A2F0B8E933109 CRC64;  
Query Match 20.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPQ 6  
Db 2 PPQ 4  
RESULT 75  
Q96F98 PRELIMINARY; PRT; 18 AA.  
AC Q96F98;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC011455; AAH11455.1; --  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 18 AA; 2114 MW; 3A6C3E2BF620B9CD CRC64;  
Query Match 20.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 PPT 11  
Db 11

Db 9 PPT 11  
Search completed: November 25, 2003, 19:34:16  
Job time : 28.1686 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 38.2849 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-34  
Perfect score: 15  
Sequence: 1 MHQPPPLPTVWFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Colostrin deriv
2	15	100.0	15	22	Colostrin peptid
3	15	100.0	15	22	Colostrin peptid
4	15	100.0	15	22	Ewe colostrin pe
5	15	100.0	15	22	Colostrin consti
6	15	100.0	15	23	Colostrin consti
7	15	100.0	15	23	Colostrin consti
8	10	66.7	10	22	Neural cell regula
9	10	66.7	10	22	Colostrin deriv

10	66.7	10	22	ABE72555	Colostrin peptid
11	66.7	10	23	ABE20252	Colostrin consti
12	66.7	10	23	AAW51059	Colostrin consti
13	66.7	10	23	AAO14601	Neural cell regula
14	60.0	11	22	AAE07192	Colostrin peptid
15	60.0	12	22	AAE07202	Modified colostrin
16	60.0	11	22	ABE59333	Ewe colostrin pe
17	60.0	11	23	ABG95549	Human novel secret
18	40.0	15	18	AAW39006	Peptide resembling
19	40.0	15	23	ABG72660	Human K-ras 10.67
20	40.0	16	18	AAW25442	Grb2 N-terminal SH
21	33.3	7	20	AAW41630	Mammalian ion chan
22	33.3	7	21	ABE17247	SH3 antagonist pep
23	33.3	7	22	ABE72269	Colostrin deriv
24	33.3	7	22	ABE72522	Colostrin peptid
25	33.3	7	22	ABE72554	Colostrin peptid
26	33.3	7	22	AAE59332	Ewe colostrin pe
27	33.3	7	23	AAE20251	Colostrin consti
28	33.3	7	23	AAW51058	Colostrin consti
29	33.3	7	23	AAO14600	Neural cell regula
30	33.3	7	23	ABE73240	Src homology3 (SH3)
31	33.3	8	22	AAW00293	Human protein frag
32	33.3	8	22	AAW00294	Human protein frag
33	33.3	9	22	AAW4971	Clone 1 scFv CDR L
34	33.3	9	24	ABR28252	Human cancer-relat
35	33.3	9	24	ABR28257	Human cancer-relat
36	33.3	10	24	ABR28346	Human cancer-relat
37	33.3	10	24	ABR28347	Human cancer-relat
38	33.3	12	22	AAW00291	Human protein frag
39	33.3	13	16	AAE93368	PI3K protein tyros
40	33.3	13	17	AAW11112	Src SH3 domain-bin
41	33.3	13	21	ABE44382	Human secreted pro
42	33.3	13	23	AAE21396	Escherichia coli 3
43	33.3	13	24	ABP81159	Human TPO peptid
44	33.3	13	24	ABP81160	Human TPO peptid
45	33.3	13	24	ABP81161	Human TPO peptid
46	33.3	13	24	ABP81162	Human TPO peptid
47	33.3	13	24	ABP81163	Human TPO peptid
48	33.3	14	20	AAW03679	Amino acid sequenc
49	33.3	14	22	AAW00448	Human protein frag
50	33.3	14	22	AAW46171	Bacille Calmette-G
51	33.3	14	22	AAW49070	BCG T-cell epitope
52	33.3	15	18	AAW38958	Peptide resembling
53	33.3	15	18	AAW39036	Peptide resembling
54	33.3	15	18	AAW38976	Peptide resembling
55	33.3	15	22	AAW78855	Growth hormone fam
56	33.3	15	24	ABR38292	Human cancer-relat
57	33.3	15	24	ABR38293	Human cancer-relat
58	33.3	15	24	ABR38294	Human cancer-relat
59	33.3	15	24	ABR38350	Human cancer-relat
60	33.3	15	24	ABR38390	Human cancer-relat
61	33.3	15	24	ABR38391	Human cancer-relat
62	33.3	15	24	ABR38392	Human cancer-relat
63	33.3	15	24	ABR38414	Human cancer-relat
64	33.3	15	24	ABR38502	Human cancer-relat
65	33.3	16	18	AAW5427	Yes SH3 domain bin
66	33.3	16	18	AAW25376	Src SH3 domain bin
67	33.3	16	18	AAW25380	Src SH3 domain bin
68	33.3	16	24	ABP82678	G protein-coupled
69	33.3	17	21	AAW39277	Gene 31 human secr
70	33.3	18	22	ABE57154	Human liver peptid
71	33.3	18	22	ABE41714	Peptide #9220 enco
72	33.3	18	22	AAW62588	Human brain expres
73	33.3	18	22	AAW75398	Human bone marrow
74	33.3	18	22	AAW35511	Peptide #9548 enco
75	33.3	18	22	AAE03955	Human gene 10 enco
76	33.3	19	20	AAW31181	Ubiquitin fusion p
77	33.3	19	20	AAW31165	Ubiquitin fusion p
78	33.3	19	22	AAW71936	MT peptid. Unide
79	33.3	20	17	AAW16997	Src SH3 domain-bin
80	33.3	20	17	AAW99513	T-cell epitope use
81	33.3	20	18	AAW35439	T-cell stimulatory
82	33.3	20	18	AAW12237	Heatshock protein

83 5 33.3 20 19 AAW60693 Mycobacteria heat  
 84 5 33.3 20 23 ABB79926 Mycobacterium heat  
 85 4 26.7 4 16 AAR80055 Peptidase substrat  
 86 4 26.7 5 21 AAY45075 Rat amelogenin N-t  
 87 4 26.7 6 13 AAR28486 Casoxin D-like vas  
 88 4 26.7 6 16 AAR83532 Zif268 zinc finger  
 89 4 26.7 6 19 AAW31463 Transcriptional ac  
 90 4 26.7 6 19 AAW31465 Transcriptional ac  
 91 4 26.7 6 20 AAW84430 HIV-1 nucleic acid  
 92 4 26.7 7 10 AAP90659 New antihypertensi  
 93 4 26.7 7 15 AAR60997 Fragment of the 3B  
 94 4 26.7 7 16 AAR73883 Rubella virus glyc  
 95 4 26.7 7 17 AAW11128 SRC SH3 domain-bin  
 96 4 26.7 7 17 AAW17010 SRC SH3 domain-bin  
 97 4 26.7 7 17 AAW07013 Synthetic peptide  
 98 4 26.7 7 18 AAW25486 SH3 domain binding  
 99 4 26.7 7 18 AAW10774 Ferritin motif #17  
 100 4 26.7 7 19 AAW79781 Proline-rich pepti

## ALIGNMENTS

RESULT 1  
 AAB72279 standard; peptide; 15 AA.

AC AAB72279;  
 DT 14-MAY-2001 (first entry)  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 34.

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

PR 17-AUG-1999; 99US-0149311.

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGG-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

PS Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHQPPQPLPPTVMFP 15  
 |||||  
 DB 1 MHQPPQPLPPTVMFP 15

## RESULT 2

AAB72531  
 ID AAB72531 standard; Peptide; 15 AA.

AC AAB72531;

DT 09-MAY-2001 (first entry)

DE Colostrinin peptide #32.

XX Dermatological; oxidative stress regulator; colostrinin.

OS Unidentified.

XX WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22665.

PR 17-AUG-1999; 99US-0149310.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -

PS Claim 6; Page 26; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.4e-09;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPLPPTVMFP 15

|||||

DB 1 MHQPPQPLPPTVMFP 15

## RESULT 3

AAB72563  
 ID AAB72563 standard; Peptide; 15 AA.

AC AAB72563;

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #32.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 22; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX Sequence 15 AA;  
 SQ

Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHQPPQPLPPTVMFP 15  
 |||||  
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 4  
 AAB59334  
 ID AAB59334 standard; Peptide; 15 AA.  
 XX  
 AC AAB59334;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment C-9.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHQPPQPLPPTVMFP 15  
 |||||  
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 5  
 AAE20261  
 ID AAE20261 standard; peptide; 15 AA.  
 XX  
 AC AAE20261;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #32.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulneryary.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15 /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22776.  
 XX  
 PR 17-AUG-2000; 2000WO-US22776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GU, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2002-269151/31.  
 XX  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 26; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQPPQPLPPTVMFP 15  
 |||||  
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 6  
 AAM51066  
 ID AAM51066 standard; Peptide; 15 AA.

XX AC AAM51066;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 159-173).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 15  
 FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 159-173. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQPPQPLPPTVMFP 15  
 |||||  
 Db 1 MHQPPQPLPPTVMFP 15

RESULT 7

AAO14610

ID AAO14610 standard; peptide; 15 AA.

XX AC AAO14610;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 32.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 15  
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPPQPLPPTVMFP 15  
DB 1 MHQPPQPLPPTVMFP 15

#### RESULT 8

AAB72270  
ID AAB72270 standard; peptide; 10 AA.

XX  
AC AAB72270;

DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 25.

XX Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX  
PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

XX  
PR 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -

PS Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX Sequence 10 AA;

Query Match 66.7%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00048;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15  
DB 1 QPLPPTVMFP 10

#### RESULT 9

AAB72523  
ID AAB72523 standard; Peptide; 10 AA.

XX  
AC AAB72523;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #24.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX  
PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22665.

PR 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -

PS Claim 6; Page 26; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.

XX Sequence 10 AA;

Query Match 66.7%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00048;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPPTVMFP 15  
DB 1 QPLPPTVMFP 10

#### RESULT 10

AAB72555  
ID AAB72555 standard; Peptide; 10 AA.

XX  
AC AAB72555;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #24.

XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.

XX Unidentified.

XX WO200112651-A2.

XX  
PD 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22774.  
 XX 17-AUG-1999; 99US-0149633.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Boldogh I;  
 XX WPI; 2001-226545/23.  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 XX regulator, for promoting neural cell differentiation and treating  
 XX damaged neural cells in a patient -  
 XX Claim 6; Page 21; 35pp; English.  
 XX The present invention relates to a method for promoting neural cell  
 XX differentiation and treating damaged neural cells, using colostrinin and  
 XX colostrinin constituent peptides (e.g. the present peptide) as a neural  
 XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX SQ Sequence 10 AA;  
 Query Match 66.7%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00048;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QPLPPTVMFP 15  
 DB 1 QPLPPTVMFP 10  
 |||||  
 RESULT 11  
 AAE20252  
 ID AAE20252 standard; peptide; 10 AA.  
 XX AC AAE20252;  
 XX 18-JUN-2002 (first entry)  
 XX Colostrinin constituent peptide #24.  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 XX transplantation; implantation; dermatological; vulnary.  
 XX Unidentified.  
 XX OS  
 XX Key Location/Qualifiers  
 XX Modified-site 10  
 XX /note= "Optionally C-terminal amide"  
 XX FT  
 XX WO200213850-A1.  
 XX 21-FEB-2002.  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2002-269151/31.  
 XX Composition useful for the modulation of blood cell proliferation in a  
 XX patient comprises a blood cell regulator selected from colostrinin, its  
 XX constituent peptide and/or analog -  
 XX Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell  
 XX regulator selected from colostrinin, its constituent peptide and/or  
 XX analogue. The invention is used for modulating the oxidative stress  
 XX level in a cell e.g. mammalian or human cell present in a cell culture,  
 XX tissue, organ, or organism; or for treating oxidative damage to the skin  
 XX of a patient e.g. animal or human; to modulate oxidative stress during/  
 XX after a premature birth or normal birth, preventing/delaying aging in a  
 XX patient, enhancing wound healing, and the reduction of side effects of  
 XX cosmetic procedures. The method changes the level of an oxidising species  
 XX in the cell, such as decreases or prevents increase in the level of  
 XX damage to a biomolecule of the patient selected from DNA, protein and/or  
 XX lipid, compared to the same conditions when the oxidative stress  
 XX regulator is not present. The modulation of oxidative stress results in  
 XX enhanced repair, regeneration, and replacement of cells, tissues and  
 XX organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 XX external organs), as well as enhanced preservation of such organs for  
 XX transplantation, implantation, or scientific research. The present  
 XX sequence is a colostrinin constituent peptide.  
 XX SQ Sequence 10 AA;  
 Query Match 66.7%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00048;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QPLPPTVMFP 15  
 DB 1 QPLPPTVMFP 10  
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 RESULT 12  
 AAM51059  
 ID AAM51059 standard; Peptide; 10 AA.  
 XX AC AAM51059;  
 XX 30-MAY-2002 (first entry)  
 XX Colostrinin constituent peptide (casein amino acids 164-173).  
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
 XX blood cell regulator; cytokine inducer; beta-casein; human.  
 XX Homo sapiens.  
 XX OS  
 XX Key Location/Qualifiers  
 XX Modified-site 10  
 XX /note= "optional C-terminal amidation"  
 XX FT  
 XX WO200213849-A1.  
 XX 21-FEB-2002.  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2002-269150/31.  
 XX Modulation of blood cell proliferation in a patient involves use of  
 XX blood cell regulator selected from colostrinin, its constituent peptide  
 XX and/or analogue -  
 XX Claim 1; Page 34; 54pp; English.  
 XX The present sequence is that of a colostrinin constituent peptide  
 XX that is used as an immunological regulator and as a blood cell  
 XX CC

AA	SQ	Sequence	10 AA;
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**Qy**      6 QFLPPTVMEF 15  
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## RESULT 14

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Age	Sex	Height (cm)	Weight (kg)	Body mass index (kg/m <sup>2</sup> )	Waist circumference (cm)	Waist-hip ratio	Trunk circumference (cm)	Trunk-hip ratio	Neck circumference (cm)	Neck-hip ratio	Neck-trunk ratio
22	Male	175	75	24.2	95	0.85	105	0.81	35	0.33	0.41
22	Female	165	65	23.8	85	0.85	95	0.81	35	0.33	0.41

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CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 8 related to the invention.  
 CC Colostrinin peptide 8 corresponds to position 165-175 of beta-caesin.  
 XX  
 SQ Sequence 11 AA;

Query Match 60.0%; Score 9; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0054;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPTVMFP 15  
 |||||  
 Db 1 PLPPTVMFP 9

RESULT 15  
 AAE07202  
 ID AAE07202 standard; peptide; 12 AA.  
 AC AAE07202;

DT 06-NOV-2001 (first entry)

DE Modified colostrinin cyclic peptide #8.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1

FT /note= "N-terminal acetyl"; this residue forms a cyclic  
 FT linkage with Gln found at the C-terminal end"

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is modified colostrinin cyclic peptide #8 related to  
 CC the invention.

SQ Sequence 12 AA;

Query Match 60.0%; Score 9; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0058;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPTVMFP 15  
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 Db 2 PLPPTVMFP 10

RESULT 16

AA859333

ID AA859333 standard; Peptide; 11 AA.

XX AA859333;

XX 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment C-8.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO2000075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -

XX Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

SQ Sequence 11 AA;

Query Match 40.0%; Score 6; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 6 QPLPPT 11  
 Db |||||  
 1 QPLPPT 6

RESULT 17  
 ABG95549  
 ID ABG95549 standard; Peptide; 11 AA.  
 XX  
 AC ABG95549;  
 XX  
 DT 15-JAN-2003 (first entry)  
 XX  
 DE Human novel secreted protein gene 86 polypeptide #1.  
 XX  
 KW Human; secreted protein; autoimmune disease; chemotaxis;  
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;  
 KW nervous system disorders; Alzheimer's disease; infection;  
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
 KW epithelial cell proliferation; organ transplantation; food additive;  
 KW preservative; nutritional.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6420526-B1.  
 XX  
 PD 16-JUL-2002.  
 XX  
 PF 08-SEP-1998; 98US-0149476.  
 XX  
 PR 07-MAR-1997; 97US-038621P.  
 PR 07-MAR-1997; 97US-040161P.  
 PR 07-MAR-1997; 97US-040182P.  
 PR 07-MAR-1997; 97US-040183P.  
 PR 07-MAR-1997; 97US-040333P.  
 PR 07-MAR-1997; 97US-040334P.  
 PR 07-MAR-1997; 97US-040336P.  
 PR 07-MAR-1997; 97US-040626P.  
 PR 11-APR-1997; 97US-043311P.  
 PR 11-APR-1997; 97US-043312P.  
 PR 11-APR-1997; 97US-043313P.  
 PR 11-APR-1997; 97US-043314P.  
 PR 11-APR-1997; 97US-043315P.  
 PR 11-APR-1997; 97US-043568P.  
 PR 11-APR-1997; 97US-043569P.  
 PR 11-APR-1997; 97US-043576P.  
 PR 11-APR-1997; 97US-043578P.  
 PR 11-APR-1997; 97US-043580P.  
 PR 11-APR-1997; 97US-043659P.  
 PR 11-APR-1997; 97US-043670P.  
 PR 11-APR-1997; 97US-043671P.  
 PR 11-APR-1997; 97US-043672P.  
 PR 11-APR-1997; 97US-043674P.  
 PR 23-MAY-1997; 97US-043674P.  
 PR 23-MAY-1997; 97US-047500P.  
 PR 23-MAY-1997; 97US-047501P.  
 PR 23-MAY-1997; 97US-047502P.  
 PR 23-MAY-1997; 97US-047503P.  
 PR 23-MAY-1997; 97US-047581P.  
 PR 23-MAY-1997; 97US-047582P.  
 PR 23-MAY-1997; 97US-047583P.  
 PR 23-MAY-1997; 97US-047584P.  
 PR 23-MAY-1997; 97US-047585P.  
 PR 23-MAY-1997; 97US-047586P.  
 PR 23-MAY-1997; 97US-047587P.  
 PR 23-MAY-1997; 97US-047588P.  
 PR 23-MAY-1997; 97US-047589P.  
 PR 23-MAY-1997; 97US-047590P.  
 PR 23-MAY-1997; 97US-047592P.  
 PR 23-MAY-1997; 97US-047593P.

PR 23-MAY-1997; 97US-047594P.  
 PR 23-MAY-1997; 97US-047595P.  
 PR 23-MAY-1997; 97US-047596P.  
 PR 23-MAY-1997; 97US-047597P.  
 PR 23-MAY-1997; 97US-047598P.  
 PR 23-MAY-1997; 97US-047599P.  
 PR 23-MAY-1997; 97US-047600P.  
 PR 23-MAY-1997; 97US-047601P.  
 PR 23-MAY-1997; 97US-047612P.  
 PR 23-MAY-1997; 97US-047613P.  
 PR 23-MAY-1997; 97US-047614P.  
 PR 23-MAY-1997; 97US-047615P.  
 PR 23-MAY-1997; 97US-047617P.  
 PR 23-MAY-1997; 97US-047618P.  
 PR 23-MAY-1997; 97US-047632P.  
 PR 23-MAY-1997; 97US-047633P.  
 PR 06-JUN-1997; 97US-048964P.  
 PR 06-JUN-1997; 97US-048974P.  
 PR 13-JUN-1997; 97US-049610P.  
 PR 08-JUL-1997; 97US-051926P.  
 PR 16-JUL-1997; 97US-052874P.  
 PR 18-AUG-1997; 97US-055724P.  
 PR 22-AUG-1997; 97US-056630P.  
 PR 22-AUG-1997; 97US-056631P.  
 PR 22-AUG-1997; 97US-056632P.  
 PR 22-AUG-1997; 97US-056636P.  
 PR 22-AUG-1997; 97US-056637P.  
 PR 22-AUG-1997; 97US-056662P.  
 PR 22-AUG-1997; 97US-056664P.  
 PR 22-AUG-1997; 97US-056845P.  
 PR 22-AUG-1997; 97US-056862P.  
 PR 22-AUG-1997; 97US-056864P.  
 PR 22-AUG-1997; 97US-056872P.  
 PR 22-AUG-1997; 97US-056874P.  
 PR 22-AUG-1997; 97US-056875P.  
 PR 22-AUG-1997; 97US-056876P.  
 PR 22-AUG-1997; 97US-056877P.  
 PR 22-AUG-1997; 97US-056878P.  
 PR 22-AUG-1997; 97US-056879P.  
 PR 22-AUG-1997; 97US-056880P.  
 PR 22-AUG-1997; 97US-056881P.  
 PR 22-AUG-1997; 97US-056882P.  
 PR 22-AUG-1997; 97US-056884P.  
 PR 22-AUG-1997; 97US-056886P.  
 PR 22-AUG-1997; 97US-056887P.  
 PR 22-AUG-1997; 97US-056888P.  
 PR 22-AUG-1997; 97US-056889P.  
 PR 22-AUG-1997; 97US-056892P.  
 PR 22-AUG-1997; 97US-056893P.  
 PR 22-AUG-1997; 97US-056894P.  
 PR 22-AUG-1997; 97US-056903P.  
 PR 22-AUG-1997; 97US-056908P.  
 PR 22-AUG-1997; 97US-056909P.  
 PR 22-AUG-1997; 97US-056910P.  
 PR 22-AUG-1997; 97US-056911P.  
 PR 22-AUG-1997; 97US-057761P.  
 PR 05-SEP-1997; 97US-057650P.  
 PR 05-SEP-1997; 97US-057659P.  
 PR 12-SEP-1997; 97US-058785P.  
 PR 02-OCT-1997; 97US-061060P.  
 PR 06-MAR-1998; 98WO-US04493.  
 XX  
 PA (HUVA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;  
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
 XX  
 DR WPI; 2002-634796/68.  
 XX  
 PT New isolated human secreted protein for diagnosing, preventing,  
 treating or ameliorating medical conditions and used as a food additive

PT or preservative -  
 PS Disclosure; Column 78; 129pp; English.  
 XX  
 CC The invention relates to an isolated protein that is one of 186 human  
 CC secreted proteins, given in the specification, encoded by one of  
 CC 309 cDNA sequences also given in the specification. The protein is used  
 CC in a pharmaceutical composition used to prevent, treat or ameliorate a  
 CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
 CC dogs, chickens or sheep. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. The present sequence represents one of the novel human  
 CC secreted proteins of the invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 40.0%; Score 6; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 HOPPOP 7  
 Db 1 HOPPOP 6  
 RESULT 18  
 AAW39006  
 ID AAW39006 standard; peptide; 15 AA.  
 AC AAW39006;  
 XX  
 XX 27-MAR-1998 (first entry)  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:405.  
 XX  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9730074-A1.  
 XX  
 PD 21-AUG-1997.  
 XX  
 PF 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX  
 DR WPI; 1997-424972/39.  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 93; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 40.0%; Score 6; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPOPLP 9  
 Db 8 PPOPLP 13  
 RESULT 19  
 ABG72660  
 ID ABG72660 standard; Peptide; 15 AA.  
 XX  
 AC ABG72660;  
 XX  
 XX 26-FEB-2003 (first entry)  
 DT  
 DE Human K-ras 10.67 proto-oncogene protein, N-terminus.  
 XX  
 KW Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;  
 KW development disorder; human immunodeficiency virus infection; HIV;  
 KW immunological disease; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CNI352063-A.  
 XX  
 PD 05-JUN-2002.  
 XX  
 PF 02-NOV-2000; 2000CN-0127155.  
 XX  
 PR 02-NOV-2000; 2000CN-0127155.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-658691/71.  
 XX  
 XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating  
 PT malignant tumors, hemopathy, development disorder, human  
 PT immunodeficiency virus infection, immunological diseases and various  
 PT inflammations -  
 XX  
 PS Example 5; Page 19 (disclosure); 33pp; Chinese.  
 XX  
 XX The present invention discloses a new kind of polypeptide,  
 CC human K-ras proto-oncogene protein 10.67, polynucleotides encoding the  
 CC polypeptide and a DNA recombination process to produce the polypeptide.  
 CC The present invention also discloses applying the polypeptide in  
 CC treating various diseases, such as malignant tumours, haemopathy,

CC development disorder, human immunodeficiency virus (HIV) infection,  
 CC immunological diseases and various inflammations. The present invention  
 CC also discloses the antagonist resisting the polypeptide and its  
 CC treatment effect. The present invention also discloses application of  
 CC the polynucleotides encoding human K-ras proto-oncogene protein 10.67.  
 CC The present sequence represents human K-ras proto-oncogene protein  
 CC 10.67, N-terminus, used in an ELISA (enzyme-linked immunosorbent assay)  
 CC experiment.

XX Sequence 15 AA;  
 SQ Query Match 40.0%; Score 6; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLPP 10  
 Db 10 PQLPP 15

RESULT 20  
 AA25442  
 ID AA25442 standard; peptide; 16 AA.

XX AC AA25442;  
 XX DT 27-MAR-1998 (first entry)

XX DE Grb2 N-terminal SH3 domain binding peptide SEQ ID NO:227.

XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX OS Synthetic.  
 OS Unidentified.

XX PN WO9730074-A1.

XX PD 21-AUG-1997.

XX PF 14-FEB-1997; 97WO-US02298.

XX PR 16-FEB-1996; 96US-0602999.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;

XX DR WPI; 1997-424972/39.

XX PT Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

XX PS Claim 20; Page 101; 131pp; English.

XX CC The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX SQ Sequence 16 AA;

Query Match 40.0%; Score 6; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 8.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13  
 Db 9 LPPTVM 14

RESULT 21  
 AAY41630  
 ID AAY41630 standard; peptide; 7 AA.

XX AC AAY41630;

XX DT 02-DEC-1999 (first entry)

XX DE Mammalian ion channel proline rich motif containing peptide #24.

XX KW SH3 domain; binding motif; potassium channel; protein tyrosine kinase;  
 KW proline rich.

XX OS Mus sp.

XX PN US5955259-A.

XX PD 21-SEP-1999.

XX PF 19-DEC-1996; 96US-0769745.

XX PR 19-DEC-1996; 96US-0769745.

XX PA (UYER-) UNIV BRANDEIS.

XX PI Holmes TC, Levitan IB;

XX DR WPI; 1999-560490/47.

XX PT Identification of compounds that modulate potassium ion channel binding  
 XX with protein tyrosine kinase SH3 domains -

XX PS Disclosure; Column 8; 18pp; English.

XX CC A method has been developed for determining if a compound modulates the  
 CC binding of a potassium ion channel to the SH3 domain of a protein  
 CC tyrosine kinase by contacting the channel with a polypeptide comprising  
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3  
 CC binding. The method is useful for assessing the ability of a compound to  
 CC modulate the formation of channel-SH3 domain complexes to improve the  
 CC understanding of mechanisms of potassium channel blockage and assess the  
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to  
 CC AAY41644 represent mammalian ion channel peptides with proline-rich  
 CC motifs.

XX SQ Sequence 7 AA;

Query Match 33.3%; Score 5; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
 Db 1 QPLPP 5

RESULT 22

```
AAB17247
ID AAB17247 standard; Peptide; 7 AA.
XX AC
XX AAB17247;
XX DT
XX 31-OCT-2000 (first entry)
XX DE
XX SH3 antagonist peptide sequence SEQ ID NO:303.
XX KW
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
XX KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
XX KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX KW vascular endothelial growth factor; matrix metalloproteinase;
XX KW asthma; thrombosis; pharmaceutical.
XX OS
XX Synthetic.
XX PN WO200024782-A2.
XX PD
XX 04-MAY-2000.
XX PF
XX 25-OCT-1999; 99WO-US25044.
XX PR
XX 23-OCT-1998; 98US-0105371.
XX PR 22-OCT-1999; 99US-0428082.
XX PA (AMGE-) AMGEN INC.
XX PI
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX DR
XX Novel composition of matter comprising an Fc domain and
XX PT pharmacologically active peptides, useful for treating cancer and
XX PT autoimmune diseases -
XX XX
XX Claim 39; Page 302; 608pp; English.
XX CC
XX The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
XX CC where P1, P2, P3, and P4 = are each independently sequences of
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
XX CC independently linkers; and a, b, c, d, e, and f = are each independently
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
XX CC activities. DNAs, vectors and host cells from the present invention can
XX CC be used for producing pharmaceutical compositions. The compositions are
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer
XX CC half-life or incorporate functions such as Fc receptor binding, protein
XX CC A binding, complement fixation, and possibly placental transfer. AAB69443
XX CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
XX CC sequences used in the exemplification of the present invention.
XX SQ
XX Sequence 7 AA;
XX Query Match 33.3%; Score 5; DB 21; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 7 PLPPT 11
XX DB 2 PLPPT 6
XX RESULT 23
XX AAB72269
XX ID AAB72269 standard; peptide; 7 AA.
XX AC
XX AAB72269;
XX DT
XX 14-MAY-2001 (first entry)
XX DE
XX Colostrinin derived cytokine inducing peptide SEQ ID 24.
XX KW
XX Colostrinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX OS
XX Synthetic.
XX PN WO200111937-A2.
XX PD
XX 22-FEB-2001.
XX PF
XX 17-AUG-2000; 2000WO-US22818.
XX PR
XX 17-AUG-1999; 99US-0149311.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX DR
XX Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostrinin as an immunological
XX PT regulator -
XX XX
XX Claim 1; Page 34; 50pp; English.
XX CC
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for
XX CC inducing cytokine production, for modulating an immunological response
XX CC and for inducing blood cell proliferation. The peptides are useful in the
XX CC treatment of disorders of the central nervous system, neurological
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,
XX CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
XX CC disorders of the immune system, bacterial and viral infections and
XX CC acquired immunological deficiencies.
XX SQ
XX Sequence 7 AA;
XX Query Match 33.3%; Score 5; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MHQPP 5
XX DB 3 MHQPP 7
XX RESULT 24
XX AAB72522
XX ID AAB72522 standard; Peptide; 7 AA.
XX AC
XX AAB72522;
XX XX
XX 09-MAY-2001 (first entry)
XX DT
XX Colostrinin peptide #23.
XX DE
XX Dermatology; oxidative stress regulator; colostrinin.
XX KW
XX OS , Unidentified.
XX XX
```

PN WO200112650-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22665.  
 XX 17-AUG-1999; 99US-0149310.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 XX Claim 6; Page 26; 48pp; English.  
 XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5  
 |||||  
 Db 3 MHQPP 7

RESULT 25  
 AAB72554  
 ID AAB72554 standard; Peptide; 7 AA.  
 XX AAB72554;  
 XX 09-MAY-2001 (first entry)  
 XX Colostrinin peptide #23.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22774.  
 XX 17-AUG-1999; 99US-0149633.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Boldogh I;  
 XX WPI; 2001-226545/23.  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5  
 |||||  
 Db 3 MHQPP 7

RESULT 26  
 AAB59332  
 ID AAB59332 standard; Peptide; 7 AA.  
 XX AAB59332;  
 XX 21-MAR-2001 (first entry)  
 XX Ewe colostrinin peptide fragment C-7.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX Ovis sp.  
 XX WO200075173-A2.  
 XX 14-DEC-2000.  
 XX 02-JUN-2000; 2000WO-GB02128.  
 XX 02-JUN-1999; 99GB-0012852.  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 XX Georgiades JA;  
 XX WPI; 2001-071058/08.  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX Claim 7; Page 27; 63pp; English.  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5  
 |||||  
 Db 3 MHQPP 7

RESULT 27  
AAE20251  
ID AAE20251 standard; peptide; 7 AA.  
XX AC AAE20251;  
XX AC AAE20251;  
XX DT 18-JUN-2002 (first entry)  
XX DE Colostrinin constituent peptide #23.  
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX KW transplantation; implantation; dermatological; vulnery.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Modified-site 7 /note= "Optionally C-terminal amide"  
XX PN WO200213850-A1.  
XX PD 21-FEB-2002.  
XX PF 17-AUG-2000; 2000WO-US22776.  
XX PR 17-AUG-2000; 2000WO-US22776.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX DR WPI; 2002-269151/31.  
XX PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
FT constituent peptide and/or analog -  
XX PS Claim 6; Page 26; 51pp; English.  
XX CC The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC after a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide.  
XX SQ Sequence 7 AA;  
Query Match 33.3%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MHQPP 5  
Db 3 MHQPP 7  
RESULT 28  
AAM51058

ID AAM51058 standard; Peptide; 7 AA.  
XX AC AAM51058;  
XX DT 30-MAY-2002 (first entry)  
XX DE Colostrinin constituent peptide (casein amino acids 157-163).  
XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
XX KW blood cell regulator; cytokine inducer; beta-casein; human.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Modified-site 7 /note= "optional C-terminal amidation"  
XX PN WO200213849-A1.  
XX PD 21-FEB-2002.  
XX PF 17-AUG-2000; 2000WO-US22775.  
XX PR 17-AUG-2000; 2000WO-US22775.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PA (REGE-) REGEN THERAPEUTICS PLC.  
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX DR WPI; 2002-269150/31.  
XX PT Modulation of blood cell proliferation in a patient involves use of  
PT blood cell regulator selected from colostrinin, its constituent peptide  
FT and/or analogue -  
XX PS Claim 1; Page 34; 54pp; English.  
XX CC The present sequence is that of a colostrinin constituent peptide  
CC that is used as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. It is classified  
CC as having a beta-casein homologue precursor, and corresponds to  
CC casin amino acids 157-163. Methods are claimed for: inducing a  
CC cytokine in a cell by contact with an immunological regulator,  
CC where the cell is present in a cell culture, a tissue, an organ  
CC or an organism, and the cell is mammalian, including human;  
CC modulating an immune response in a cell by contact with the  
CC immunological regulator under conditions effective to induce a  
CC cytokine; modulating an immune response in a patient by administering  
CC an immunological regulator under conditions effective to induce a  
CC cytokine, where the immunological regulator is administered topically  
CC or as part of a dietary supplement, and where the immune response is  
CC specific or non specific, an interferon response or an antibody  
CC response; modulating blood cell proliferation by contacting blood  
CC cells with a blood cell regulator, where the blood cells are present  
CC in a cell culture or an organism, are mammalian or human, and where  
CC the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patent. A  
CC claimed cytokine-inducing composition comprises a pharmaceutical  
CC carrier and an active agent such as the present peptide.  
XX SQ Sequence 7 AA;  
Query Match 33.3%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MHQPP 5  
Db 3 MHQPP 7  
RESULT 29  
AAM51058

AAO14600  
 ID AAO14600 standard; peptide; 7 AA.  
 XX  
 AC AAO14600;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX  
 DE Neural cell regulatory colostrinin peptide 23.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optional C-terminal amide"  
 FT  
 XX  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22777.  
 XX  
 PR 17-AUG-2000; 2000WO-US22777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 33.3%; Score 5; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHOPP 5  
 |||||  
 Db 3 MHOPP 7  
 RESULT 30  
 ABB73240  
 ID ABB73240 standard; Peptide; 7 AA.  
 XX  
 AC ABB73240;  
 XX  
 DT 05-APR-2002 (first entry)  
 XX  
 DE Src homology3 (SH3) antagonist peptide SEQ ID NO:303.  
 XX  
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;  
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;

TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
 antianaemic; anorectic; antiinfertility; haemostatic; dermatological;  
 neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 sleep disorder; neurological degenerative disease; anaemia;  
 thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 Fanconi's syndrome.  
 KW  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX  
 PN WO200183525-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14310.  
 XX  
 PR 03-MAY-2000; 2000US-0563286.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 XX  
 DR WPI; 2002-130313/17.  
 XX  
 PT Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility -  
 XX  
 PS Claim 39; Page 55; 176pp; English.  
 XX  
 CC The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising  
 CC EPO-mimetic compounds are useful for treating disorders characterised by  
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB735695 to ABB73777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 33.3%; Score 5; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PLPPT 11  
 |||||  
 Db 2 PLPPT 6  
 RESULT 31  
 AAM00293  
 ID AAM00293 standard; Peptide; 8 AA.  
 XX  
 AC AAM00293;  
 XX

```

DT 01-OCT-2001 (first entry)
XX Human protein fragment SEQ ID NO: 837.
DE
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX
XX Homo sapiens.
OS
XX WO200151670-A2.
PN
XX 19-JUL-2001.
PD
XX 05-JAN-2001; 2001WO-US00322.
PF
XX 07-JAN-2000; 2000US-0174962.
PR (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach MD;
PA
XX WPI; 2001-451871/48.
PI N-PSDB; AAH89406.
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
PT
XX Disclosure; Page 344; 475pp; English.
XX
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercu-
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.
XX
XX Sequence 8 AA;
SQ
XX
XX Query Match 33.3%; Score 5; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 QPLPP 10
XX Db 1 QPLPP 5
XX
XX RESULT 32
XX AAM00294
XX ID AAM00294 standard; Peptide; 8 AA.
XX AC AAM00294;
XX
XX 01-OCT-2001 (first entry)
XX
XX Human protein fragment SEQ ID NO: 838.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX
XX Homo sapiens.
OS
XX WO200151670-A2.
PN
XX 19-JUL-2001.
PD
XX 05-JAN-2001; 2001WO-US00322.
PF
XX
XX Query Match 33.3%; Score 5; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 QPLPP 10
XX Db 1 QPLPP 5
XX
XX RESULT 32
XX AAB84971
XX ID AAB84971 standard; protein; 9 AA.
XX AC AAB84971;
XX
XX 06-AUG-2001 (first entry)
XX
XX Clone 1 scFv CDR L3 region binding to target antigen M.
XX
XX Antiinflammatory; antiallergic; cytostatic; antibacterial; antiviral;
XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
XX antiarthritic; dermatological; immune response; modulator; enzyme;
XX antigen M; T-cell receptor; complementary determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200140312-A2.
PN
XX 07-JUN-2001.
PD
XX
XX 04-DEC-2000; 2000WO-GB04629.
PF
XX
XX 03-DEC-1999; 99GB-0028789.
PR (DIVE-) DIVERSYS LTD.
XX
XX Holt LJ, De Wildt RMT, Tomlinson I;
PI
XX WPI; 2001-374801/39.
XX
XX Isolating a polypeptide of interest from a naive polypeptide repertoire
PT which has not been preselected with a specific target ligand involves
PT direct screening of naive polypeptide repertoire with the target ligand

```



PT  
XX  
PS  
XX  
XX  
Example 2; Page 29; 41pp; English.

CC The invention relates to isolating, from a naive polypeptide (I) repertoire (antibody or T-cell receptor polypeptides), which has not been preselected with a specific target ligand, a polypeptide of interest (II) capable of interacting with the specific target ligand. The method involves direct screening of (I) with the target ligand in order to identify (II). The polypeptides selected by the method may be used in any process which involves ligand-polypeptide binding including in vivo diagnostic and prophylactic applications, in vitro and in vivo diagnostic applications, in vitro assay and reagent applications. Enzyme variants generated and selected by the method may be assayed for activity, either in vitro or in vivo using standard techniques. Antibody polypeptides selected by the method are used diagnostically in Western analysis and in situ protein detection. The selected antibodies are useful for preventing, suppressing or treating inflammatory states, allergic hypersensitivity, cancer, bacterial or viral infection and autoimmune disorders e.g., type I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and myasthenia gravis. The selected polypeptides may be used extracorporeally or in vitro selectively to kill, deplete or effectively remove a target cell population from a heterogeneous collection of cells. Sequences AAB84968-979 represent complementary determining regions (CDRs) of scFv heavy and light chains binding to target antigens M and D.

XX  
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
DB 3 QPLPP 7  
|||||

RESULT 34  
ABR28252  
ID ABR28252 standard; Peptide; 9 AA.  
XX  
AC ABR28252;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1087.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response

PT  
XX  
PS  
XX  
XX  
in cancer patients -  
Claim 13; Page 413; 1021pp; English.

CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX  
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
DB 1 QPPQP 5  
|||||

RESULT 35  
ABR28257  
ID ABR28257 standard; Peptide; 9 AA.  
XX  
AC ABR28257;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1092.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients -  
Claim 13; Page 413; 1021pp; English.

XX  
PS  
XX  
CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
 DB 4 QPPQP 8  
 |||||  
 |||||

RESULT 36  
 ABR28346  
 ID ABR28346 standard; Peptide; 10 AA.

XX AC ABR28346;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 187P3F2 HLA peptide #1181.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX OS Homo sapiens.

PN WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
 DB 4 QPPQP 8  
 |||||  
 |||||

RESULT 38  
 AAM00291

Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
 DB 4 QPPQP 8  
 |||||  
 |||||

RESULT 37  
 ABR28347  
 ID ABR28347 standard; Peptide; 10 AA.

XX AC ABR28347;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 187P3F2 HLA peptide #1182.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX OS Homo sapiens.

PN WO200283921-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 CC proteins and polynucleotides, useful for therapeutic, prognostic and  
 CC diagnostic reagents for eliciting cellular or humoral immune response  
 CC in cancer patients

XX Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
 DB 1 QPPQP 5  
 |||||  
 |||||

```

ID  AAW00291 standard; Peptide; 12 AA.
XX
AC  AAM00291;
XX
DT  01-OCT-2001 (first entry)
XX
DE  Human protein fragment SEQ ID NO: 835.
XX
KW  Human; single nucleotide polymorphism; SNP; paternity test;
KW  forensic test; aberrant protein expression.
XX
OS  Homo sapiens.
XX
PN  WO200151670-A2.
XX
PD  19-JUL-2001.
XX
PF  05-JAN-2001; 2001WO-US00322.
XX
PR  07-JAN-2000; 2000US-0174962.
XX
PA  (CURA-) CURAGEN CORP.
XX
PI  Shimkets RA, Leach MD;
XX
DR  WPI; 2001-451871/48.
XX
DR  N-PSDB; AAH89404.
XX
PT  Isolated human polynucleotides containing single nucleotide
PT  polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT  infection and diabetes -
XX
PS  Disclosure; Page 344; 475pp; English.
XX
CC  The present invention relates to human nucleic acids containing single
CC  nucleotide polymorphisms (SNPs). These can be used in forensic and
CC  paternity tests, and to aid in the treatment of diseases associated with
CC  aberrant protein expression, including cancer, amyloidosis, diabetes,
CC  Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC  glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC  meningitis, muscular disorders, dementia, neurological diseases, tuberos
CC  sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC  osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC  autoimmunity. The present sequence is a peptide encoded by a
CC  polymorphism-containing oligonucleotide fragment of the invention.
XX
SQ  Sequence 12 AA;

Query Match 33.3%; Score 5; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 5 QPLPP 9

RESULT 39
AAR93368
ID AAR93368 standard; peptide; 13 AA.
XX
AC AAR93368;
XX
DT 24-APR-1996 (first entry)
XX
DE P13K protein tyrosine kinase derived peptide #3.
XX
KW SH3 ligand; SH3 binding agent; biased phage library;
KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
KW p67; complex; chronic myelogenous leukaemia; cancer.
XX
OS Synthetic.

Query Match 33.3%; Score 5; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 5 PLPPT 9

RESULT 40
AAW11112
ID AAW11112 standard; peptide; 13 AA.
XX
AC AAW11112;
XX
DT 25-JUN-1997 (first entry)
XX
DE Src SH3 domain-binding peptide used in signal transduction modulation.
XX
KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX
OS Synthetic.
XX
PN WO9603649-A1.
XX
PD 08-FEB-1996.
XX
PF 24-JUL-1995; 95WO-US09382.

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XX 07-JUN-1995; 95US-0483555.  
 PR 22-JUL-1994; 94US-0278865.  
 XX (UYN-C-) UNIV NORTH CAROLINA.  
 PA  
 XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;  
 PI WPI; 1996-117151/12.  
 XX  
 XX Peptide with binding affinity for Src homology region 3 (SH3)  
 PT domains of proteins - useful for e.g. modulating signal transduction  
 PT pathways at the cellular level, esp. protein tyrosine  
 PT kinase-mediated  
 XX  
 XX Claim 38; Page 87; 116pp; English.  
 PS  
 XX AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3  
 CC binding peptides are useful in modulating signal transduction pathways  
 CC at the cellular level (especially protein tyrosine kinase-mediated),  
 CC modulating oncogenic protein activity, or providing compounds for the  
 CC development of drugs with the ability to modulate broad classes, as  
 CC well as specific classes, of proteins involved in signal transduction  
 CC and also for regulating the processing, trafficking or translocation of  
 CC RNA. Conjugates of the peptides with detectable labels or imaging agents  
 CC are useful for imaging cells, tissues and organs in which Src or  
 CC Src-related proteins are expressed.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 33.3%; Score 5; DB 17; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PLPPT 11  
 Db |||||  
 5 PLPPT 9  
 RESULT 41  
 AAB44382  
 ID AAB44382 standard; Protein; 13 AA.  
 XX  
 AC AAB44382;  
 XX  
 XX 14-FEB-2001 (first entry)  
 DT  
 XX Human secreted protein encoded by gene 49 clone HPWAV82.  
 DE  
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200058358-A1.  
 PN  
 XX 05-OCT-2000.  
 PD  
 XX 23-MAR-2000; 2000WO-US07725.  
 PF  
 XX 26-MAR-1999; 99US-0126602.  
 PR  
 XX 14-JAN-2000; 2000US-0176063.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 PI WPI; 2000-594640/56.  
 XX  
 DR N-PSDB; AAC79045.  
 XX

PT Forty nine nucleic acid molecules encoding human secreted proteins,  
 PT useful in the prevention, treatment and diagnosis of cancer, immune  
 PT disorders, cardiovascular disorders and neurological diseases -  
 XX  
 XX Claim 11; Page 356; 367pp; English.  
 PS  
 XX Sequences AAB44335-B44382 represent the amino acid sequences of 49  
 CC human secreted proteins encoded by the genes AAC69084-C69119. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 33.3%; Score 5; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPQPL 8  
 Db |||||  
 6 PPQPL 10  
 RESULT 42  
 AAE21396  
 ID AAE21396 standard; peptide; 13 AA.  
 XX  
 AC AAE21396;  
 XX  
 XX 01-JUL-2002 (first entry)  
 DT  
 XX Escherichia coli 3-isopropylmalate dehydrogenase (IPMDH) peptide #1.  
 DE  
 XX Protein thermostability; 3-isopropylmalate dehydrogenase; IPMDH;  
 KW isocitrate dehydrogenase; ICDH; enzyme.  
 KW  
 XX Escherichia coli.  
 OS  
 XX EP1182253-A2.  
 PN  
 XX 27-FEB-2002.  
 PD  
 XX 03-JUL-2001; 2001EP-0115642.  
 PF  
 XX 04-JUL-2000; 2000JP-0201920.  
 PR  
 XX 31-MAY-2001; 2001JP-0164332.  
 PR  
 XX (AJIN) AJINOMOTO CO INC.  
 PA  
 XX Yamagishi A;  
 PI WPI; 2002-294076/34.  
 DR  
 XX Improving protein thermostability of protein by estimating amino acid  
 XX sequence of ancestral protein (AP), and replacing amino acids of  
 PT desired protein, which differ from those of AP with the same amino  
 PT acids of AP -  
 XX  
 XX Example 4; Fig 9; 73pp; English.  
 PS  
 XX The invention relates to a method for improving thermostability of  
 CC proteins. The method involves comparing amino acid sequences derived  
 CC

CC from two or more species which evolutionarily correspond to each other  
 CC in phylogenetic tree; estimating amino acid sequence of ancestral  
 CC protein and replacing amino acids of desired protein, which differ  
 CC from those of ancestral protein with the same amino acids of ancestral  
 CC protein. The method is used for improving thermostability of proteins  
 CC preferably 3-isopropylmalate dehydrogenase (IPMDH) and isocitrate  
 CC dehydrogenase (ICDH). The invention also relates to a protein having  
 CC an improved thermostability and a nucleic acid encoding such protein.  
 CC The present sequence is Escherichia coli IPMDH peptide.  
 XX  
 SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
 Db 1 QPLPP 5  
 |||||

RESULT 43  
 ABP81159  
 ID ABP81159 standard; peptide; 13 AA.

XX AC ABP81159;  
 XX 27-FEB-2003 (first entry)  
 XX Human TPO peptide with MCH class II binding activity #112.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 XX MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 KW Homo sapiens.  
 XX WO200268469-A2.

XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.

XX Carr FJ, Carter G;  
 XX WPI; 2003-103168/09.  
 XX Modified thrombopoietin molecule for use in pharmaceutical  
 PT compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -  
 XX  
 PS Disclosure; Page 12; 36pp; English.

CC The invention relates to a novel modified molecule having the biological  
 CC activity of human thrombopoietin (TPO) and being substantially  
 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 XX invention.

SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 7 PLPPT 11  
 |||||

RESULT 44  
 ABP81160  
 ID ABP81160 standard; peptide; 13 AA.

XX AC ABP81160;  
 XX 27-FEB-2003 (first entry)  
 XX Human TPO peptide with MCH class II binding activity #113.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 XX MHC class II; immunosuppressive; antiallergic; autoimmune disease.

XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.

XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.

XX Carr FJ, Carter G;  
 XX WPI; 2003-103168/09.  
 XX Modified thrombopoietin molecule for use in pharmaceutical  
 PT compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -  
 XX  
 PS Disclosure; Page 12; 36pp; English.

CC The invention relates to a novel modified molecule having the biological  
 CC activity of human thrombopoietin (TPO) and being substantially  
 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 XX invention.

SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 5 PLPPT 9  
 |||||

RESULT 45

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ABP81161
ID ABP81161 standard; peptide; 13 AA.
XX
AC ABP81161;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #114.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
XX MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
PA (MERE.) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G;
XX
DR WPI; 2003-103168/09.
XX
PT Modified thrombopoietin molecule for use in pharmaceutical
PT compositions, has same activity of human thrombopoietin, but is
PT non-immunogenic or less immunogenic than other non-modified molecules
PT with same activity -
XX
PS Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
CC invention.
XX
SQ Sequence 13 AA;
Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PLPPT 11
DB 4 PLPPT 8
RESULT 46
ABP81162
ID ABP81162 standard; peptide; 13 AA.
XX
AC ABP81162;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #115.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
XX MHC class II; immunosuppressive; antiallergic; autoimmune disease.

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XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
PA (MERE.) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G;
XX
DR WPI; 2003-103168/09.
XX
PT Modified thrombopoietin molecule for use in pharmaceutical
PT compositions, has same activity of human thrombopoietin, but is
PT non-immunogenic or less immunogenic than other non-modified molecules
PT with same activity -
XX
PS Disclosure; Page 12; 36pp; English.
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
CC invention.
XX
SQ Sequence 13 AA;
Query Match 33.3%; Score 5; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PLPPT 11
DB 2 PLPPT 6
RESULT 47
ABP81163
ID ABP81163 standard; peptide; 13 AA.
XX
AC ABP81163;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #116.
XX
KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
XX MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200268469-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
PR 26-FEB-2001; 2001EP-0104702.
XX

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PA (WERE ) MERCK PATENT GMBH.

XX Carr FJ, Carter G;

XX WPI; 2003-103168/09.

XX Modified thrombopoietin molecule for use in pharmaceutical  
PT compositions, has same activity of human thrombopoietin, but is  
PT non-immunogenic or less immunogenic than other non-modified molecules  
PT with same activity -

XX Disclosure; Page 12; 36pp; English.

XX The invention relates to a novel modified molecule having the biological  
CC activity of human thrombopoietin (TPO) and being substantially  
CC non-immunogenic or less immunogenic than any non-modified molecule having  
CC the same biological activity when used in vivo. The invention also  
CC discloses T-cell epitope peptides created from non-modified TPO, and  
CC having potential MHC class II binding activity. The protein of the  
CC invention has immunosuppressive and antiallergic activity. A peptide of  
CC the invention is useful in the manufacture of TPO having substantially no  
CC or less immunogenicity than any non-modified molecule with the same  
CC biological activity when used in vivo. The protein is useful in  
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
CC allergies and autoimmune disease treatment. The sequences shown in  
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
CC invention.

XX Sequence 13 AA;

Query Match 33.3%; Score 5; DB 24; Length 13;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
Db 1 PLPPT 5

RESULT 48

AAI03679  
ID AAY03679 standard; peptide; 14 AA.

XX AC AAY03679;

XX DT 07-JUN-1999 (first entry)

XX DE Amino acid sequence of the malaria (M) string CTL epitope BCG.

XX CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;  
KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;  
KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;  
KW melanoma; HIV; breast; colon; vaccination.

XX OS Mycobacterium tuberculosis.

XX PN WO9856919-A2.

XX PD 17-DEC-1998.

XX PF 09-JUN-1998; 98WO-GB01681.

XX PR 09-JUN-1997; 97GB-0011957.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Blanchard T, Gilbert SC, Hanke T, Hill AVS, McMichael AJ;  
PI Plebanski M, Schneider J, Smith GL;

XX WPI; 1999-070325/06.

XX DR N-PSDB; AAX29219.

XX PT Generating CD8-positive T cell response to target antigen using

PT recombinant poxvirus - for treating or preventing malaria and HIV  
PT infection, also epitope strings from Plasmodium and HIV

XX Claim 38; Page 19; 85pp; English.

XX The invention relates to methods and reagents for generating a  
CC protective CD8+ T-cell immune response against at least one target  
CC antigen. The kits of the invention comprises (i) as priming composition,  
CC a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)]  
CC epitopes of the target antigen, plus a carrier, and (ii) as boosting the  
CC composition a source of CTL epitopes, with at least one CTL epitope the  
CC same as used in (i), with this source being a non-replicating or  
CC replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If  
CC the source of CTL epitopes in (i) is a viral vector, then the vector in  
CC (ii) is from a different virus. The kits are used to generate an immune  
CC response (prophylactic or therapeutic) against pathogens or tumours,  
CC specifically against malaria parasites such as P. falciparum, or HIV, and  
CC also many other bacterial, viral or parasitic pathogens. The kits are  
CC also used for protective response against melanoma and cancer of breast  
CC or colon, and generally wherever a strong CD8+ response is protective.  
CC The boosting composition may be used alone to boost a naturally primed  
CC response against malaria. The specified PVV provide an excellent booster  
CC effect, better than that from wild-type poxvirus, resulting in complete  
CC rather than partial protection against sporozoite challenge. Also PVV are  
CC safer to use than wild-type virus. Sequences AAY03661-680 represent CTL  
CC peptide epitopes of the malaria (M) string.

XX Sequence 14 AA;

Query Match 33.3%; Score 5; DB 20; Length 14;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
Db 5 QPLPP 9

RESULT 49

AAM00448

ID AAM00448 standard; Peptide; 14 AA.

XX AC AAM00448;

XX DT 01-OCT-2001 (first entry)

XX DE Human protein fragment SEQ ID NO: 996.

XX KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression.

XX OS Homo sapiens.

XX PN WO200151670-A2.

XX PD 19-JUL-2001.

XX PF 05-JAN-2001; 2001WO-US00322.

XX PR 07-JAN-2000; 2000US-0174962.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX DR N-PSDB; AAH89565.

XX PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes -

XX PS Disclosure; Page 389; 475pp; English.

XX The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a peptide encoded by a  
CC polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 14 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
DB 5 QPLPP 9

RESULT 50  
AAB46171  
ID AAB46171 standard; peptide; 14 AA.  
AC AAB46171;  
XX 04-APR-2001 (first entry)  
DE Bacille Calmette-Guérin universal T epitope.  
XX  
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
KW amyloid precursor protein; Alzheimer's disease.  
XX  
OS Mycobacterium tuberculosis.  
XX WO200072880-A2.  
XX 07-DEC-2000.  
XX 26-MAY-2000; 2000WO-US14810.  
XX 28-MAY-1999; 99US-0322289.  
XX (NEUR-) NEURALAB LTD.  
XX Schenk DB, Bard F, Vasquez NU, Yednock T;  
XX WPI; 2001-032104/04.  
XX Preventing or treating a disease associated with amyloid deposits,  
XX especially Alzheimer's disease, comprises administering amyloid  
XX specific antibody -  
XX Disclosure; Page 28; 143pp; English.

This invention describes a novel method of preventing or treating a  
CC disease associated with amyloid deposits of amyloid precursor protein  
CC (APP) Abeta fragments in the brain of a patient, which comprises  
CC administering to the patient: (a) an antibody that binds to Abeta, the  
CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
CC that induces an immunogenic response against residues 1-3 to 7-11 of  
CC Abeta. The products of the invention have neurotropic and neuroprotective  
CC activity. The method is also useful for monitoring a course of treatment  
CC being administered to a patient e.g. active and passive immunization. The  
CC methods are useful for prophylactic and therapeutic treatment of  
CC Alzheimer's disease.

XX Sequence 14 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
DB 5 QPLPP 9

RESULT 51  
AAB49070  
ID AAB49070 standard; peptide; 14 AA.  
XX  
AC AAB49070;  
XX 27-MAR-2001 (first entry)  
DT BCG T-cell epitope, SEQ ID NO:6.  
DE  
XX  
KW Amyloid disease; amyloid fibril deposition; amyloid plaque;  
KW immunogenic; antibody; vaccine; Alzheimer's disease;  
KW type 2 diabetes; reactive system amyloidosis;  
KW systemic senile amyloidosis; familial amyloid cardiomyopathy;  
KW transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;  
KW haemodialysis-associated beta-2-microglobulin deposition;  
KW carrier protein; universal T-cell epitope.  
XX  
OS Mycobacterium bovis.  
XX WO200072876-A2.  
XX 07-DEC-2000.  
XX 01-JUN-2000; 2000WO-US15239.  
XX 01-JUN-1999; 99US-0137010.  
XX (NEUR-) NEURALAB LTD.  
XX Schenk DB;  
XX WPI; 2001-070921/08.  
XX Pharmaceutical composition comprising immunogen against amyloid  
XX component such as fibril peptide or protein, or antibody against  
XX amyloid component useful for treating amyloid diseases or amyloidoses -  
XX Disclosure; Page 43; 140pp; English.

The invention relates to a novel pharmaceutical composition for  
CC preventing or treating a disease characterised by amyloid fibril  
CC deposits (amyloid plaques) in a patient. The pharmaceutical composition  
CC comprises an agent that will induce an immune response against an amyloid  
CC component, or an antibody or antibody fragment that binds to an amyloid  
CC component. The invention also relates to a method for determining  
CC the prognosis of a patient undergoing treatment for an amyloid disorder  
CC which involves measuring a patient serum amount of immunoreactivity  
CC against a selected amyloid component. A patient serum immunoreactivity  
CC of at least four times a base line serum immunoreactivity control level  
CC indicates a prognosis of improved status with respect to the disorder.  
CC The pharmaceutical compositions of the invention are useful for treating  
CC a wide variety of disorders characterised by amyloid fibril deposition in  
CC a patient. Such disorders include Alzheimer's disease characterised by  
CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by  
CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic  
CC amyloidosis associated with systemic inflammatory diseases (e.g.,  
CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA  
CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile  
CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR  
CC fibrils derived from transthyretin (TTR); transmissible spongiform





Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
| | | | |  
Db 2 QPLPP 6

RESULT 54  
AAW38976  
ID AAW38976 standard; peptide; 15 AA.  
XX AC AAW38976;  
XX  
XX  
XX 27-MAR-1998 (first entry)  
XX  
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:373.  
XX  
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
XX  
XX Synthetic.  
XX  
XX WO9730074-A1.  
FN  
XX 21-AUG-1997.  
PD  
XX 14-FEB-1997; 97WO-US02298.  
PF  
XX 16-FEB-1996; 96US-0602999.  
PR  
XX (CYTO-) CYTOGEN CORP.  
PA (UYN-) UNIV NORTH CAROLINA.  
PA  
FI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
PI Sparks AB, Thorn JM;  
XX  
XX WPI; 1997-424972/39.  
XX  
XX Src homology region 3 binding peptide - used to activate Src  
PT tyrosine kinase(s) and to stimulate immune response by increasing  
PT production of certain lymphokine(s), e.g. interleukin-1  
XX  
XX Claim 22; Page 92; 131pp; English.  
PS  
XX  
XX The present sequence represents a peptide which resembles a Src homology  
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
CC domain of Crk; (h) peptides which bind the SH3 domain of Grb2. The purified  
CC binding peptides can be used in the method to identify inhibitors of  
CC their binding to their respective SH3 domains, which could be used to  
CC modulate the pharmacological activity of proteins or polypeptide  
CC containing the SH3 domain. The peptides can also be used to activate  
CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
CC response by increasing the production of certain lymphokines, e.g.  
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
CC conjugated molecule to certain cellular compartments containing Src or  
CC Src related proteins.  
XX  
XX Sequence 15 AA;  
SQ

Query Match 33.3%; Score 5; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
| | | | |

Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QPPQP 14

RESULT 55  
AAG78855  
ID AAG78855 standard; Peptide; 15 AA.  
XX  
XX AAG78855;  
AC  
XX 12-DEC-2001 (first entry)  
DT  
XX  
XX Growth hormone family protein 11 peptide fragment.  
DE  
XX  
XX Growth hormone; cytostatic; virucidal; immunomodulator; antiinflammatory;  
KW haemostatic; gene therapy; malignant tumour; haemopathy; HIV infection;  
KW immunological disease; inflammation.  
XX  
XX Unidentified.  
OS  
XX WO200172832-A1.  
FN  
XX 04-OCT-2001.  
PD  
XX 26-MAR-2001; 2001WO-CN00489.  
PF  
XX 27-MAR-2000; 2000CN-0115180.  
PR  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2001-602854/68.  
DR  
XX  
XX New polypeptide for the diagnosis and treatment of malignant neoplasm,  
PT hemopathy, HIV infection, immunological diseases and inflammations,  
PT comprises protein 11 of the growth hormone family -  
XX  
XX Example 5; Page 19; 35pp; Chinese.  
PS  
XX  
XX The present invention relates to protein 11 of the growth hormone family  
CC (see AAI65179 and AAG78854). The growth hormone protein and its coding  
CC sequence are useful in the diagnosis and treatment of malignant tumours,  
CC haemopathy, HIV infection, immunological diseases and various  
CC inflammations. The present sequence is an N-terminal peptide fragment of  
CC the growth hormone protein which was used in an example from the present  
CC invention.  
XX  
XX Sequence 15 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
| | | | |  
Db 8 PLPPT 12

RESULT 56  
ABR38292  
ID ABR38292 standard; Peptide; 15 AA.  
XX  
XX ABR38292;  
AC  
XX 19-MAY-2003 (first entry)  
DT  
XX  
XX Human cancer-related protein 187P3F2 HLA peptide #1423.  
DE  
XX  
XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
XX Homo sapiens.  
OS  
XX

```

PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
XX
PF 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX (AGEN-) AGENSYS INC.
PS Claim 13; Page 616; 1021pp; English.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 616; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 33.3%; Score 5; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QPPQP 7
Db 8 QPPQP 12
RESULT 57
ABR38293
ID ABR38293 standard; Peptide; 15 AA.
XX
XX ABR38293;
AC
XX 19-MAY-2003 (first entry)
DT
DE Human cancer-related protein 187P3F2 HLA peptide #1424.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US11654.
PF
XX 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 616; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 33.3%; Score 5; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QPPQP 7
Db 8 QPPQP 12
RESULT 58
ABR38294
ID ABR38294 standard; Peptide; 15 AA.
XX
XX ABR38294;
AC
XX 19-MAY-2003 (first entry)
DT
DE Human cancer-related protein 187P3F2 HLA peptide #1425.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US11654.
PF
XX 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 616; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC directing the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 33.3%; Score 5; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QPPQP 7
Db 7 QPPQP 11

```



Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7  
Db 11 QPPQP 15

## RESULT 61

ABR38391  
ID ABR38391 standard; Peptide; 15 AA.

XX AC ABR38391;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 187P3F2 HLA peptide #1522.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of  
proteins and polynucleotides, useful for therapeutic, prognostic and  
diagnostic reagents for eliciting cellular or humoral immune response  
in cancer patients

XX PS Claim 13; Page 618; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
proteins are useful for eliciting a humoral or cellular immune response.  
The genes are useful as probes and primers for the amplification and/or  
detection of genes, mRNAs or their fragments, as reagents for the  
diagnosis and/or prognosis of cancer, as coding sequences capable of  
directing the expression of the protein, as tools for modulating or  
inhibiting the expression of genes and/or translation of transcripts, and  
as therapeutic agents. The proteins and peptides are useful as  
therapeutic, prognostic and diagnostic reagents for cancer. The present  
sequence is a human leukocyte antigen (HLA) peptide, used in an example  
from the invention.

XX SQ Sequence 15 AA;

## Query Match

Best Local Similarity 33.3%; Score 5; DB 24; Length 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7  
Db 5 QPPQP 9

## RESULT 62

ABR38392

ID ABR38392 standard; Peptide; 15 AA.

XX AC ABR38392;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 187P3F2 HLA peptide #1523.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of  
proteins and polynucleotides, useful for therapeutic, prognostic and  
diagnostic reagents for eliciting cellular or humoral immune response  
in cancer patients

XX PS Claim 13; Page 618; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
proteins are useful for eliciting a humoral or cellular immune response.  
The genes are useful as probes and primers for the amplification and/or  
detection of genes, mRNAs or their fragments, as reagents for the  
diagnosis and/or prognosis of cancer, as coding sequences capable of  
directing the expression of the protein, as tools for modulating or  
inhibiting the expression of genes and/or translation of transcripts, and  
as therapeutic agents. The proteins and peptides are useful as  
therapeutic, prognostic and diagnostic reagents for cancer. The present  
sequence is a human leukocyte antigen (HLA) peptide, used in an example  
from the invention.

XX SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 24; Length 15;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7  
Db 3 QPPQP 7

## RESULT 63

ABR38414

ID ABR38414 standard; Peptide; 15 AA.

XX AC ABR38414;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 187P3F2 HLA peptide #1545.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
human leukocyte antigen.

```

OS Homo sapiens.
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 10-APR-2001; 2001US-283112P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 13; Page 619; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 33.3%; Score 5; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 84;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QPPQP 7
XX | | | | |
XX Db 10 QPPQP 14
XX
XX RESULT 64
XX ABR38502
XX ID ABR38502 standard; Peptide; 15 AA.
XX
XX AC ABR38502;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 187P3P2 HLA peptide #1633.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 10-APR-2001; 2001US-283112P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 13; Page 619; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 33.3%; Score 5; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 84;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QPPQP 7
XX | | | | |
XX Db 10 QPPQP 14
XX
XX RESULT 65
XX AAW25427
XX ID AAW25427 standard; peptide; 16 AA.
XX
XX AC AAW25427;
XX
XX 27-MAR-1998 (first entry)
XX
XX Yes SH3 domain binding peptide SEQ ID NO:213.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX Unidentified.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UYN-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JW;
XX WPI; 1997-424972/39.

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PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 13; Page 620; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 33.3%; Score 5; DB 24; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 84;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QPPQP 7
XX | | | | |
XX Db 10 QPPQP 14
XX
XX RESULT 65
XX AAW25427
XX ID AAW25427 standard; peptide; 16 AA.
XX
XX AC AAW25427;
XX
XX 27-MAR-1998 (first entry)
XX
XX Yes SH3 domain binding peptide SEQ ID NO:213.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX Unidentified.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UYN-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JW;
XX WPI; 1997-424972/39.

```

XX PT Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX PS Claim 19; Page 100; 131pp; English.  
 XX CC The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 5 PLPPT 9

RESULT 66  
 AAW25376  
 ID AAW25376 standard; peptide; 16 AA.  
 XX AC AAW25376;  
 XX DT 27-MAR-1998 (first entry)  
 XX DE Src SH3 domain binding peptide SEQ ID NO:158.  
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX OS Synthetic.  
 OS Unidentified.  
 XX PN WO9730074-A1.  
 XX PD 21-AUG-1997.  
 XX PF 14-FEB-1997; 97WO-US02298.  
 XX PR 16-FEB-1996; 96US-0602999.  
 XX PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX PI Der CU, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX DR WPI; 1997-424972/39.  
 XX PT Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 131pp; English.  
 XX PS The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 5 PLPPT 9

RESULT 67  
 AAW25380  
 ID AAW25380 standard; peptide; 16 AA.  
 XX AC AAW25380;  
 XX DT 27-MAR-1998 (first entry)  
 XX DE Src SH3 domain binding peptide SEQ ID NO:147.  
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX OS Synthetic.  
 OS Unidentified.  
 XX PN WO9730074-A1.  
 XX PD 21-AUG-1997.  
 XX PF 14-FEB-1997; 97WO-US02298.  
 XX PR 16-FEB-1996; 96US-0602999.  
 XX PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX DR WPI; 1997-424972/39.  
 XX PT Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 16; Page 99; 131pp; English.  
 XX CC The present sequence represents a Src homology region 3 (SH3) binding

CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53b2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX  
 CC Sequence 16 AA;

Query Match 33.3%; Score 5; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 5 PLPPT 9  
 |||||

RESULT 68  
 ABP82678  
 ID ABP82678 standard; Peptide; 16 AA.

XX  
 CC ABP82678;

DT 04-MAR-2003 (first entry)

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1351.

XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.

XX  
 OS Homo sapiens.

XX  
 PN WO200261087-A2.

XX  
 PD 08-AUG-2002.

XX  
 PF 19-DEC-2001; 2001WO-US50107.

XX  
 PR 19-DEC-2000; 2000US-257144P.

XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX  
 PI Burner GC, Roush CL, Brown JP;

XX  
 DR WPI; 2003-046718/04.

XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases -

XX  
 PS Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, host  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

XX  
 CC Sequence 16 AA;

Query Match 33.3%; Score 5; DB 24; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
 Db 10 PLPPT 14  
 |||||

RESULT 69  
 AAB39277  
 ID AAB39277 standard; Protein; 17 AA.

XX  
 AC AAB39277;

XX  
 DT 02-FEB-2001 (first entry)

XX  
 DE Gene 31 human secreted protein homologous amino acid sequence #157.

XX  
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;  
 KW ophthalmological; autoimmune disease; rheumatoid arthritis; angio genesis;  
 KW hyperproliferative disorder; cardiovascular disorder; infection;  
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; chemotaxis.

XX  
 OS Homo sapiens.

XX  
 PN WO2000056754-A1.

XX  
 PD 28-SEP-2000.

XX  
 PF 16-MAR-2000; 2000WO-US06792.

XX  
 PR 19-MAR-1999; 99US-0125362.

XX  
 PR 10-DEC-1999; 99US-0169980.

XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

XX  
 PI Rosen GA, Ruben SM, Komatsoulis G;

XX  
 DR WPI; 2000-579483/54.



PT Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition -  
 XX  
 XX Disclosure; Page 52; 434pp; English.

XX The polynucleotide sequences given in AAC74223-C74279 encode the human  
 CC secreted proteins represented in AAB39179-B39226. Sequences  
 CC AAB39227-B39308 are alternative proteins encoded by the genes, and also  
 CC protein sequences with which they share homology. The proteins have  
 CC activities based on the tissues and cells in which they are expressed.  
 CC Examples of activities include: immunosuppressive; antiarthritic;  
 CC antirheumatic; antiproliferative; cytostatic; cardiact; vasotropic;  
 CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 CC fungicide; and ophthalmological. The human secreted proteins,  
 CC polynucleotides, antagonists and agonists of the invention may be useful  
 CC in the treatment, prevention, and/or diagnosis of various disease,  
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation, to  
 CC regenerate tissues, maintain organs before transplantation, in  
 CC chemotaxis and as a food additive or preservative e.g. to increase  
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used  
 CC during the isolation and characterisation of the genes of the invention.

XX Sequence 17 AA;

Query Match 33.3%; Score 5; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
 DB 1 QPLPP 5

RESULT 70  
 ABB57154  
 ID ABB57154 standard; Peptide; 18 AA.

XX ABB57154;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX Human liver peptide, SEQ ID No 35802.  
 DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KW hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.  
 OS  
 XX WO200157273-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000664.  
 PF  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI  
 XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human adult liver -  
 XX  
 XX Claim 27; SEQ ID No 35802; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. ABB47348-ABG53930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLPL 9  
 DB 9 PQLPL 13

RESULT 71  
 ABB41714  
 ID ABB41714 standard; Peptide; 18 AA.

XX ABB41714;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX Peptide #9220 encoded by human foetal liver single exon probe.  
 DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
 KW Homo sapiens.  
 OS  
 XX WO200157277-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI  
 XX WPI; 2001-483447/52.  
 DR  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human fetal liver -

XX Claim 27; SEQ ID No 34349; 639pp + sequence listing; English.  
 PS  
 XX The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred.No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 PQPLP 9  
|||||  
Db 9 PQPLP 13

RESULT 72  
AAM62588  
ID ID AAM62588 standard; Protein; 18 AA.  
XX AC AAM62588;  
XX DT 05-NOV-2001 (first entry)  
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 34693.  
DE XX  
DE Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
KW epilepsy; cancer.  
XX Homo sapiens.  
OS WO200157275-A2.  
PN 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US00667.  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
PT  
XX Example 4; SEQ ID NO: 34693; 650pp + Sequence Listing; English.  
PS  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention.

XX

SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred.No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

XX KW Probe: microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-488897/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX XX
XX PS Claim 27; SEQ ID No 35780; 654pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AA131315-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders.
XX XX
XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQLP 9
Db 9 PQLP 13

RESULT 75
AAE03955
ID AAE03955 standard; peptide; 18 AA.
XX AC
XX AC AAE03955;
XX DT
XX DT 09-AUG-2001 (first entry)
XX DE
XX DE Human gene 10 encoded secreted protein fragment, SEQ ID NO:126.
XX KW
XX KW Human; secreted protein; proliferative disorder; cancer; tumour;
XX KW foetal abnormality; developmental abnormality; haematopoietic disorder;
XX KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX KW inflammation; allergy; neurological disorder; Alzheimer's disease;
XX KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX KW cardiovascular disorder; angiogenic disorder; kidney disorder;
XX KW gastrointestinal disorder; pregnancy-related disorder;
XX KW endocrine disorder; infection; wound healing; vulnery;
XX KW cell culture; chemotaxis; food additive; gene therapy;
XX KW binding partner identification.
XX OS
XX OS Homo sapiens.

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PN WO200077022-A1.
XX XX
XX PD 21-DEC-2000.
XX XX
XX PF 01-JUN-2000; 2000WO-US15136.
XX PR 11-JUN-1999; 99US-0138629.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Ruben SM, Komatsoulis GA;
XX XX
XX DR WPI; 2001-367020/38.
XX XX
XX PT Nucleic acids encoding 50 human secreted polypeptides, useful for
XX PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX PT disease, botulism, cancers and Scimitar syndrome -
XX XX
XX PS Disclosure; Page 566-567; 614pp; English.
XX XX
XX CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
XX CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
XX CC The genes and their secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Pathological conditions can be diagnosed by determining the
XX CC amount of the new protein in a sample or by determining the presence of
XX CC mutations in the new genes. Specific uses are described for each of the
XX CC 50 genes, based on the tissues in which they are most highly expressed,
XX CC and include developing products for the diagnosis or treatment of
XX CC proliferative disorders, cancer, tumours, foetal and developmental
XX CC abnormalities, haematopoietic disorders, diseases of the immune system,
XX CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX CC allergies, neurological disorders (e.g., Alzheimer's disease,
XX CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX CC cardiovascular disorders, angiogenic disorders, kidney disorders,
XX CC gastrointestinal disorders, pregnancy-related disorders, endocrine
XX CC disorders, and infections. The proteins can also be used to aid wound
XX CC healing and epithelial cell proliferation, to prevent skin aging due to
XX CC sunburn, to maintain organs before transplantation, for supporting cell
XX CC culture of primary tissues, to regenerate tissues, to identify their
XX CC cognate ligands or binding partners, and in chemotaxis, and can be used
XX CC as a food additive or preservative to modify storage properties.
XX CC Antibodies specific for a protein of the invention can be used in
XX CC alleviating symptoms associated with the disorders mentioned above, and
XX CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX CC immunosorbent assay (ELISA). The present sequence represents a human
XX CC secreted protein fragment referred to in the disclosure of the invention.
XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 11 QPLPP 15

Search completed: November 25, 2003, 19:27:24
Job time : 39.2849 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 24.0698 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-34

Perfect score: 15

Sequence: 1 MHQPRQLPPTWFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*

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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-10-281-652-34	Sequence 34, Appl
2	10	66.7	10	US-10-281-652-25	Sequence 25, Appl
3	8	53.3	10	US-10-185-815-89	Sequence 89, Appl
4	6	40.0	11	US-09-809-391-689	Sequence 689, Appl
5	6	40.0	11	US-09-882-171-689	Sequence 689, Appl
6	6	40.0	15	US-10-161-791-405	Sequence 405, Appl
7	6	40.0	16	US-10-161-791-227	Sequence 227, Appl
8	5	33.3	7	US-10-286-457-359	Sequence 359, Appl
9	5	33.3	7	US-10-281-652-24	Sequence 24, Appl
10	5	33.3	9	US-10-062-109A-382	Sequence 382, Appl
11	5	33.3	9	US-10-062-109A-458	Sequence 458, Appl
12	5	33.3	9	US-10-062-109A-382	Sequence 382, Appl
13	5	33.3	9	US-10-005-480A-382	Sequence 382, Appl
14	5	33.3	9	US-10-005-480A-458	Sequence 458, Appl
15	5	33.3	9	US-10-005-480A-563	Sequence 563, Appl

16	5	33.3	10	US-09-794-346-1	Sequence 1, Appl
17	5	33.3	12	US-10-148-936-1	Sequence 93, Appl
18	5	33.3	13	US-09-938-315-93	Sequence 69, Appl
19	5	33.3	13	US-09-897-107-69	Sequence 90, Appl
20	5	33.3	13	US-10-161-791-90	Sequence 93, Appl
21	5	33.3	13	US-10-161-791-93	Sequence 38, Appl
22	5	33.3	14	US-10-079-167-38	Sequence 18, Appl
23	5	33.3	14	US-10-367-405-18	Sequence 30, Appl
24	5	33.3	15	US-10-302-896-30	Sequence 355, Appl
25	5	33.3	15	US-10-161-791-355	Sequence 373, Appl
26	5	33.3	15	US-10-161-791-373	Sequence 437, Appl
27	5	33.3	16	US-10-161-791-213	Sequence 213, Appl
28	5	33.3	16	US-10-225-567A-1351	Sequence 1351, Appl
29	5	33.3	17	US-10-029-386-31396	Sequence 31396, A
30	5	33.3	18	US-09-864-761-45132	Sequence 45132, A
31	5	33.3	18	US-10-302-896-31	Sequence 31, Appl
32	5	33.3	19	US-09-964-201A-17	Sequence 17, Appl
33	5	33.3	20	US-09-308-511-11	Sequence 11, Appl
34	5	33.3	20	US-10-161-791-147	Sequence 147, Appl
35	5	33.3	20	US-09-500-700-104	Sequence 104, Appl
36	4	26.7	6	US-10-092-219-11	Sequence 11, Appl
37	4	26.7	6	US-09-019-679-4	Sequence 4, Appl
38	4	26.7	7	US-09-879-957-45	Sequence 45, Appl
39	4	26.7	7	US-09-938-315-9	Sequence 9, Appl
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58	4	26.7	9	US-09-834-765-546	Sequence 546, Appl
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63	4	26.7	9	US-09-780-053-620	Sequence 620, Appl
64	4	26.7	9	US-09-945-917-34	Sequence 34, Appl
65	4	26.7	9	US-09-945-917-34	Sequence 29, Appl
66	4	26.7	9	US-03-745-078A-29	Sequence 26, Appl
67	4	26.7	9	US-09-932-165-3	Sequence 3, Appl
68	4	26.7	9	US-09-932-165-3	Sequence 648, Appl
69	4	26.7	9	US-09-932-165-648	Sequence 34, Appl
70	4	26.7	9	US-10-374-624-29	Sequence 29, Appl
71	4	26.7	9	US-10-161-791-11	Sequence 11, Appl
72	4	26.7	9	US-10-042-202-49	Sequence 49, Appl
73	4	26.7	9	US-10-158-596A-102	Sequence 102, Appl
74	4	26.7	9	US-10-254-446A-102	Sequence 102, Appl
75	4	26.7	10	US-08-344-824-204	Sequence 204, Appl
76	4	26.7	10	US-08-344-824-205	Sequence 205, Appl
77	4	26.7	10	US-09-834-765-468	Sequence 468, Appl
78	4	26.7	10	US-09-780-053-490	Sequence 490, Appl
79	4	26.7	10	US-09-780-053-505	Sequence 505, Appl
80	4	26.7	10	US-09-780-053-569	Sequence 569, Appl
81	4	26.7	10	US-09-780-053-588	Sequence 588, Appl
82	4	26.7	10	US-09-780-053-675	Sequence 675, Appl
83	4	26.7	10	US-09-908-322-53	Sequence 53, Appl
84	4	26.7	10	US-09-745-078A-28	Sequence 28, Appl
85	4	26.7	10	US-09-783-931-53	Sequence 53, Appl
86	4	26.7	10	US-09-572-404B-22	Sequence 22, Appl
87	4	26.7	10	US-09-572-404B-636	Sequence 636, Appl
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 99                   4   26.7   10 12 US-10-192-381-61  
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## ALIGNMENTS

RESULT 1  
 US-10-281-652-34  
 ; Sequence 34, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 34  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-34

Query Match                   100.0%; Score 15; DB 15; Length 15;  
 Best Local Similarity   100.0%; Pred. No. 6.1e-08;  
 Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;  
 QY   1 MHQPPQLPPTVMFP 15  
 DB   1 MHQPPQLPPTVMFP 15

RESULT 2  
 US-10-281-652-25  
 ; Sequence 25, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-25

Query Match                   66.7%; Score 10; DB 15; Length 10;  
 Best Local Similarity   100.0%; Pred. No. 0.0021;  
 Matches   10; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   6 QPLPPTVMFP 15  
 DB   1 QPLPPTVMFP 10

RESULT 3  
 US-10-185-815-89  
 ; Sequence 89, Application US/10185815  
 ; Publication No. US20030096354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elan Corporation, plc  
 ; APPLICANT: O'Mahony, Daniel  
 ; APPLICANT: Lambkin, Imelda  
 ; APPLICANT: Higgins, Lisa  
 ; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands  
 ; FILE REFERENCE: E1067-20093  
 ; CURRENT APPLICATION NUMBER: US/10/185,815  
 ; CURRENT FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: 60/302,591  
 ; PRIOR FILING DATE: 2001-07-02  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 89  
 ; LENGTH: 10  
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 US-10-185-815-89

Query Match                   53.3%; Score 8; DB 15; Length 10;  
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QY   1 MHQPPQPL 8  
 DB   3 MHQPPQPL 10

RESULT 4  
 US-09-809-391-689  
 ; Sequence 689, Application US/09809391  
 ; Publication No. US20030049618A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P2  
 ; CURRENT APPLICATION NUMBER: US/09/809,391  
 ; CURRENT FILING DATE: 2001-03-16  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 761  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 689  
 ; LENGTH: 11  
 ; TYPE: PRT  
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 US-09-809-391-689  
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 Best Local Similarity   100.0%; Pred. No. 12;

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Matches      6;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      2  HQPPQP 7
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Db      1  HQPPQP 6

RESULT 5
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; Publication No. US20030175858A1
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
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; PRIOR APPLICATION NUMBER: 60/056,864
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;; PRIOR FILING DATE: 1997-08-22  
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;; PRIOR APPLICATION NUMBER: 60/056,845  
;; PRIOR FILING DATE: 1997-08-22  
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;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,761  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/047,595  
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;; PRIOR APPLICATION NUMBER: 60/056,908  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/048,964  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Query Match 40.0%; Score 6; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOPPOP 7  
Db 1 HOPPOP 6

RESULT 6  
US-10-161-791-405  
; Sequence 405, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 405:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-405

Query Match 40.0%; Score 6; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQPLP 9  
Db 8 PPQPLP 13

RESULT 7  
US-10-161-791-227  
; Sequence 227, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME





QY 8 LPPTV 12  
 |||||  
 Db 1 LPPTV 5

## RESULT 11

US-10-062-109A-458  
 ; Sequence 458, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 458  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-458

Query Match 33.3%; Score 5; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12  
 |||||  
 Db 1 LPPTV 5

## RESULT 12

US-10-062-109A-563  
 ; Sequence 563, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 563  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-563

Query Match 33.3%; Score 5; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12  
 |||||  
 Db 1 LPPTV 5

## RESULT 13

US-10-005-480A-382  
 ; Sequence 382, Application US/10005480A  
 ; Publication No. US20030191073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.00  
 ; CURRENT APPLICATION NUMBER: US/10/005,480A  
 ; CURRENT FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 382  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-005-480A-382

Query Match 33.3%; Score 5; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12  
 |||||  
 Db 1 LPPTV 5

## RESULT 14

US-10-005-480A-458  
 ; Sequence 458, Application US/10005480A  
 ; Publication No. US20030191073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.00  
 ; CURRENT APPLICATION NUMBER: US/10/005,480A  
 ; CURRENT FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 458  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-005-480A-458

Query Match 33.3%; Score 5; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12  
 |||||

Db 1 LPPTV 5

RESULT 15  
US-10-005-480A-563  
; Sequence 563, Application US/10005480A  
; Publication No. US20030191073A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; TITLE OF INVENTION: Cancer  
; FILE REFERENCE: 51158-20062.00  
; CURRENT APPLICATION NUMBER: US/10/005,480A  
; CURRENT FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 563  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-005-480A-563

Query Match 33.3%; Score 5; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTV 12  
Db 1 LPPTV 5

RESULT 16  
US-09-794-346-1  
; Sequence 1, Application US/09794346  
; Patent No. US20010031857A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharma Deutschland GmbH  
; FILE REFERENCE: 02481.1728  
; CURRENT APPLICATION NUMBER: US/09/794,346  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: EP 00104114.4  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661  
; PRIOR FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Description of Artificial Sequence: Memnoniella echinata, FH 227  
; OTHER INFORMATION: 1, DSM 1319  
US-09-794-346-1

Query Match 33.3%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
Db 6 QPLPP 10

RESULT 17  
US-10-148-936-1  
; Sequence 1, Application US/10148936  
; Publication No. US20030113819A1  
; GENERAL INFORMATION:  
; APPLICANT: Horton, Jeffrey  
; APPLICANT: Smith, John  
; APPLICANT: Teear, Michelle  
; APPLICANT: Kendall, Jonathan  
; APPLICANT: Michael, Nigel  
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells  
; FILE REFERENCE: PA9963  
; CURRENT APPLICATION NUMBER: US/10/148,936  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/GB00/04593  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: GB 9928674.2  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligomer  
US-10-148-936-1

Query Match 33.3%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
Db 4 PLPPT 8

RESULT 18  
US-09-938-315-93  
; Sequence 93, Application US/09938315  
; Patent No. US20020091085A1  
; GENERAL INFORMATION:  
; APPLICANT: KAY, BRIAN K.  
; SPARKS, ANDREW B.  
; THORN, JUDITH M.  
; QUILLIAM, LAWRENCE A.  
; DER, CHANNING J.  
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUFSTADT,  
; P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,315  
; FILING DATE: 23-Aug-2001  
; CLASSIFICATION: <unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-007-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000

```
/
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 93:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 13 amino acids
/   TYPE: amino acid
/   TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-938-315-93

Query Match      33.3%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPPT 11
Db      5 PLPPT 9

RESULT 19
US-09-897-107-69
/ Sequence 69, Application US/09897107
/ Patent No. US20020137094A1
/ GENERAL INFORMATION:
/ APPLICANT: YAMAGISHI, Akihiko
/ TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING
/ TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODIN
/ FILE REFERENCE: 2103830S0
/ CURRENT APPLICATION NUMBER: US/09/897,107
/ CURRENT FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: JP2000-201920
/ PRIOR FILING DATE: 2000-07-04
/ PRIOR APPLICATION NUMBER: JP2001-164332
/ PRIOR FILING DATE: 2001-05-31
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 69
/ LENGTH: 13
/ TYPE: PPT
/ ORGANISM: Escherichia coli
US-09-897-107-69

Query Match      33.3%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QPLPP 10
Db      1 QPLPP 5

RESULT 20
US-10-161-791-90
/ Sequence 90, Application US/10161791
/ Publication No. US20030186863A1
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
```

```
/
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
US-10-161-791-90

Query Match      33.3%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPPT 11
Db      8 PLPPT 12

RESULT 21
US-10-161-791-93
/ Sequence 93, Application US/10161791
/ Publication No. US20030186863A1
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/161,791
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999
/ FILING DATE: 16-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-93

```

```

Query Match          33.3%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPPT 11
Db      5 PLPPT 9

```

```

RESULT 22
US-10-079-167-38
; Sequence 38, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-38

```

```

Query Match          33.3%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 QPLPP 10
Db      5 QPLPP 9

```

```

RESULT 23
US-10-367-405-18
; Sequence 18, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch

```

```

; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-18

```

```

Query Match          33.3%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 POPLP 9
Db      10 POPLP 14

```

```

RESULT 24
US-10-302-896-30
; Sequence 30, Application US/10302896
; Publication No. US20030180307A1
; GENERAL INFORMATION:
; APPLICANT: GUISSO-MACLOUP, NICOLE
; APPLICANT: BOURSAX-ETUDE, CAROLINE
; TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS
; TITLE OF INVENTION: OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS,
; TITLE OF INVENTION: AND BORDETELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 02356.0081
; CURRENT APPLICATION NUMBER: US/10/302,896
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/EP01/06457
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/206,969
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bordetella sp.
US-10-302-896-30

```

```

Query Match          33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 QPPQP 7
Db      2 QPPQP 6

```

```

RESULT 25
US-10-161-791-355

```

; Sequence 355, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 355:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-355  
  
Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 PLPPT 11  
Db 9 PLPPT 13  
  
RESULT 26  
US-10-161-791-373  
; Sequence 373, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 373:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-373  
  
Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 OPPQP 7  
Db 10 OPPQP 14  
  
RESULT 27  
US-10-161-791-437  
; Sequence 437, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 437:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-437

Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
|||  
Db 2 QPLPP 6

RESULT 28  
US-10-161-791-213  
Sequence 213, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 213:  
SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-213

Query Match 33.3%; Score 5; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
|||  
Db 5 PLPPT 9

RESULT 29  
US-10-225-567A-1351  
Sequence 1351, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 1351  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-1351

Query Match 33.3%; Score 5; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
|||  
Db 10 PLPPT 14

RESULT 30  
US-10-029-386-31396  
Sequence 31396, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: A60MICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 31396  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO ALL18558.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.6  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4  
US-10-029-386-31396

US-09-864-761-45132

Query Match 33.3%; Score 5; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
 |||||  
 Db 8 QPLPP 12

RESULT 31  
 US-09-864-761-45132  
 ; Sequence 45132, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Acomica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263,6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 49117  
 ; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 45132  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AC015670.4  
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.76  
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.63  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76  
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.84

US-09-864-761-45132

Query Match 33.3%; Score 5; DB 9; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLPP 9  
 |||||  
 Db 9 QPLPP 13

RESULT 32  
 US-10-302-896-31  
 ; Sequence 31, Application US/10302896  
 ; Publication No. US20030180307A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GUISSO-MACLOUF, NICOLE  
 ; APPLICANT: BOURSAX-UEDE, CAROLINE  
 ; TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS  
 ; TITLE OF INVENTION: OF PERTACTIN IN BORDETTELLA PERTUSSIS, BORDETTELLA PARAPERTUSSIS,  
 ; TITLE OF INVENTION: AND BORDETTELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN  
 ; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS  
 ; FILE REFERENCE: 02356.0081  
 ; CURRENT APPLICATION NUMBER: US/10/302,896  
 ; CURRENT FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06457  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: 60/206,969  
 ; PRIOR FILING DATE: 2000-05-25  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 31  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Bordetella sp.  
 ; US-10-302-896-31

US-10-302-896-31

Query Match 33.3%; Score 5; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
 |||||  
 Db 2 QPPQP 6

RESULT 33  
 US-09-964-201A-17  
 ; Sequence 17, Application US/09964201A  
 ; Publication No. US20030091575A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kanten, John H  
 ; APPLICANT: Tramontano, Alfonso  
 ; APPLICANT: Pilon, Aprile L  
 ; APPLICANT: Lohnas, Gerald L  
 ; APPLICANT: Roberts, Steven F  
 ; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
 ; FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09\026,276  
 ; CURRENT APPLICATION NUMBER: US/09/964,201A  
 ; CURRENT FILING DATE: 2002-05-21  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; US-09-964-201A-17

US-09-964-201A-17

Query Match 33.3%; Score 5; DB 11; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10

Db           |||||  
              6 QPLPP 10

## RESULT 34

US-09-308-511-11  
; Sequence 11, Application US/09308511  
; Patent No. US20020103145A1  
; GENERAL INFORMATION:  
; APPLICANT: BOT and BONA  
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue &  
;           Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/308,511  
; FILING DATE: 19-May-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: 29889-165/29528  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2558  
; TELEFAX: 212-765-2519  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacteria  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 350...369  
; OTHER INFORMATION: Heat Shock Protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-308-511-11

Query Match           33.3%; Score 5; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY           6 QPLPP 10

Db           |||||  
              6 QPLPP 10

## RESULT 35

US-10-161-791-147  
; Sequence 147, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 147:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-147

Query Match           33.3%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY           7 PLPPT 11

Db           |||||  
              7 PLPPT 11

## RESULT 36

US-09-500-700-104  
; Sequence 104, Application US/09500700  
; Publication No. US20030059767A1  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: BARBAS III, Carlos F.  
; APPLICANT: GOTTESFELD, Joel M.  
; APPLICANT: WRIGHT, Peter E.  
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR  
; FILE REFERENCE: SCRIPI160-4  
; CURRENT APPLICATION NUMBER: US/09/500,700  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: US 08/863,813  
; PRIOR FILING DATE: 1997-05-27  
; PRIOR APPLICATION NUMBER: US 08/676,318  
; PRIOR FILING DATE: 1996-12-30  
; PRIOR APPLICATION NUMBER: PCI/US95/00829  
; PRIOR FILING DATE: 1995-01-18  
; PRIOR APPLICATION NUMBER: US 08/312,604  
; PRIOR FILING DATE: 1994-09-28  
; PRIOR APPLICATION NUMBER: US 08/183,119



; PRIOR FILING DATE: 1994-01-18  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 104  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Modified sequence of finger 2 of zif268  
US-09-500-700-104

Query Match 26.7%; Score 4; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PQPL 8  
|||  
Db 1 PQPL 4

RESULT 37  
US-10-092-219-11  
; Sequence 11, Application US/10092219  
; Publication No. US20020115114A1  
; GENERAL INFORMATION:  
; APPLICANT: Domini, Jan  
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase  
; FILE REFERENCE: 1064HG/50947  
; CURRENT APPLICATION NUMBER: US/10/092,219  
; CURRENT FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: PCT/GB98/00244  
; PRIOR FILING DATE: 1998-01-27  
; PRIOR APPLICATION NUMBER: 03/355,160  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 9701652.1  
; PRIOR FILING DATE: 1997-01-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-219-11

Query Match 26.7%; Score 4; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
|||  
Db 2 PLPP 5

RESULT 38  
US-09-019-679-4  
; Sequence 4, Application US/09019679  
; Patent No. US20020012943A1  
; GENERAL INFORMATION:  
; APPLICANT: Fowlkes, Dana M  
; APPLICANT: Thorp, H. Holden  
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular  
; TITLE OF INVENTION: Interactions and Drug Discovery  
; FILE REFERENCE: 97082-B  
; CURRENT APPLICATION NUMBER: US/09/019,679  
; CURRENT FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: 60/036,919  
; EARLIER FILING DATE: 1997-02-06  
; EARLIER APPLICATION NUMBER: 60/059,049  
; EARLIER FILING DATE: 1997-09-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3  
; OTHER INFORMATION: Binding motif  
US-09-019-679-4

Query Match 26.7%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
|||  
Db 2 PLPP 5

RESULT 39  
US-09-879-957-45  
; Sequence 45, Application US/09879957  
; Patent No. US20020034755A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; HOFFMAN, No. US20020034755A1h  
; KAY, Brian K.  
; FOWLKES, Dana M.  
; MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,957  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,915  
; FILING DATE: 03-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELE: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-09-879-957-45

Query Match 26.7%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
|||

Db 2 PLPP 5

RESULT 40  
US-09-938-315-9  
; Sequence 9, Application US/09938315  
; Patent No. US20020091085A1  
; GENERAL INFORMATION:  
; APPLICANT: KAY, BRIAN K.  
; SPARKS, ANDREW B.  
; THORN, JUDITH M.  
; QUILLIAM, LAWRENCE A.  
; DER, CHANNING J.  
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patencin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,315  
; FILING DATE: 23-Aug-2001  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.  
; REGISTRATION NUMBER: 34,038  
; REFERENCE/DOCKET NUMBER: 4980-007-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-938-315-9

Query Match 26.7%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 41  
US-10-052-578-286  
; Sequence 286, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

; FILE REFERENCE: 11746/46003  
; CURRENT APPLICATION NUMBER: US/10/052,578  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-052-578-286

Query Match 26.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 4 PLPP 7

RESULT 42  
US-10-053-520-286  
; Sequence 286, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 286  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-520-286

Query Match 26.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 4 PLPP 7

RESULT 43  
US-10-161-791-9  
; Sequence 9, Application US/10161791  
; Publication No. US20030186663A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.

```
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 2 PLPP 5

RESULT 44
US-10-053-498B-286
; Sequence 286, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 286
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

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; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-498B-286

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10
Db 4 PLPP 7

RESULT 45
US-09-894-018-76
; Sequence 76, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-76

Query Match 26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PQPL 8
Db 5 PQPL 8

RESULT 46
US-09-745-078A-30
; Sequence 30, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
```

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-30

Query Match          26.7%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 47
US-10-052-578-82
; Sequence 82, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-052-578-82

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 48
US-10-053-520-82
; Sequence 82, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31

```

```

; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-82

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 4 PLPP 7

RESULT 49
US-10-374-624-30
; Sequence 30, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-30

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12
Db 5 PPTV 8

RESULT 50
US-10-053-498B-82
; Sequence 82, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707

```

; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 82  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-498B-82

Query Match 26.7%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
|  
|  
|  
|  
Db 4 PLPP 7

RESULT 51  
US-08-344-824-102  
; Sequence 102, Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: SIDNEY, John  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-344-824-102  
Query Match 26.7%; Score 4; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7  
|  
|  
|  
|  
Db 2 PPQP 5

RESULT 52  
US-08-344-824-322  
; Sequence 322, Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: SIDNEY, John  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 322:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-344-824-322  
Query Match 26.7%; Score 4; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPQP 7  
|  
|  
|  
|  
Db 5 PPQP 8

RESULT 53  
US-08-344-824-323  
; Sequence 323, Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: SIDNEY, John  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 323:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-344-824-323  
Query Match 26.7%; Score 4; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US/08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-323

Query Match          26.7%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPQP 7
Db      1 PPQP 4

RESULT 54
US-08-854-825-43
; Sequence 43, Application US/08854825
; Publication No. US20020115061A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; APPLICANT: Cerny, Andreas
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,825
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silvert, Donald J.
; REGISTRATION NUMBER: 37552
; REFERENCE/DOCKET NUMBER: 61230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-854-825-43

Query Match          26.7%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      1 PLPP 4

RESULT 55
US-09-834-765-48
; Sequence 48, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-48

Query Match          26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PQPL 8
Db      4 PQPL 7

RESULT 56
US-09-834-765-130
; Sequence 130, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-834-765-130

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 57
US-09-834-765-356
; Sequence 356, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-356

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 2 PQPL 5

RESULT 58
US-09-834-765-462
; Sequence 462, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-462

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 59
US-09-834-765-546
; Sequence 546, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-546

  Query Match          26.7%; Score 4; DB 9; Length 9;
  Best Local Similarity 100.0%; Pred. No. 6e+05;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8
Db 6 PQPL 9

RESULT 60
US-09-938-315-11
; Sequence 11, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
```

```
/
/
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Villacorta, Gilberto M.
/ REGISTRATION NUMBER: 34, 038
/ REFERENCE/DOCKET NUMBER: 4980-007-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-315-11

Query Match          26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      2 PLPP 5

RESULT 61
US-09-780-053-165
/ Sequence 165, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 165
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-165

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      6 PPTV 9

RESULT 62
US-09-780-053-456
/ Sequence 456, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
```

```
/
/
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 456
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-456

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      5 PPTV 8

RESULT 63
US-09-780-053-517
/ Sequence 517, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 517
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-517

Query Match          26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      5 PPTV 8

RESULT 64
US-09-780-053-620
/ Sequence 620, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Mary Faris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
```



; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83PEG4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: HIGHLY EXPRESSED IN PROSTATE CANCER  
; CURRENT APPLICATION NUMBER: 129.5USU1  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 620  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-620

Query Match 26.7%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPTV 12  
Db 5 PPTV 8

RESULT 65  
US-09-945-917-34  
; Sequence 34, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-34

Query Match 26.7%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
Db 4 PLPP 7

RESULT 66  
US-09-745-078A-29  
; Sequence 29, Application US/09745078A  
; Publication No. US20030050434A1  
; GENERAL INFORMATION:  
; APPLICANT: Garth J. S. COOPER  
; APPLICANT: Christina M. BUCHANAN  
; TITLE OF INVENTION: PEPTIDE  
; FILE REFERENCE: 441842000100  
; CURRENT APPLICATION NUMBER: US/09/745,078A  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: NZ336359  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Analog of human preptin  
US-09-745-078A-29

Query Match 26.7%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPTV 12  
Db 5 PPTV 8

RESULT 67  
US-09-972-656-26  
; Sequence 26, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-26

Query Match 26.7%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPPT 11  
Db 6 LPPT 9

RESULT 68  
US-09-932-165-3  
; Sequence 3, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-3

```

Query Match	26.7%	Score 4;	DB 12;	Length 9;
Best Local Similarity	100.0%	Pred. No. 6e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	11	TVMF	14
Db	6	TVMF	9

```

RESULT 69
US-09-932-165-648
; Sequence 648, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 648
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-648

```

Query Match	26.7%	Score 4;	DB 12;	Length 9;
Best Local Similarity	100.0%	Pred. No. 6e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	11	TVMF	14
Db	6	TVMF	9

RESULT 70  
US-09-845-917A-34  
; Sequence 34, Application US/09845917A  
; Publication No. US20030167538A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR. THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 9

```

; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-34

```

Query Match	26.7%	Score 4;	DB 12;	Length 9;
Best Local Similarity	100.0%;	Pred. No. 6e+05;		
Matches 4;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy	7 PLPP 10
pb	4 PLPP 7

```

RESULT 71
US-10-374-624-29
; Sequence 29, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: N2336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-29

```

Query Match	26.7%	Score 4;	DB 12;	Length 9;
Best Local Similarity	100.0%;	Pred. No. 68+05;		
Matches 4;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy 9 p pTV 12  
p 5 p pTV 8

RESULT 72  
US-10-161-791-11  
; Sequence 11, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pernie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-11

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLPP 10
Db      2 PLPP 5

RESULT 73
US-10-042-202-49
; Sequence 49, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PIEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESS: WENDEROOTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordpad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
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; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-042-202-49

Query Match      26.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PLPP 10
Db      3 PLPP 6

RESULT 74
US-10-158-596A-102
; Sequence 102, Application US/10158596A
; Publication No. US20030068900A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela
; APPLICANT: Flynn, Christine
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL
; FILE REFERENCE: 119927-1052
; CURRENT APPLICATION NUMBER: US/10/158,596A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-102

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPQP 7
Db      2 PPQP 5

RESULT 75
US-10-254-446A-102
; Sequence 102, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-102

Query Match      26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPQP 7
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db      2 PPQP 5
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Search completed: November 25, 2003, 20:37:09  
Job time : 24.0698 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 12,1221 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-34  
Perfect score: 15  
Sequence: 1 MHQPPQLPPTVMFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	10	66.7	10	4	US-09-641-803-25
3	6	40.0	11	4	US-09-149-476-689
4	6	40.0	15	3	US-08-602-999A-405
5	6	40.0	15	4	US-09-500-124-405
6	6	40.0	16	3	US-08-602-999A-227
7	6	40.0	16	4	US-09-500-124-227
8	5	33.3	7	2	US-08-769-745-26
9	5	33.3	7	4	US-09-641-803-24
10	5	33.3	11	1	US-08-336-343A-24
11	5	33.3	11	3	US-08-652-877-34
12	5	33.3	11	3	US-08-476-515A-34
13	5	33.3	13	3	US-08-602-999A-90
14	5	33.3	13	3	US-08-602-999A-93
15	5	33.3	13	4	US-08-278-865-93
16	5	33.3	13	4	US-09-500-124-90
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18	5	33.3	15	3	US-08-602-999A-355
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23	5	33.3	15	4	US-09-500-124-437
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25	5	33.3	16	4	US-09-500-124-213
26	5	33.3	19	4	US-09-026-276-17
27	5	33.3	20	2	US-08-363-276B-11
28	5	33.3	20	3	US-08-602-999A-147
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33	4	26.7	4	4	US-09-355-160D-11
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36	4	26.7	7	1	US-08-482-847-7
37	4	26.7	7	2	US-08-340-283-38
38	4	26.7	7	2	US-08-769-745-7
39	4	26.7	7	3	US-08-602-999A-9
40	4	26.7	7	4	US-08-278-865-9
41	4	26.7	7	4	US-08-630-915A-45
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43	4	26.7	7	5	PCT-US94-01840-11
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48	4	26.7	8	5	PCT-US91-05177-19
49	4	26.7	9	1	US-08-214-650-43
50	4	26.7	9	1	US-08-615-181-110
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55	4	26.7	9	2	US-08-146-028-446
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69	4	26.7	9	4	US-09-500-124-11
70	4	26.7	10	1	US-08-230-047-12
71	4	26.7	10	1	US-08-212-190A-8
72	4	26.7	10	2	US-08-146-028-444
73	4	26.7	10	2	US-08-769-745-5
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75	4	26.7	10	2	US-08-900-321-8
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83	4	26.7	10	4	US-08-439-157-43
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85	4	26.7	10	4	US-09-437-895-12
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87	4	26.7	10	4	US-09-437-895-65
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89	4	26.7	11	1	US-07-794-288D-24
90	4	26.7	11	1	US-08-336-343A-25
91	4	26.7	11	1	US-08-323-531-22
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93	4	26.7	11	3	US-08-602-999A-260
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96	4	26.7	11	3	US-08-652-877-32
97	4	26.7	11	3	US-08-652-877-35
98	4	26.7	11	3	US-08-652-877-36
99	4	26.7	11	3	US-08-107-794A-22
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Sequence 22, Appl  
Sequence 32, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
Sequence 22, Appl

## ALIGNMENTS

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RESULT 1
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match          100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQPPQLPPTVMFP 15
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Db 1 MHQPPQLPPTVMFP 15

RESULT 2
US-09-641-803-25
; Sequence 25, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-25

Query Match          66.7%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QLPPTVMFP 15
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Db 1 QLPPTVMFP 10

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RESULT 3
US-09-149-476-689
; Sequence 689, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
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; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,583
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; EARLIER APPLICATION NUMBER: 60/047,617
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
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; EARLIER APPLICATION NUMBER: 60/047,632
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; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580

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; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
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; EARLIER APPLICATION NUMBER: 60/043,314  
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; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/056,888  
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; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 40.0%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOPPOP 7  
|||  
Db 1 HOPPOP 6

## RESULT 4

US-08-602-999A-405  
; Sequence 405, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLESCULE TYPE: peptide  
US-08-602-999A-405  
Query Match 40.0%; Score 6; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPQPLP 9  
Db 8 PPQPLP 13  
RESULT 5  
US-09-500-124-405  
Sequence 405, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLESCULE TYPE: peptide  
US-09-500-124-405  
Query Match 40.0%; Score 6; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPQPLP 9  
Db 8 PPQPLP 13  
RESULT 6  
US-08-602-999A-227  
Sequence 227, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLESCULE TYPE: peptide  
US-09-500-124-405



TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 227:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-227

Query Match 40.0%; Score 6; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13  
Db 9 LPPTVM 14

## RESULT 7

US-09-500-124-227  
Sequence 227, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 227:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-227

Query Match 40.0%; Score 6; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPTVM 13  
Db 9 LPPTVM 14

## RESULT 8

US-08-769-745-26  
Sequence 26, Application US/08769745  
Patent No. 595259  
GENERAL INFORMATION:  
APPLICANT: Holmes, Todd C.  
APPLICANT: Levitan, Irwin B.  
APPLICANT: Brandeis University  
TITLE OF INVENTION: Mechanism for the Regulation of Ion  
TITLE OF INVENTION: Channel Activity  
FILE REFERENCE: BRU96-02  
CURRENT FILING DATE: 1996-12-19  
CURRENT APPLICATION NUMBER: US/08/769,745  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Mouse  
US-08-769-745-26

Query Match 33.3%; Score 5; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
Db 1 QPLPP 5

## RESULT 9

US-09-641-803-24  
Sequence 24, Application US/09641803  
Patent No. 6500798  
GENERAL INFORMATION:  
APPLICANT: STANTON, G. John  
APPLICANT: HUGHES, Thomas K.  
APPLICANT: BOLDOGH, Istvan  
TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
FILE REFERENCE: 265.00220101  
CURRENT APPLICATION NUMBER: US/09/641,803  
CURRENT FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: 60/149,310  
PRIOR FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn ver. 2.1  
SEQ ID NO 24  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: peptide  
US-09-641-803-24

Query Match 33.3%; Score 5; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQPP 5  
Db 3 MHQPP 7

## RESULT 10

US-08-336-343A-24

Sequence 24, Application US/08336343A  
Patent No. 5677144  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
APPLICANT: Alves, Frauke  
TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,343A  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-065  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-336-343A-24

Query Match 33.3%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
Db 7 PLPPT 11

RESULT 11  
US-08-652-877-34  
Sequence 34, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh

OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15203  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355E-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-652-877-34

Query Match 33.3%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
Db 7 PLPPT 11

RESULT 12  
US-08-476-515A-34  
Sequence 34, Application US/08476515A  
Patent No. 6239270  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Martin Savitzky  
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,  
STREET: 3C43,  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Compaq PC  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Word 7.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,515A  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA: WO PCT/SE94/00483  
APPLICATION NUMBER: 29,699  
FILING DATE: 24-MAY-1994  
PRIOR APPLICATION DATA: SE 9301764-8  
FILING DATE: 24-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355D  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-476-515A-34

Query Match 33.3%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
|||||  
Db 7 PLPPT 11

RESULT 13  
US-08-602-999A-90  
Sequence 90, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-93

Query Match 33.3%; Score 5; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
|||||

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-90

Query Match 33.3%; Score 5; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
|||||  
Db 8 PLPPT 12

RESULT 14  
US-08-602-999A-93  
Sequence 93, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-93

Query Match 33.3%; Score 5; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 PLPPT 9

## RESULT 15

US-08-278-865-93  
 ; Sequence 93, Application US/08278865  
 ; Patent No. 6303574  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAY, BRIAN K.  
 ; APPLICANT: SPARKS, ANDREW B.  
 ; APPLICANT: THORN, JUDITH M.  
 ; APPLICANT: QUILLIAM, LAWRENCE A.  
 ; APPLICANT: DER, CHANNING J.  
 ; TITLE OF INVENTION: SFC SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 106  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESS: P.C.  
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/278,865  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Villacorta, Gilberto M.  
 ; REGISTRATION NUMBER: 34,038  
 ; REFERENCE/DOCKET NUMBER: 4980-007-0  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 413-3000  
 ; TELEFAX: (703) 413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 93:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; US-08-278-865-93

Query Match 33.3%; Score 5; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11

Db 5 PLPPT 9

## RESULT 16

US-09-500-124-90  
 ; Sequence 90, Application US/09500124  
 ; Patent No. 6432920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, ANDREW B.  
 ; APPLICANT: KAY, BRIAN K.  
 ; APPLICANT: THORN, JUDITH M.  
 ; APPLICANT: QUILLIAM, LAWRENCE A.  
 ; APPLICANT: DER, CHANNING J.  
 ; APPLICANT: FOWLKES, DANA M.  
 ; APPLICANT: RIDER, JAMES E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mistrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 90:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; US-09-500-124-90

Query Match 33.3%; Score 5; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11

Db 8 PLPPT 12

## RESULT 17

US-09-500-124-93  
 ; Sequence 93, Application US/09500124  
 ; Patent No. 6432920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, ANDREW B.  
 ; APPLICANT: KAY, BRIAN K.  
 ; APPLICANT: THORN, JUDITH M.  
 ; APPLICANT: QUILLIAM, LAWRENCE A.  
 ; APPLICANT: DER, CHANNING J.  
 ; APPLICANT: FOWLKES, DANA M.  
 ; APPLICANT: RIDER, JAMES E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124

;  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-09-500-124-93

Query Match 33.3%; Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11  
Db 5 PLPPT 9

RESULT 18  
US-08-602-999A-355  
; Sequence 355, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 355:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid

;  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-355

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11  
Db 9 PLPPT 13

RESULT 19  
US-08-602-999A-373  
; Sequence 373, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 373:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-373

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPPQP 7  
Db 10 QPPQP 14

RESULT 20  
US-08-602-999A-437  
; Sequence 437, Application US/08602999A  
; Patent No. 6184205

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 437:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-437

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
DB 2 QPLPP 6

RESULT 21  
US-09-500-124-355  
Sequence 355, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.

ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 355:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-355

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
DB 9 PLPPT 13

RESULT 22  
US-09-500-124-373  
Sequence 373, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 373:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-373

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPQP 7  
DB 10 QPPQP 14

RESULT 23  
US-09-500-124-437  
Sequence 437, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
OPERATING SYSTEM: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 437:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-437

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10  
DB 2 QPLPP 6

RESULT 24  
US-08-602-999A-213  
Sequence 213, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
OPERATING SYSTEM: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 213:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-213

Query Match 33.3%; Score 5; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11  
DB 5 PLPPT 9

RESULT 25  
US-09-500-124-213  
Sequence 213, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James F.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 213:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-213

Query Match 33.3%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPPT 11  
Db 5 PLPPT 9

RESULT 26  
US-09-026-276-17  
Sequence 17, Application US/09026276  
Patent No. 6319503  
GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Tramontano, Alfonso  
APPLICANT: Pilon, Aprile L  
APPLICANT: Lohnas, Gerald L  
APPLICANT: Roberts, Steven F  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 6319503 09/026,276  
CURRENT APPLICATION NUMBER: US/09/026,276  
CURRENT FILING DATE: 1998-02-19  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 17  
LENGTH: 19  
TYPE: PPT  
ORGANISM: Mycobacterium tuberculosis  
US-09-026-276-17

Query Match 33.3%; Score 5; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPLPP 10  
Db 6 QPLPP 10

RESULT 27  
US-08-363-276B-11  
Sequence 11, Application US/08363276B  
Patent No. 5969109  
GENERAL INFORMATION:  
APPLICANT: BONA ET AL.  
TITLE OF INVENTION: CHIMERIC ANTIBODIES  
TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue &  
ADDRESSEE: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,276B  
FILING DATE: 22-DECEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 07/486,546  
FILING DATE: 28-FEBRUARY-1990 (ABANDONED)  
APPLICATION NUMBER: USSN 07/687,376  
FILING DATE: 18-APRIL-1991 (ABANDONED)  
APPLICATION NUMBER: USSN 08/327,636  
FILING DATE: 24-OCTOBER-1994 (ABANDONED)  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Richard S  
REGISTRATION NUMBER: 26,154  
REFERENCE/DOCKET NUMBER: 29889-165/29528  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2558  
TELEFAX: 212-765-2519  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Mycobacteria  
FEATURE:  
NAME/KEY:  
LOCATION: 350...369  
OTHER INFORMATION: Heat Shock Protein  
US-08-363-276B-11

Query Match 33.3%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPLPP 10  
Db 6 QPLPP 10



```

RESULT 28
US-08-602-999A-147
; Sequence 147, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-147

Query Match 33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPPT 11
Db 7 PLPPT 11

RESULT 29
US-08-755-034-11
; Sequence 11, Application US/08755034
; Patent No. 6204250
; GENERAL INFORMATION:
; APPLICANT: BOT and BONA
; TITLE OF INVENTION: IMMUNIZATION OF INFANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA

```

```

; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,034
; FILING DATE: 22-NOVEMBER-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
; US-08-755-034-11

Query Match 33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPLPP 10
Db 6 QPLPP 10

RESULT 30
US-09-500-124-147
; Sequence 147, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 147:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-09-500-124-147

Query Match 33.3%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 PLPPT 11  
Db 7 PLPPT 11

## RESULT 31

PCT-US95-16718-11  
; Sequence 11, Application PC/TUS9516718  
; GENERAL INFORMATION:  
; APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE  
; APPLICANT: CITY UNIVERSITY OF NEW YORK  
; TITLE OF INVENTION: CHIMERIC ANTIBODIES  
; TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue &  
; ADDRESSEE: Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/16718  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: 29889-165/29528  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2558  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacteria  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 350...369  
; OTHER INFORMATION: Heat Shock Protein  
; PCT-US95-16718-11

Query Match 33.3%; Score 5; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QPLPP 10  
Db 6 QPLPP 10

## RESULT 32

PCT-US96-08995-11  
; Sequence 11, Application PC/TUS9608995  
; GENERAL INFORMATION:  
; APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY  
; APPLICANT: UNIVERSITY OF NEW YORK  
; TITLE OF INVENTION: PEGYLATED MODIFIED PROTEINS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/08995  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,421  
; FILING DATE: 7-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: 29889-165/29528  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2558  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacteria  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 350...369  
; OTHER INFORMATION: Heat Shock Protein  
; PCT-US96-08995-11

Query Match 33.3%; Score 5; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      6 QPLPP 10
Db      6 QPLPP 10

RESULT 33
US-09-355-160D-11
; Sequence 11, Application US/09355160D
; Patent No. 6436671
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. 6436671el Lipid Kinase
; FILE REFERENCE: 2332-1-004
; CURRENT APPLICATION NUMBER: US/09/355,160D
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-355-160D-11

Query Match      26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      2 PLPP 5

RESULT 34
US-08-127-499A-7
; Sequence 7, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid

QY      6 QPLPP 10
Db      6 QPLPP 10

RESULT 33
US-09-355-160D-11
; Sequence 11, Application US/09355160D
; Patent No. 6436671
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. 6436671el Lipid Kinase
; FILE REFERENCE: 2332-1-004
; CURRENT APPLICATION NUMBER: US/09/355,160D
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-355-160D-11

Query Match      26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      2 PLPP 5

RESULT 34
US-08-127-499A-7
; Sequence 7, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
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; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-7

Query Match      26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPOP 7
Db      1 PPOP 4

RESULT 35
US-08-230-047-40
; Sequence 40, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-40

Query Match      26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 36
US-08-482-847-7
; Sequence 7, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
```

;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Foley & Lardner  
;; STREET: 3000 K Street, N.W., Suite 500  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20007-5109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,847  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/127,499  
;; FILING DATE: 28-SEP-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BENT, Stephen A.  
;; REGISTRATION NUMBER: 29,768  
;; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; US-08-482-847-7  
  
Query Match 26.7%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 PPQP 7  
Db 1 PPQP 4  
  
RESULT 37  
US-08-340-283-38  
; Sequence 38, Application US/08340283  
; Patent No. 5861318  
; GENERAL INFORMATION:  
; APPLICANT: Elhammer, Ake P.  
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR  
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY  
; NUMBER OF SEQUENCES: 205  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law  
; ADDRESSEE: (1920-32-1)  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: U.S.A.  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/340,283  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Wootton, Thomas A.  
;; REGISTRATION NUMBER: 35,004  
;; REFERENCE/DOCKET NUMBER: 4828  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (616) 385-7914  
;; TELEFAX: (616) 385-6897  
;; TELEX: 224401  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; US-08-340-283-38  
  
Query Match 26.7%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 PLPP 10  
Db 4 PLPP 7  
  
RESULT 38  
US-08-769-745-7  
; Sequence 7, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Rat  
; US-08-769-745-7  
  
Query Match 26.7%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 PLPP 10  
Db 2 PLPP 5  
  
RESULT 39  
US-08-602-999A-9  
; Sequence 9, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/602,999A  
;; FILING DATE: 16-FEB-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Misrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-602-999A-9

Query Match 26.7%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 40  
US-08-278-865-9  
; Sequence 9, Application US/08278865  
; Patent No. 6303574  
; GENERAL INFORMATION:  
; APPLICANT: KAY, BRIAN K.  
; APPLICANT: SPARKS, ANDREW B.  
; APPLICANT: THORN, JUDITH M.  
; APPLICANT: QUILLIAM, LAWRENCE A.  
; APPLICANT: DER, CHANNING J.  
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/278,865  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Villacorta, Gilberto M.

;; REGISTRATION NUMBER: 34,038  
;; REFERENCE/DOCKET NUMBER: 4980-007-0  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 413-3000  
;; TELEFAX: (703) 413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-278-865-9

Query Match 26.7%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 41  
US-08-630-915A-45  
; Sequence 45, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-630-915A-45

Query Match 26.7%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
 Db ||||  
 2 PLPP 5

## RESULT 42

US-09-500-124-9  
 ; Sequence 9, Application US/09500124  
 ; Patent No. 6432920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; NUMBER OF SEQUENCES: ISOLATING AND USING SAME  
 ; CORRESPONDENCE ADDRESS: 467  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; US-09-500-124-9

Query Match 26.7%; Score 4; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
 Db ||||  
 2 PLPP 5

## RESULT 43

PCT-US94-01840-11  
 ; Sequence 11, Application PC/TUS9401840  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Christopher E. Rudd  
 ; APPLICANT: Prasad Kanteti  
 ; APPLICANT: Lewis Cantley  
 ; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF

; TITLE OF INVENTION: LIPID KINASES  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 502 or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/01840  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/023,915  
 ; FILING DATE: February 26, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Janis K. Fraser  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00530/063001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: Linear  
 ; PCT-US94-01840-11

Query Match 26.7%; Score 4; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
 Db ||||  
 3 PLPP 6

## RESULT 44

US-09-641-640-8  
 ; Sequence 8, Application US/09641640  
 ; Patent No. RE37952  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SCHWEIGHOFFER, Fabien  
 ; TOCQUE, Bruno  
 ; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 ; STREET: 500 Arcola Rd. 3C43  
 ; CITY: Collegeville  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19426  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/641,640  
 ; FILING DATE: 15-Aug-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/612,857

```

; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith Ph.D., Julie K.
;   REGISTRATION NUMBER: 38,619
;   REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (610)454-3839
;   TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..8
;   OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match          26.7%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 45
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/612,857
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93-10971
; FILING DATE: 15-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:

```

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..8
;   OTHER INFORMATION: /note= "3BP1 peptide"
US-08-612-857-8

Query Match          26.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PLPP 10
Db      3 PLPP 6

RESULT 46
US-08-747-221B-43
; Sequence 43, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-747-221B-43

Query Match          26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPTV 12
Db      2 PPTV 5

```

RESULT 47  
US-09-005-051-43  
; Sequence 43, Application US/09005051  
; Patent No. 6291222  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary W.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,051  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/747,221  
; FILING DATE: No. 6291222ember 12, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: FC-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-005-051-43

Query Match 26.7%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPTV 12  
Db 2 PPTV 5

RESULT 48  
PCT-US91-05177-19  
; Sequence 19, Application PC/TUS9105177  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathy L  
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/05177  
; FILING DATE: 19910722  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/557,220  
; FILING DATE: 23-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 990008.544PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal  
PCT-US91-05177-19

Query Match 26.7%; Score 4; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQPL 8  
Db 2 PQPL 5

RESULT 49  
US-08-214-650-43  
; Sequence 43, Application US/08214650  
; Patent No. 5709995  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; APPLICANT: Certy, Andreas  
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voigt & Mayer  
; STREET: Two Prudential Plaza, Suite 4900  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/214,650  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silver, Donald J.  
; REGISTRATION NUMBER: 37552  
; REFERENCE/DOCKET NUMBER: 61230  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5600  
; TELEFAX: (312) 616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-214-650-43



Query Match 26.7%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 1 PLPP 4

## RESULT 50

US-08-615-181-110  
; Sequence 110, Application US/08615181  
; Patent No. 5756666  
; GENERAL INFORMATION:  
; APPLICANT: MASAFUMI, TAKIGUCHI  
; APPLICANT: MIWA, KIYOSHI  
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE  
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
; TITLE OF INVENTION: CURING AIDS  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/615,181  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/01756  
; FILING DATE: 19-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 261302/1993  
; FILING DATE: 19-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-110

Query Match 26.7%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPPT 11  
Db 1 LPPT 4

## RESULT 51

US-08-146-028-441

; Sequence 441, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:  
; APPLICANT:

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,028  
; INFORMATION FOR SEQ ID NO: 441:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-441

Query Match 26.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 6 PLPP 9

## RESULT 52

US-08-146-028-442  
; Sequence 442, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:  
; APPLICANT:

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,028  
; INFORMATION FOR SEQ ID NO: 442:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-442

Query Match 26.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 5 PLPP 8

## RESULT 53

US-08-146-028-443  
; Sequence 443, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 443:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-443

Query Match 26.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
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|  
Db 4 PLPP 7

RESULT 54  
US-08-146-028-445  
; Sequence 445, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 445:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-445

Query Match 26.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
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|  
Db 2 PLPP 5

RESULT 55  
US-08-146-028-446  
; Sequence 446, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,028

; INFORMATION FOR SEQ ID NO: 446:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-146-028-446

Query Match 26.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
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|  
Db 1 PLPP 4

RESULT 56  
US-08-318-856A-49  
; Sequence 49, Application US/08318856A  
; Patent No. 5972351  
; GENERAL INFORMATION:

; APPLICANT: Adrian V.S. Hill, et al.  
; TITLE OF INVENTION: PHASMODIUM FALCIPARUM MHC CLASS I-  
; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-BRYTHROCYTIC STAGE  
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1+

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,856A

; FILING DATE: October 3, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 92 08 068.8

; FILING DATE: April 3, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 92 17 704.7

; FILING DATE: August 20, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB93/00711

; FILING DATE: April 5, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee Cheng

```
;
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-856A-49

Query Match 26.7%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 5 PLPP 8

RESULT 57
US-08-723-425A-441
; Sequence 441, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-441

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 6 PLPP 9

RESULT 58
US-08-723-425A-442
; Sequence 442, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-442

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10
Db 5 PLPP 8

RESULT 59
US-08-723-425A-443
; Sequence 443, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 443:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-443

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 4 PLPP 7

RESULT 60  
US-08-723-425A-445  
Sequence 445, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 445:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-723-425A-445

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 61  
US-08-723-425A-446  
Sequence 446, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 446:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-446

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 1 PLPP 4

RESULT 62  
US-08-602-999A-11  
Sequence 11, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James F.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-11

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 63  
US-09-112-206-441  
; Sequence 441, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 441:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-441  
Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 6 PLPP 9

RESULT 64  
US-09-112-206-442  
; Sequence 442, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 442:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-442

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 5 PLPP 8

RESULT 65  
US-09-112-206-443  
; Sequence 443, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/112.206  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/146,028  
 ; FILING DATE:  
 ; INFORMATION FOR SEQ ID NO: 443:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-09-112-206-443

Query Match 26.7%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
 Db 4 PLPP 7

RESULT 66  
 US-09-112-206-445  
 ; Sequence 445, Application US/09112206  
 ; Patent No. 6210903  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
 ; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
 ; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
 ; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 ; NUMBER OF SEQUENCES: 453  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/112.206  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/146,028  
 ; FILING DATE:  
 ; INFORMATION FOR SEQ ID NO: 445:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-09-112-206-445

Query Match 26.7%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
 Db 2 PLPP 5

RESULT 67  
 US-09-112-206-446  
 ; Sequence 446, Application US/09112206  
 ; Patent No. 6210903  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
 ; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
 ; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
 ; NUMBER OF SEQUENCES: 453  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/112.206  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/146,028  
 ; FILING DATE:  
 ; INFORMATION FOR SEQ ID NO: 446:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-09-112-206-446

Query Match 26.7%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10  
 Db 1 PLPP 4

RESULT 68  
 US-08-278-865-11  
 ; Sequence 11, Application US/08278865  
 ; Patent No. 6303574  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAY, BRIAN K.  
 ; APPLICANT: SPARKS, ANDREW B.  
 ; APPLICANT: THORN, JUDITH M.  
 ; APPLICANT: QUILLIAM, LAWRENCE A.  
 ; APPLICANT: DER, CHANNING J.  
 ; TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 106  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/278,865  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Villacorta, Gilberto M.  
 ; REGISTRATION NUMBER: 34,038  
 ; REFERENCE/DOCKET NUMBER: 4980-007-0  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 413-3000  
 ; TELEFAX: (703) 413-2220  
 ; TELEX: 248855 OPAT UR  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-278-865-11

Query Match 26.7%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 69  
US-09-500-124-11  
; Sequence 11, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-11

Query Match 26.7%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 2 PLPP 5

RESULT 70  
US-08-230-047-12  
; Sequence 12, Application US/08230047  
; Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-12

Query Match 26.7%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PLPP 10  
Db 7 PLPP 10

RESULT 71  
US-08-212-190A-8  
; Sequence 8, Application US/08212190A  
; Patent No. 5652223  
; GENERAL INFORMATION:  
; APPLICANT: KOHN, Elise C.  
; APPLICANT: LIOTTA, Lance A.  
; APPLICANT: KIM, Young Sook  
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/POCKET NUMBER: 15280-204US
; REFERENCE/POCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-212-190A-8

```

```

Query Match      26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPP 10
        ||||
DB      7 PLPP 10

```

## RESULT 72

```

US-08-146-028-444
; Sequence 444, Application US/08146028
; Patent No. 5891640

```

```

; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 444:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-146-028-444

```

```

Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPP 10
        ||||
DB      3 PLPP 6

```

## RESULT 73

```

US-08-769-745-5
; Sequence 5, Application US/08769745
; Patent No. 5955259

```

```

; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Rat
; US-08-769-745-5

```

```

Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPP 10
        ||||
DB      4 PLPP 7

```

## RESULT 74

```

US-08-769-745-6
; Sequence 6, Application US/08769745
; Patent No. 5955259

```

```

; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02

```

```

; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
; US-08-769-745-6

```

```

Query Match      26.7%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PLPP 10
        ||||
DB      4 PLPP 7

```

## RESULT 75

```

US-08-900-321-8
; Sequence 8, Application US/08900321
; Patent No. 5981712

```

```

; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

```



ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/900,321  
FILING DATE: 25-JUL-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,190  
FILING DATE: 14-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-204100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-900-321-8

Query Match 26.7%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PLPP 10

Db 7 PLPP 10

Search completed: November 25, 2003, 20:30:09  
Job time : 12.1221 secs